

Curriculum Vitae **Consolandi Clarissa**

Macroarea of competence

OMICS Technologies: Genomics, Transcriptomics, Metagenomics, Single-cell approach applied in different field (human pathologies; studies of microorganisms)

Employer

Institute of Biomedical Technologies, National Research Council, via Cervi 93, 20090 Segrate (Mi)

Field of activity

Single-cell sequencing activity by 10X Genomics platform for the characterization of the molecular states of individual cells through their transcriptional profiles. This approach, differently from the in “bulk” RNA-seq, allows studying cell-to-cell variability in terms of transcriptomic dynamics and cellular heterogeneity.

The study of Human Gut Microbiome, by the analysis of the composition and structure by sequencing the 16S gene amplicons and by shotgun sequencing, in health (supercentenarians) and diseased states [after allogeneic HCT in pediatric patients suffering from hematological disorders (time-course study), Parkinson’s disease and Parkinsonism, Rheumatoid arthritis, Behcet’s syndrome, gastric cancer, ulcerative rettocolitis, type 2 diabetes, Down Syndrome, Barrett’s esophagus and esophageal adenocarcinoma, atherosclerosis]

Date

2007-2009

Occupation or position held

Triennial temporary position as Researcher III professional Level – at the Institute of Biomedical Technologies, National Research Council

Main activities and responsibilities

Scientific Responsible for CNR in a triennial Project, entitled "Multifunctional microfluidic platform for biomedical applications based on the analysis of nucleic acids", with regard to Programma Strategico “Nuove applicazioni dell’industria biomedicale”

Employer

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Field of activity

Development of different array platform : 1) microarrays (glass slides or other substrates such as beads); 2) micro-fluidics lab-on-chips, which involve the movement and processing of samples and reagents inside the micro-channels of a chip, and 3) fully integrated lab-on-chips, which combine micro-arrays, micro-fluidics, active electrical components, detection systems and all the technology needed to perform total automated biochemical analysis, from sample preparation to detection, in a single micro-device. Application of the microarray technology in different fields, such as the biomedical analysis, environmental diagnostics and food analysis.

Employer

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Field of activity	Application of the microarray technology in different fields, such as the biomedical analysis, environmental diagnostics and food analysis.
Date	2003 – 2005
Occupation or position held	Biennial research fellowship at the Department of Science and Biomedical Technologies – University of Milan - with a Project entitled “Manipolazione di biomolecole, fluidi, sistemi e dati per la tecnologia Bio-Chip” (0/01/2003 - 10/01/2007) Rif. 1583/2002-RBNE01TZZ8
Main activities and responsibilities	Participation in a three-years European Project, entitled "Oliv-Track" (“Traceability of origin and authenticity of olive oil by combined genomic and metabolomic approaches”), supported by the European Community (01/01/2003 - 31/12/2005) rif. QLK1-CT-2002-02386
Employer	Department of Science and Biomedical Technologies – University of Milan – Palazzo LITA
Field of activity	Application of the microarray technology in food analysis.
<u>Education and training</u>	
Date	2004
Title of qualification awarded	PhD in Molecular Medicine, Curriculum Genomics & Proteomics”, at the Department of Biomedical Technology, University of Milan, with the discussion of the thesis “DNA microarrays technology applied to polymorphisms detection in HLA complex”
Date	2000
Title of qualification awarded	Master Degree in Biology at the University of Milan, with the discussion of the thesis “DNA microarrays technology applied to mutations and polymorphisms detection”
Main subjects	Molecular Biology
Organisation providing education and training	University of Milan
Date	1993
Title of qualification awarded	Classical High school Diploma (Liceo Classico “S. Weil” di Treviglio (BG).

Job-related skills

Extremely interested in high-tech methodologies exploration and exploitation in different scientific fields (such as human pathologies and microbiology).

Wide experience in molecular biology and biotechnology, focusing the attention mainly on microarrays, ultra-massive sequencing and single-cell platforms through the exploration of methodological and technological hurdles in Genomic and Transcriptomic fields.

Great experience in the experimental process to prepare custom DNA microarrays, evaluating all the crucial steps involved in this methodology, and generating a series of analytical tools to address the manufacturing, detection and data analysis components of a microarray experiment.

Application of the microarray technology in different fields, such as the biomedical analysis.

Wide experience on three categories of Biochips: 1) microarrays (glass slides or other substrates such as beads), with biomolecules immobilized on their surface; 2) micro-fluidics lab-on-chips, which involve the movement and processing of samples and reagents inside the micro-channels of a chip, and 3) fully integrated lab-on-chips, which combine micro-arrays, micro-fluidics, active electrical components, detection systems and all the technology needed to perform total automated biochemical analysis, from sample preparation to detection, in a single micro-device.

Wide experience on ultra-massive sequencing technology (GS-FLX and Junior, by Roche and Genome Analyzer IIx and MiSeq System, by Illumina), by using different sequencing protocols regarding the entire genome sequencing, the resequencing of particular regions of interest for identification of single nucleotide variants (coupled with targeted capture systems, either in *solido* (Nimblegen) or in *liquido* (Agilent SureSelect) (Cifola I. et al., 2013), the evaluation of transcriptome amplification methods, the development of innovative technologies to study gene expression profiling of high antibiotic producing microorganisms, the metagenomics an Genomic and Transcriptomic analysis in Prokaryotes: sequencing of the whole genomes of high antibiotic producer microorganisms or of producers of new potential bioactive molecules; study of the gene expression profiles through RNA sequencing in time course experiments, in the analysis of high and low antibiotic producer microorganisms and, in the case of pathogens, in host-mimicking growing conditions.

Studies regarding the animal microbiome.

Studies regarding the human gut microbiome (GM), in particular in the study of adaptation of the GM to different diets and lifestyles; the analysis of the correlation between GM and health and human diseases and the characterization of the GM (cell-based *ex vivo* model. she is focusing her attention in the taxonomic characterization of the human gut microbiome in different populations or in people affected by different pathologies respect to healthy controls; in the understanding the potential of the microbiota-host bionetwork through the analysis of bioactive metabolites produced by bacteria in comparison of the phylogenetic diversity and taxonomic relative abundance; in the exploration of the bacterial functional pathways and in the analysis of human GM resistome, which is important for understanding the proliferation of pathogen antibiotic resistance. In the study of the relation between host/microbial communities, dual RNAseq/Metatranscriptomics analysis are performed onto intestinal and gastric biopsies from patients.

Studies regarding the oral, rectal and vaginal human microbiome.

Single-cell transcriptomics in Exploring transcriptional single-cell signatures in a mouse model of epilepsy caused by a polyalanine expansion mutation in Aristaless-related homeobox gene by 10X Genomics platform.

International Ids

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Scopus Author ID: 6603386746

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