Pre-Conference Workshops and Symposia

Sunday 26th June, 9:00-10:30 | **Workshop C – Auditorium III & IV**

SINGLE CELL OMICS

Organized by Colin Clarke (NIBRT) and Antonio Roldão (iBET)

The study of cellular biology has been transformed over the last decade through advances in analytical technology such as next generation sequencing (NGS) and the development of new approaches for deep proteomics. While these analyses have greatly improved our understanding of cellular processes, to date the majority of this knowledge gained has been elucidated from the study of millions of pooled cells as a "bulk" sample. A critical drawback of this approach is that heterogeneity, a universal characteristic of all biological systems, is ignored. Bulk sample analysis provides only a "population average" limiting our understanding of complex systems, obscuring heterogeneity and in some cases describing an inferred cellular state in which very few cells (or none at all) may exist.

In recent years rapid technological advances in areas such as cell isolation methods using microfluidics or microwell devices, preparation of NGS libraries from ultra-low quantities of nucleic acids and innovative labelling strategies for MS-based proteomics have enabled the characterisation of DNA, RNA and proteins at single cell resolution. In particular, transcriptome analysis of single cells (scRNA-seq), has matured rapidly and the technique is now cost effective, highly accurate and capable of determining the distribution of expression levels in tens of thousands of single cells.

This workshop will focus on the application of single cell analysis for studies seeking to gain deep understanding of cell factories and cell therapies. The first part of the workshop will introduce participants to scRNA-seq experimental methods and data analyses, including examples of the successful application of single cell transcriptomics to cell factories and cell therapies. In the second part, participants will join working groups to discuss the opportunities and challenges related to the widespread application of the technology to enhance manufacturing of recombinant proteins, gene and cell therapies.

Section 1. Thematic presentations (15 min each + 5 min Q&A at the end)

- Presentation 1: Overview of experimental methods for single cell omics.
    - *Understanding of single cell libraries preparation (incl. QC, cell isolation methods, sequencing, …), assessing cost-benefit, and examples of applications for production of biopharmaceuticals.*
- Presentation 2: Bioinformatics analysis of single cell omics data.
    - *What are the stages one needs to go through for data analysis? What are the different platforms available?*

Section 2. Working groups (40 min)

- Working groups defined according to thematic lines
    - Thematic 1: Recombinant protein
    - Thematic 2: Gene therapy
    - Thematic 3: Cell therapy
- Topics/questions to address by each working group:
    - Where´s the high value in using single cell omics?
    - Single cell *vs* bulk omics – which approach is optimal?
    - Do you see value in creating working groups for better annotation of genomes for non-model organisms or creating a cell atlas?
    - What are the major barriers and limitations in using single cell omics? Is it the cost? Is it the lack of bioinformatic platforms? Other?

Section 3. Wrap-up (10 min)

- Summary of major outcomes from working groups activity:
    - Identification of key barriers
    - Definition of pathways to move the field forward
    - Tentative timeframe to solidify the field