



3rd Annual Workshop on Genomics

July 11-12, 2025 • Lisbon, Portugal

Friday, July 11

12:00-13:00 **REGISTRATION & LUNCH**

13:00-13:15 **WELCOME**
Shaji Kumar and Maria-Victoria Mateos

13:15-14:45 **CURRENT DEFINITION AND MANAGEMENT
OF PRECURSOR CONDITIONS**

Chairs: Kenneth Anderson and Philippe Moreau

13:15-13:25	Lessons from large scale population screenings	TBC
13:25-13:35	The importance of risk-stratifying for precursor conditions	TBC
13:35-13:45	IMWG risk stratification model for SMM	Maria-Victoria Mateos
13:45-13:55	How do current risk stratification perform in clinical trials and pitfalls	Shaji Kumar
13:55-14:05	Dynamic model	Irene Ghobrial
14:05-14:15	Immune microenvironment and risk of progression	Nikhil Munshi
14:15-14:45	Panel	Session faculty + Sagar Lonial

14:45-15:00 **BREAK**

15:00-16:30 **PRECURSOR DISEASE GENOMICS AND MICROENVIRONMENT**

Chairs: Nikhil Munshi and Noopur Raje

15:00-15:10	Differentiating between MM like and MGUS like SMM	Mehmet Samur
15:10-15:20	Single-cell RNA-sequencing from patients with MGUS and SMM to evaluate tumor and microenvironment cells	Romanos Sklavenitis-Pistofidis
15:20-15:30	Staging MGUS and SMM using minimally invasive methods: MMyeRisk	Bruno Paiva
15:30-15:40	Transcriptional evolution of multiple myeloma precursor disease	TBC
15:40-15:50	Transcriptional Remodeling of the Stromal and Endothelial Microenvironment in MGUS	Felipe Prosper
15:50-16:00	Genetic subtypes of smoldering multiple myeloma	Mark Bustoros
16:00-16:30	Round table discussion on next generation stratification for precursor conditions	Sundar Jagannath, Shaji Kumar, Maria-Victoria Mateos, Jesus San Miguel

16:30-16:45

BREAK

16:45-18:00

**THE FUTURE OF PRECURSOR DISEASE:
BALANCING TREATMENT AND INNOVATION**

Chairs: Sundar Jagannath and Jesus San Miguel

16:45-16:55	Are we under or over treating under current guidelines?	Suzanne Lentzsch
16:55-17:05	How do we design new clinical studies for precursor conditions based on what we have learned from current and previous enrollment criteria?	Sagar Lonial
17:05-17:15	Liquid Biopsy Approaches for Detection and Characterization of Precursor Disease Progression	TBC
17:15-17:25	Prior cancer and risk of MGUS	TBC
17:25-17:35	How do we use AI to integrate the multimodal genomic platforms	TBC
17:35-18:00	Panel	Session faculty + Jens Lohr

Saturday, July 12

8:30-10:00

DECIPHERING SINGLE CELLS IN MM

Chairs: Herve Avet-Loiseau and Marc Raab

8:30-8:40	Breakout Lesions as Hotspots of Tumor-Immune Cell Interactions	Niels Weinhold
8:40-8:50	Genotypic identification of polyclonal plasma cells in myeloma	Matteo DaVia
8:50-9:00	Single-cell profiling and multiscale integration for risk stratification and disease subtyping in myeloma	Alessandro Lagana
9:00-9:10	Single-cell spatial organization of tumor microenvironment	Leo Rasche
9:10-9:20	Integrating Multi-Omics Approaches to Decode Spatial Heterogeneity and Therapy Resistance	TBC
9:20-9:30	Long non-coding RNA landscape of tumor microenvironment	Manoj Bhasin
9:30-10:00	Panel	Session faculty + Jonathan Keats

10:00-10:15

BREAK

10:15-11:45

GENOMICS IN MM AND OTHER PLASMA CELL DYSCRASIAS

Chairs: Faith Davies and Martin Kaiser

10:15-10:25	Epigenetic Dysregulation and the Promise of Catalytic Inhibition in t(4;14)	Ben Barwick
10:25-10:35	Imaging based genomics	Jens Hillengass
10:35-10:45	Exploring Ancestral Differences in Multiple Myeloma Biology Through Whole-Genome Sequencing	Kylee Maclachlan

10:45-10:55	Utilizing Genomics to Identify Novel Immunotherapeutic Targets in Multiple Myeloma High-Risk Subgroups	Brian Walker
10:55-11:05	Genomic Determinants of Clinical Outcomes in t(11;14) MM	Linda Baughn
11:05-11:15	Genomic Determinants of Resistance to Anti-BCMA Therapies	Francesco Maura
11:15-11:45	Panel	Session faculty + Gareth Morgan and Keith Stewart
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11:45-12:30	LUNCH	
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12:30-14:00	NOVEL TARGETS IN PLASMA CELL DYSCRASIAS	
	<i>Chairs: Nizar Bahlis and Lawrence Boise</i>	
12:30-12:40	Large scale dependancy and drug screen	TBC
12:40-12:50	Genome-scale CRISPR activation and knockout studies to reveal sensitive and resistance MM cells to inhibitors	Constantine Mitsiades
12:50-13:00	Developing in-vitro models to study high risk phenotypes	Mariateresa Fulciniti
13:00-13:10	Mitochondrial vulnerabilities against multiple myeloma	Simone Cenci
13:10-13:20	Advancing bench side research using immunocompetent mouse models	Marta Chesi
13:20-13:30	The Role of TRAF3 Loss and NF-kB Signaling in Anti-BCMA Immunotherapy Failure	Paola Neri
13:30-14:00	Panel	Session faculty + Leif Bergsagel and Adam Sperling
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14:00-14:30	BREAK	
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14:30-16:00	MM AND OTHER PLASMA CELL DISORDERS	
	<i>Chair: Saad Usmani</i>	
14:30-14:40	Treatment approaches for genomically defined high risk WM	Steven Treon
14:40-14:50	From Plasma Cells to Immune Microenvironment: A Comprehensive Single-Cell Analysis of AL Amyloidosis	Raphael Szalat
14:50-15:00	Genomic determinants of primary PCL and secondary PCL	Hamza Hassan
15:00-15:10	Marrow Independence of Malignant Plasma Cells in the Context of Extramedullary Disease	TBC
15:10-15:20	Clonal hematopoiesis in myeloma	TBC
15:20-15:30	Transcriptional and chromatin accesibility of myeloma cells	Frank Zhan
15:30-16:00	Panel	Session faculty + Ajai Chari
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16:00-16:15	BREAK	
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16:15-17:45

PROTEOMICS AND METHYLATION

Chairs: Suzanne Trudel and Kwee Yong

16:15-16:25	Targeting Methylation in MM	Jonathan Licht
16:25-16:35	Extrachromosomal DNA and outcome	Parth Shah
16:35-16:45	RNA Methylation	Eugenio Morelli
16:45-16:55	Streamlining Crosslinking Mass Spectrometry Data Analysis for High-Throughput Structural Biology	Arun Wiita
16:55-17:05	Proteomics-Driven Insights into Multiple Myeloma Onset in the UK Biobank	Anjan Thakurta
17:05-17:15	The proteogenomic landscape of multiple myeloma	Jan Krönke
17:15-17:45	Panel	Session faculty + Ajay Nooka

17:45-18:00

CLOSING