



# Advanced novel flow cytometry applications

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### Abstract

Over time, flow cytometry has undergone a constant transformation. Current equipment is capable to detect more than 30 parameters simultaneously from each studied particle in suspension. The analysis can be performed at high speed, reaching up to 30,000 particles per second, in some cases even more. Consequently, flow cytometry is currently one of the most powerful technology for cell analysis. Within conventional applications, the one that has evolved most in recent years is the immunophenotyping. Currently, high-dimensional flow cytometry analysis allows as to address multiparametric cell-analysis to elucidate most complex phenotypes.

On the other hand, lots of efforts are focused to develop new flow cytometry strategies and applications to address any biological question. We are currently focused on developing strategies that allow us to exceed the theoretical resolution limit of existing equipment. Recently, we have developed strategies to detect single Nano-sized particles (such as viruses, extracellular vesicles or chromosomes) of interest to the scientific community. 2- Identify and isolate EVs from different origins in the search for new biomarkers associated with pathologies of interest. 3- Finally, we have adapted the sorting of chromosomes to their subsequent sequencing without amplification to give light to some "dark zones" of known genomes that to date have low resolution in sequencing.

# Biography

Oscar is the Head of Flow Cytometry Unit at Centre for Genomic Regulation and Pompeu Fabra University in Barcelona, Spain, since 2001, where coordinates the assistance, supervision and training of one of the most advanced flow cytometry platforms in Europe. The Unit assists, supervise and advise more than 300 users from around 120 research groups in Spain and Europe. He supports the use of most flow cytometry applications, develops and implements new ones under scientific community needs. He received his Ph.D in Biochemistry from Autonomous University of Barcelona, Spain and he started to develop advanced Flow Cytometry applications during his first post-doc, at Cancer Research Institute (IRO) in Barcelona, Spain. Oscar has published relevant research papers in leading scientific journals, developing advanced Flow Cytometry methodologies and specific cell sorting. One of those was a relevant new methodological approach for hematopoietic stem cells detection and enumeration by Flow Cytometry with clinical implications. In 2012 he implemented flow karyotyping for chromosomes sorting and, currently is the unique Flow Cytometry Unit in Europe providing this special application as a service. Additionally, he recently combined this application with subsequent chromosome sequencing without amplification by using Oxford Nanopore technologies as a new methodology to assemble structurally very complex chromosomes. Currently, Oscar is focused in develop strategies to detect and isolate nanoparticles by Flow Cytometry. Recently, he has developed an approach for Single-Virus sorting for subsequent single-virus genomics. This methodology allows the possibility to explore the diversity of viruses in different ecosystems and to elucidate the global microbiome, in special, the global virosphere. He has also developed a new approach to identify and isolate Extracellular Vesicles (smaller than 100nm) by Flow Cytometry, to study cell communication and, based on Extracellular Vesicles' cargo transfer, looking for biomarkers related with diseases. His Unit is becoming a reference site for advanced Flow Cytometry applications and sorting at the single-particle level. Oscar also participates, as membership, in alliances of excellence, as Core4life, an "Excellence Alliance of Life Science Core Facilities in Europe".

# Publications

1. Kuderna LFK, Solís-Moruno M, Batlle-Masó L, Julià E, Lizano E, Anglada R, Ramírez E, Bote A, Tormo M, Marquès-Bonet T, Fornas Ò and Casals F (2020) Flow Sorting Enrichment and Nanopore Sequencing of Chromosome 1 From a Chinese Individual. Front. Genet. 10:1315.

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