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## BIOGRAPHICAL SKETCH

**NAME:** CLELIA PEANO

**POSITION TITLE:**

Head of Genomics Unit at Humanitas Clinical and Research Center  
Tenured Researcher at Institute of Genetic and Biomedical Research, National Research Council

**EDUCATION/TRAINING:**

2005. PhD accomplishment in Biotechnologies at the University of Parma  
2002. Licensed as Professional Biologist.  
2001. Magna cum laude Master Degree in Biology at the Department of Genetics, University of Parma

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### **Personal Statement**

During her career she focused her research activity on the application of microarray technology and deep sequencing for the analysis of Genomics, Transcriptomics and Epigenetics in Humans, Bacteria, and Plants as evidenced by her publications and involvement in scientific projects. She has great experience in the field of Next Generation Sequencing with both 454 and Illumina sequencing platforms. In the last three years she acquired great experience in Single-cell sequencing analysis with 10x Genomics Chromium Controller platform; she has also good skills in Bioinformatic Data Analysis and webtools development.

### **Experience acquired as Head of Humanitas Genomic Unit**

From January 2018 she is the Head of the Genomic Unit of Humanitas Clinical and Research Center, she coordinates a Team of highly qualified and specialized personnel composed of three senior Laboratory technicians with both technical and scientific documented experience in the application of Next Generation Sequencing technology in many different research fields

She is currently responsible of the management of all the NGS and single-cell sequencing platforms available at Humanitas Genomic Unit, of all the instruments for qualitative and quantitative evaluation of samples and of the Automation systems for samples preparation:

2 Nextseq 550 (Illumina); 1 MiSeq (Illumina); 1 iScan (Illumina)  
1 Chromium Controller (10x Genomics)  
1 Genetic Analyzer 3500DX (Applied Biosystems)  
1 TapeStation 4200 (Agilent); 1 Fluorometer Qubit 3.0 (Invitrogen); 1 MicroPlate Reader GloMax Discover (Promega)  
1 QiaCube Connect extractor system (QIAGEN); 1 TECAN Liquid Handler (Hewlett-Packard); 1 NGS Express Workstation (Perkin Elmer)

The main application fields of Next Generation Sequencing and single-cell sequencing that she set-up and implemented at Humanitas Genomic Unit are:

1) Transcriptomics: mRNA-seq, totalRNAseq, smallRNAseq

- 2) Epigenomics: CHIP-seq, Methyl-seq, ATAC-seq
- 3) Human Genetics Studies: Exome-seq, Target resequencing, Whole Genome seq
- 4) Oncogenomics: cancer genes-panel sequencing, single-cell CNV/genome/exome sequencing.
- 5) Single-cell omics: single-cell gene expression, single-cell immune profiling, single-cell ATACseq, Spatial Transcriptomics.
- 6) Microbiome and Metagenomic profiling: Microbiome-seq (16s rDNA amplicon sequencing), Metagenome-seq (shotgun whole metagenomic sequencing).

Every year she promotes and organizes a theoretical and practical course on Single-cell sequencing with 10x Genomics technology .

She strictly collaborates with the Humanitas Bioinformatic Unit for the management of the computational infrastructures dedicated to the sequencing machines, and for the continuous implementation of computational platforms for bioinformatics data analysis.

### **Research activities**

- Analysis of the immune infiltrate at single-cell level in cardiopathies and solid tumors.
- Immune profiling at single-cell level of hematological cancers and autoimmune diseases.
- Epigenomics analysis of stem cells differentiation.
- Analysis of the Human GUT microbiome/metagenome in correlation with different diets and lifestyles or with the onset of diseases.
- Study of Host Pathogens interactions to unravel structural and functional determinants behind pathogenesis and persistence.
- Genomics, Transcriptomics, and Metabolic profiling of antibiotic producers.

### **Research in the field of Single-cell omics:**

From the beginning of 2018 she is responsible of the single-cell sequencing facility (10xGenomics).

She is currently involved in many different research projects focused mainly on the application of single-cell sequencing technology to the analysis of the immune infiltrate both in heart (in mouse models of cardiopathies) (Martini et. Al. Circulation, 2019) and in solid tumors directly on patients' samples (Ponzetta et al. Cell, 2019; Donadon et. al, JEM, 2020) and for the identification of new subsets of immune cells (Galletti et. al. Nat. Immunol. 2020).

She recently received a funding as Principal Investigator of the IRGB-CNR Research Unit for a project in which she will be responsible of the single-cell level immune profiling in patients affected by Depressive Syndrome (Cariplo Foundation grant).

### **Research in the field of Epigenomics:**

From 2016 till 2019 she was the principal investigator of the ITB-CNR research Unit in the EPIGEN Flagship Project (sub-project 7.1 CUP: B92I16000070006). She was responsible of the Genome-wide definition of regulatory regions (regulome) and transcripts (transcriptome) during the transition from pluripotent to neural restricted stem cells in physiological conditions and in rare genetic neurodegenerative diseases. Her research activity, in the context of this project, and of a FIRB-FUTURO in RICERCA (RBFR100S4G\_002) grant that she obtained in 2011, was focused on the understanding how Epigenetic mechanisms regulate biological processes, determine phenotypic variation and contribute to the onset and progression of diseases. She focused her work on the Genome-Wide Definition of Promoter and Enhancer Usage during Neural Induction of Human Embryonic Stem Cells (Poletti et al. PLOS ONE 2015), on the definition of transcriptional, epigenetic and retroviral signatures for the

identification of regulatory regions involved in hematopoietic lineage commitment (Miccio and Peano, Epigenetics and Chromatin, 2013; Romano and Peano, Sci. Reports, 2016, Romano et al. iScience 2020) and on the analysis of transcriptional regulation and Chromatin dynamics in Human Epithelial Cell differentiation (Cavazza et al., Stem Cell Reports, 2016).

#### Research in the field of Human Gut Microbiome analysis:

From 2011 she is involved in many collaborations regarding the analysis of the Human GUT Microbiome in correlation with different diets and lifestyles or with the onset of diseases. She analyzed the diversity of Bifidobacteria within the infant gut microbiota (Turrone and Peano, PLOS ONE, 2011, Centanni et al., PLOS ONE, 2013). She participated to the study of the Gut microbiome and metagenome of the Hadza hunter-gatherers (Schnorr et al., Nature Comm, 2014; Rampelli et al. Curr. Biol. 2015, Turrone et al. Front. Microbiol, 2016), to understand how the lifestyle correlates with the shaping of microbiota both from an evolutionary than from an adaptational point of view. She was also involved in many studies regarding the analysis of Gut Microbiome dysbiosis in relation to the onset of different pathologies such as: Behcet's syndrome (Consolandi et al., Autoimmun Reviews, 2014; Van Der Houwen, Frontiers Immunol. 2020), Graft Versus Host Disease (GVHD) in pediatric patients (Biagi et al., BMT, 2015), in Down Syndrome (Biagi et al., PLOS ONE, 2014), in Type2 Diabetes (Candela et al., British J. of Nutrition, 2016).

She studied the correlation between a dysbiotic microbiome and the predisposition to infections such as in tuberculosis or in enteritis induced by *S. typhimurium* (Majlessi et al., Mucosal Immunology, 2017, Del Bel Belluz et al., PLoS Pathogens, 2016). She was part of the Scientific and Organizing Committee of an International Congress that was held in Milan, the 25-26 of June 2015, focusing on the analysis of HUMAN GUT MICROBIOME AND DISEASES.

She recently took part to the Gut Microbiome for Health World Summit (Rome 10-11 March 2018) presenting her recent work on the association between Gut Microbiota, Carotid vascular damage and major cardiovascular risk factors in a population based study analyzing a cohort of 700 patients (paper in preparation).

She recently received a funding as Principal Investigator of the IRGB-CNR Research Unit for a PRIN project in which she will be responsible of the GUT metagenomics analysis 450 patients affected by Difficult to Control Hypertension (MIUR PRIN grant).

#### Research in the field of host-pathogens interactions analysis:

In 2012 she obtained a grant from Italian Ministry of Research and University as principal investigator of the ITB-CNR research Unit for a PRIN project (2010P3S8BR\_002) focused on the unravelling of structural and functional determinants behind *Helicobacter pylori* pathogenesis and persistence. In this project her research activity was focused on the identification of *H. pylori* epitopes responsible for host immune-response modulation through Interactome-sequencing (Puccio et al., Helicobacter, 2014; Soluri et al. JOVE, 2018) and on the integration of ChIP-seq and RNA-seq data to systematically define the role of different transcriptional factors in *H. pylori* Transcriptional Regulatory Networks (Vannini and Pinatel, Scientific Reports, 2017; Pellicciari and Pinatel, Scientific Reports, 2017; Pepe et al., Frontiers in Microbiol. 2018). In the last two years she was also involved in the study of *Pseudomonas aeruginosa* and *Escherichia coli* virulence factors (Falchi et al., J Bacteriol 2017; Raneri et al., Scientific Reports 2018; Soluri et. al. Frontiers Microbiol. 2020)

She was involved in a CARIPLO-Vaccines project promoting innovative approaches for the development of an effective vaccine against *B. pseudomallei*, the etiological agent of melioidosis. In this project her activity was focused on the whole transcriptomic analysis of *B. thailandensis* and *B. pseudomallei* strains in conditions mimicking host infection, in order to elucidate the gene networks regulating the virulence

factors involved in the first phase of interaction (Peano et al., PLoS ONE, 2014; Gourlay and Peano, Acta D, 2015).

#### Research in the field of Genomics and Transcriptomics of antibiotic producers (industrial research)

She was involved into two MIUR projects, one LIFA (Inter-disciplinary laboratory for anti-infective drugs), and one PON project in collaboration with Sanofi-Aventis and with the University of Salento for the development and application of new technologies to implement the production process of drugs and of new bioactive molecules from natural sources. Her research activity in this projects was focused on the development of innovative technologies to study gene expression profiling of high antibiotic producing microorganisms.

She studied the Erythromycin producer *S. erythraea* by comparing genomics and transcriptomics profiles of wild type, mutants and classically improved over-producers (Peano et al., MCF 2007; Carata and Peano, MCF, 2009, Peano et al., MCF, 2012). She worked on Rifampicin high and low producers strains, to reveal, through genomic comparison, key molecular targets to rapidly convert an *A. mediterranei* wt strain into an overproducer (Peano et al., Metabol Engineer, 2014). Recently she was involved in the genomics and transcriptomic analysis of the industrial Spiramycin producer, *S. ambofaciens*, to identify new target of metabolic engineering by the implementation of its metabolic model (Fondi et al. Frontiers Microbiol. 2017; Talà et al. Metabolic Engineering 2018).

#### Research in the field of Regulatory Networks

She is strongly active in studying the role of small-non coding RNAs in bacteria and in developing molecular techniques to discover and/or predict new ncRNAs and RNA binding proteins as documented by three published works regarding: the use of Tet-Trap, as a genetic approach to the identification of bacterial RNA thermometers (Devillani et al., RNA, 2014); the use of In Vitro Transcription profiling and Chromatin Immunoprecipitation-sequencing to characterize Escherichia coli  $\sigma(S)$  core regulon (Maciag and Peano, NAR, 2011; Peano et al., Sci Reports, 2015) and the identification of novel RNA binding proteins through the selection of open reading frames (Patrucco et al., RNA Biol, 2015). She was involved also in the study of human RNA binding proteins and transposable element sequences (Fasolo et. al. FASEB J. 2019)

#### Research in the field of Bioinformatics:

She built up a solid experience in the field of bioinformatics data analysis taking part in the development of a computational procedure to identify significant overlap of differentially expressed and genomic imbalanced regions in cancer datasets, in the development of a webtool for the regional expression analysis in prokaryotes, in the development of a webtool for Interactome-sequencing data analysis and in the development of a metabolic model for the identification of new targets for improving antibiotic (Bicciato et al., NAR , 2009; Puccio et al. NAR 2017; Fondi et al. Frontiers Microbiol. 2017; Puccio et al, NAR, 2020).

## **Positions and Employment**

From January 2005 till May 2017 Researcher at the Institute of Biomedical Technologies, National Research Council (2005 till 2011 with fixed term contracts, from 2011 till 2017 Tenured Researcher position)

From June 2017 to present Tenured Researcher at the Institute of Genetic and Biomedical Research, National Research Council

From November 2018 to present Head of Genomics Unit and Sequencing Facility at Humanitas Clinical and Research Center

## **Academic experience**

In 2017 she obtained the National academic qualification as Associate Professor in Molecular Biology BANDO D.D. 1532/2016 SETTORE CONCORSUALE 05/E2

In 2018 she obtained the National academic qualification as Associate Professor in Genetics BANDO D.D. 1532/2016 SETTORE CONCORSUALE 05/11

Teaching activity for Humanitas University PhD course in Molecular and Experimental Medicine “Application of single-cell sequencing technology to Immunology” October-November 2019.

Teaching activity for the 6<sup>th</sup> and 7<sup>th</sup> GWAS Summer School “From GWAS to Function”, Pula, Cagliari, 2017-2018

Teaching activity for the University of Milan, Nutrigenomics and Nutrigenomics degree course in Applied Biology and Nutritional Sciences, from 2015 till 2018.

Teaching activity for the PhD School of Molecular and Translational Medicine of the University of Milan, from 2008 till 2013

Co-tutor of the PhD thesis of Dr. Patrizia Pinciroli, PhD School of Molecular and Translational Medicine of the University of Milan, Ciclo XXII, Academic year 2008/2009, title of the thesis: “An Advanced Transcription Profiling approach to reveal signaling and interactions of the embryonic olfactory system, a model of regeneration in the nervous system”.

Co-tutor of the PhD thesis of Dr. Luca Petiti, PhD School of Molecular and Translational Medicine of the University of Milan, Ciclo XXVII, Academic year 2013/2014, title of the thesis: “Next-Generation Sequencing Approach for Transcriptome and Epigenome Definition of human Hematopoietic Stem/Progenitors Cells and Their Early Erythroid and Myeloid Committed Progeny”

Co-tutor of the PhD thesis of Dr. Simone Puccio, PhD School of Molecular and Translational Medicine of the University of Milan, Ciclo XXIX, Academic year 2015/2016, title of the thesis: “Development of a Webtool for the interactome-sequencing data analysis and identification of H. pylori epitopes responsible for host immuno-response modulation”

Co-tutor of the Specialization Thesis in Medical Genetics of Dr. Carola Conca Dioguardi, Academic year 2018/2019, title of the thesis: “High-dimensional single-cell immunomonitoring for esophageal adenocarcinoma prevention and treatment”

### **Teaching and Training Activity in private companies**

Teaching activity for PFIZER Immunology course: “Application of single-cell sequencing technology to Immunology” November 2019.

Training course in 2009 and in 2013 at Sanofi-Aventis S.p.A, Brindisi, Italy. Training course for highly qualified researchers in the development of new processes and products in the field of anti-infective drugs .

### **Memberships**

Member of the SIMGBM (Italian Society of General Microbiology and Microbial Biotechnologies)

Member of the ICPeMed: International Consortium for Personalised Medicine (she was part of the Working Panel 5: Impact of New Tools and Research Strategies on PM in the First ICPeMed Workshop)

Faculty Member of the 6<sup>th</sup> and 7<sup>th</sup> GWAS Summer School “From GWAS to Function”, Pula, Cagliari, 2017-2018

### **Honors**

In 2011 she was awarded with a FEMS Congress Grant for attending the Congress of European Microbiologists, “Advancing Knowledge on Microbes” from 26-30 June, in Geneva.

In 2018 the poster entitled “Single-cell characterization and therapeutic manipulation of immune cells in pressure overload-induced heart failure” in which she is co-author was awarded as best work of the Humanitas Research day 2018, 28<sup>th</sup> November.

### **Research Support and Scientific Collaborations**

#### **Ongoing Research Support**

From 01/05/2020 CARIPO Project 2019-3392, Title: miR-34 regulates the autoimmune T cells response in the depressive syndrome (REMEDY). Budget: 80.000 Euro

From 31/08/2019 PRIN Project 2017HTKLR03\_003, Title: DIFFICULT TO CONTROL HYPERTENSION: an integrated approach for the identification of the metagenomics, molecular, biochemical and therapeutic determinants in large populations. Budget: 178.000 Euro

#### **Completed Research Support**

From 08/03/2012 to 08/07/2015 FIRB-Futuro in Ricerca RBF100S4G\_002. Title: Genome-wide analysis of promoter and enhancer usage in hematopoietic stem cell differentiation. Budget: 205.000 Euro

From 01/02/2013 to 01/02/2016 PRIN 2010P3S8BR\_002. Title: Unravelling structural and functional determinants behind *Helicobacter pylori* pathogenesis and persistence. Budget: 188.000 Euro.

From 01/01/2016 to 31/12/2019 EPIGEN-Flagship Project; sub-project: Epigenetic drugs for therapeutic use. Budget: 70.000 Euro

A total of 10 Fixed term Researcher Contracts (one year duration) and 1 fixed term Technician contract (one year duration) (assigned from 01/10/2012 till 12/11/2020), were payed on the previously listed projects.

### **International Collaborations**

International Collaboration Agreement signed the 08/03/2016 involving:

Institute of Biomedical Technologies – National Research Council (ITB-CNR)

Karolinska Institutet, Centre for Translational Microbiome Research (CTMR)

University of Florence – Department of Experimental and Clinical Medicine

The Research Collaboration was constituted with the aim to analyse the human and microbial gene expression in Behcet's disease using metatranscriptomic RNA sequencing.

International Collaboration Agreement signed the 27/09/2016 involving:

Institute of Biomedical Technologies – National Research Council (ITB-CNR)

Karolinska Institutet, Centre for Translational Microbiome Research (CTMR)

University of Florence – Department of Experimental and Clinical Medicine

The Research Collaboration was constituted with the aim to analyse the human and microbial gene expression in Gastric cancer and *Helicobacter pylori* infection using metatranscriptomic RNA sequencing.

International Collaboration Agreement signed the 28/02/2017 involving:

Institute of Biomedical Technologies – National Research Council (ITB-CNR)

L'UNIVERSITE PIERRE ET MARIE CURIE, of Paris.

The Research Collaboration was constituted with the aim to exchange confidential information regarding the metatranscriptomic analysis of the bacterial community residing in human biopsies deriving from patients affected by gastric cancer and Behcet syndrome

### **Contribution to Science**

**Complete List of Published Work in Scopus:**

<https://www.scopus.com/authid/detail.uri?authorId=13403279300>

### **Scientific Publications**

Total number of peer-reviewed scientific articles: 69  
Book Chapters: 3  
H-index in Scopus is 23  
Her total number of Citations in Scopus is 4003

### **Selection of the most relevant/recent papers (listed by field of research)**

#### Single-cell omics:

Donadon M, Torzilli G, Cortese N, Soldani C, Di Tommaso L, Franceschini B, Carriero R, Barbagallo M, Rigamonti A, Anselmo A, Colombo FS, Maggi G, Lleo A, Cibella J, Peano C, Kunderfranco P, Roncalli M, Mantovani A, Marchesi F. Macrophage morphology correlates with single-cell diversity and prognosis in colorectal liver metastasis. **J Exp Med.** **2020** Nov 2;217(11):e20191847. doi: 10.1084/jem.20191847. PMID: 32785653

Galletti G, De Simone G, Mazza EMC, Puccio S, Mezzanotte C, Bi TM, Davydov AN, Metsger M, Scamardella E, Alvisi G, De Paoli F, Zanon V, Scarpa A, Camisa B, Colombo FS, Anselmo A, Peano C, Polletti S, Mavilio D, Gattinoni L, Boi SK, Youngblood BA, Jones RE, Baird DM, Gostick E, Llewellyn-Lacey S, Ladell K, Price DA, Chudakov DM, Newell EW, Casucci M, Lugli E. Two subsets of stem-like CD8+ memory T cell progenitors with distinct fate commitments in humans. **Nat Immunol.** **2020** Oct 12. doi: 10.1038/s41590-020-0791-5. Epub ahead of print. PMID: 33046887.

Martini E, Kunderfranco P, Peano C, Carullo P, Cremonesi M, Schorn T, Carriero R, Termanini A, Colombo FS, Jachetti E, Panico C, Faggian G, Fumero A, Torracca L, Molgora M, Cibella J, Pagiatakis C, Brummelman J, Alvisi G, Mazza EMC, Colombo MP, Lugli E, Condorelli G, Kallikourdis M. Single-Cell Sequencing of Mouse Heart Immune Infiltrate in Pressure Overload-Driven Heart Failure Reveals Extent of Immune Activation. **Circulation.** **2019** Dec 17;140(25):2089-2107. doi: 10.1161/CIRCULATIONAHA.119.041694. Epub 2019 Oct 30. PMID: 31661975.

Ponzetta A, Carriero R, Carnevale S, Barbagallo M, Molgora M, Perucchini C, Magrini E, Gianni F, Kunderfranco P, Polentarutti N, Pasqualini F, Di Marco S, Supino D, Peano C, Cananzi F, Colombo P, Pilotti S, Alomar SY, Bonavita E, Galdiero MR, Garlanda C, Mantovani A, Jaillon S. Neutrophils Driving Unconventional T Cells Mediate Resistance against Murine Sarcomas and Selected Human Tumors. **Cell.** **2019** Jul 11;178(2):346-360.e24. doi: 10.1016/j.cell.2019.05.047. Epub 2019 Jun 27. PMID: 31257026; PMCID: PMC6630709

#### Epigenomics:

Romano O, Petiti L, Felix T, Meneghini V, Portafax M, Antoniani C, Amendola M, Bicciato S, Peano C, Miccio A. GATA Factor-Mediated Gene Regulation in Human Erythropoiesis. **iScience.** **2020** Apr 24;23(4):101018. doi: 10.1016/j.isci.2020.101018. Epub 2020 Mar 30. PMID: 32283524; PMCID: PMC7155206.

Alvisi G, Brummelman J, Puccio S, Mazza EM, Tomada EP, Losurdo A, Zanon V, Peano C, Colombo FS, Scarpa A, Alloisio M, Vasanthakumar A, Roychoudhuri R, Kallikourdis M, Pagani M, Lopci E, Novellis P, Blume J, Kallies A, Veronesi G, Lugli E. IRF4 instructs effector Treg differentiation and immune



suppression in human cancer. **J Clin Invest.** 2020 Jun 1;130(6):3137-3150. doi: 10.1172/JCI130426. PMID: 32125291; PMCID: PMC7260038.

Romano O and Peano C, et al.. Transcriptional, epigenetic and retroviral signatures identify regulatory regions involved in hematopoietic lineage commitment. **Scientific Reports.** 2016 Apr 20;6:24724. doi: 10.1038/srep24724. PubMed PMID: 27095295; PubMed Central PMCID: PMC4837375.

Cavazza A, et al. Dynamic Transcriptional and Epigenetic Regulation of Human Epidermal Keratinocyte Differentiation. **Stem Cell Reports.** 2016 Mar 23. pii: S2213-6711(16)00084-9. doi: 10.1016/j.stemcr.2016.03.003.

#### Genomics-Transcriptomics-Metagenomics:

De Simone G, Mazza EMC, Cassotta A, Davydov AN, Kuka M, Zanon V, De Paoli F, Scamardella E, Metsger M, Roberto A, Pilipow K, Colombo FS, Tenedini E, Tagliafico E, Gattinoni L, Mavilio D, Peano C, Price DA, Singh SP, Farber JM, Serra V, Cucca F, Ferrari F, Orrù V, Fiorillo E, Iannaccone M, Chudakov DM, Sallusto F, Lugli E. CXCR3 Identifies Human Naive CD8+ T Cells with Enhanced Effector Differentiation Potential. **J Immunol.** 2019 Dec 15;203(12):3179-3189. doi: 10.4049/jimmunol.1901072. Epub 2019 Nov 18. PMID: 31740485; PMCID: PMC6900484.

Bongiovanni D, Santamaria G, Klug M, Santovito D, Felicetta A, Hristov M, von Scheidt M, Aslani M, Cibella J, Weber C, Moretti A, Laugwitz KL, Peano C, Bernlochner I. Transcriptome Analysis of Reticulated Platelets Reveals a Prothrombotic Profile. **Thromb Haemost.** 2019 Nov;119(11):1795-1806. doi: 10.1055/s-0039-1695009. Epub 2019 Sep 1. PMID: 31473989.

Talà A, et al. Pirin: A novel redox-sensitive modulator of primary and secondary metabolism in *Streptomyces*. **Metabolic Engineering** 2018 Jul;48:254-268. doi: 10.1016/j.ymben.2018.06.008. Epub 2018 Jun 23. PubMed PMID: 29944936.

Rampelli S, et al. Metagenome Sequencing of the Hadza Hunter-Gatherer Gut Microbiota. **Current Biology** 2015 Jun 29;25(13):1682-93. doi: 10.1016/j.cub.2015.04.055. PubMed PMID: 25981789.

Peano C, et al. Comparative genomics revealed key molecular targets to rapidly convert a reference rifamycin-producing bacterial strain into an overproducer by genetic engineering. **Metabolic Engineering** 2014 Aug 19;26C:1-16. doi: 10.1016/j.ymben.2014.08.001.

Schnorr SL, et al. Gut microbiome of the Hadza hunter-gatherers. **Nature Communications** 2014 Apr 15;5:3654. doi: 10.1038/ncomms4654. PubMed PMID: 24736369; PubMed Central PMCID: PMC3996546.

Consolandi C, et al. Behçet's syndrome patients exhibit specific microbiome signature. **Autoimmunity Reviews** 2014 Nov 27. pii: S1568-9972(14)00281-X. doi: 10.1016/j.autrev.2014.11.009. Review. PubMed PMID: 25435420.

Tomato Genome Consortium. The tomato genome sequence provides insights into fleshy fruit evolution. **Nature**. 2012 May 30;485(7400):635-41. doi: 10.1038/nature11119. PubMed PMID: 22660326; PubMed Central PMCID: PMC3378239.

#### Host-pathogens interaction:

Soluri MF, Puccio S, Caredda G, Edomi P, D'Elios MM, Cianchi F, Troilo A, Santoro C, Sblattero D, Peano C. Defining the Helicobacter pylori Disease-Specific Antigenic Repertoire. **Front Microbiol**. 2020 Jul 9;11:1551. doi: 10.3389/fmicb.2020.01551. PMID: 32849324; PMCID: PMC7396715.

Majlessi L, et al. Colonization with Helicobacter is concomitant with modified gut microbiota and drastic failure of the immune control of Mycobacterium tuberculosis. **Mucosal Immunology** 2017 Feb 1. doi: 10.1038/mi.2016.140. PubMed PMID: 28145441.

Del Bel Belluz L, et al. The Typhoid Toxin Promotes Host Survival and the Establishment of a Persistent Asymptomatic Infection. **PLoS Pathogens**. 2016 Apr 7;12(4):e1005528. doi: 10.1371/journal.ppat.1005528.

#### Bioinformatics:

Puccio S, Grillo G, Consiglio A, Soluri MF, Sblattero D, Cotella D, Santoro C, Liuni S, Bellis G, Lugli E, Peano C, Licciulli F. InteractomeSeq: a web server for the identification and profiling of domains and epitopes from phage display and next generation sequencing data. **Nucleic Acids Res**. 2020 Jul 2;48(W1):W200-W207. doi: 10.1093/nar/gkaa363. PMID: 32402076; PMCID: PMC7319578.

Puccio S, Grillo G, Licciulli F, Severgnini M, Liuni S, Biciato S, De Bellis G, Ferrari F, Peano C. WoPPER: Web server for Position Related data analysis of gene Expression in Prokaryotes. **Nucleic Acids Res**. 2017 Jul 3;45(W1):W109-W115. doi: 10.1093/nar/gkx329. PMID: 28460063; PMCID: PMC5570229.

Biciato S, et al. A computational procedure to identify significant overlap of differentially expressed and genomic imbalanced regions in cancer datasets. **Nucleic Acids Research** 2009 Aug;37(15):5057-70. doi: 10.1093/nar/gkp520. Epub 2009 Jun 19. PubMed PMID: 19542187; PubMed Central PMCID: PMC2731905.

#### **Organization of National or International Congresses**

She was part of the Organizing and Scientific Committee of the HUMAN GUT MICROBIOME AND DISEASES

International Congress, Palazzo Delle Stelline , 25-26 June, 2015.

She attended also as a Speaker and Chairman.

#### **Participation to National or International Congresses as invited Speaker**

Oral Communication: Genome-wide mapping of regulatory elements in human somatic stem cells. EPIGEN, Progetto Bandiera EPIGENOMICA, Annual Meeting 2013. 15-17 Aprile.

Oral Communication: Genome-wide mapping of regulatory elements in human somatic stem cells. EPIGEN, Progetto Bandiera EPIGENOMICA, Annual Meeting 2014. 17-20 February

Selected Poster Oral Communication: Identification of H. pylori epitopes responsible for host immunoresponse modulation through ORF-filtered phage display libraries and Interactome-sequencing. 11th International Workshop on Pathogenesis and Host response in Helicobacter Infections. 2-5 July 2014, Helsingor Denmark.

Oral Communication: Genome-wide mapping of regulatory elements in human somatic stem cells. EPIGEN, Progetto Bandiera EPIGENOMICA, Annual Meeting 2016. 24-27 May 2016.

Invited Speaker with the talk: Definition of a Common Immune Signature in Solid Tumors. 10x Genomics User Group Meeting, INGM, Milan, 24<sup>th</sup> September 2018.

Invited Speaker with the talk: Definition of a Common Immune Signature in Solid Tumors. 10x Genomics User Group Meeting, Prague, 20<sup>th</sup> November 2020.

She attended more than 40 National and/or International Congresses by presenting more than 100 abstracts and posters, about 15 were selected for oral communications.

*In compliance with the Italian legislative Decree no. 196 dated 30/06/2003, I hereby authorize you to use and process my personal details contained in this document.*

*Yours faithfully*

*Clelia Peano*



Clelia Peano, PhD

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