CURRICULUM VITAE
Dr D'ARGENIO VALERIA

PERSONAL INFORMATION **Valeria D'Argenio, MD, PhD**

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Present position

Researcher in Clinical Biochemistry and Molecular Biology (SSD 05/E3 - BIO12), Department of Molecular Medicine and Medical Biotechnologies, University Federico II c/o CEINGE Biotecnologie Avanzate, Naples Italy
Principal Investigator (PI) c/o CEINGE Biotecnologie Avanzate, Naples, Italy
Responsible for molecular diagnostics c/o CEINGE Biotecnologie Avanzate, Naples, Italy

National Scientific Qualification to function as Associate Professor in the SSD 05/E3 - BIO12
National Scientific Qualification to function as Associate Professor in the SSD 06/N1 – MED46

WORK EXPERIENCE

January 2015 to date

Researcher
CEINGE Biotecnologie Avanzate, Naples Italy

- Whole genome *de novo* sequencing of bacteria of biotechnological interest
- Study of human microbiome composition and its correlations with specific human diseases onset and/or development
- Application of Next generation Sequencing-based approaches to the study of the molecular basis of human diseases (DNA and RNA levels and epigenetic mechanisms)
- Development and implementation of next generation sequencing-based protocol for diagnostic purposes.

April 2011 – March 2014

Researcher
Federico II University, Naples, Italy

Clinical Biochemistry, Molecular Biology and Biotechnologies

- Whole genome *de novo* sequencing of bacteria of biotechnological interest
- Study of human microbiome composition and its correlation with disease onset and/or development
- Application of Next generation Sequencing-based approaches to the study of the molecular basis of human diseases (DNA and RNA levels and epigenetic mechanisms)
- Development and implementation of next generation sequencing-based protocol for diagnostic purposes.

From April 2011 – to date
Principal Investigator (PI) at CEINGE Biotecnologie Avanzate, Naples, Italy

From April 2011 – to September 2018
Next Generation Sequencing Facility Responsible

CEINGE Biotecnologie Avanzate, Naples, Italy

Clinical Biochemistry, Molecular Biology and Biotechnologies

From July 2006 to January 2011
Post-MD Medical Specialization in Clinical Biochemistry and Molecular Biology

Federico II University, Naples, Italy

EDUCATION AND TRAINING

From February 2011 to January 2015
Ph.D. in Human Genetics

European School of Molecular medicine (SEMM), University Federico II and CEINGE Biotecnologie Avanzate, Naples, Italy II. Ph.D. Project: Molecular alterations in human genetic diseases through Next Generation Sequencing Technologies.

Next Generation Sequencing technologies: *de novo* bacteria sequencing, amplicon sequencing, target capture resequencing, miRNAs profiling, RNA-Seq.

From July 2006 to January 2011
Post-MD Medical Specialization

Postgraduated in Clinical Biochemistry and Molecular Biology, Federico II University, Naples, Italy. Thesis: Molecular basis of inherited cardiomyopathies through next generation sequencing technologies.

Next Generation Sequencing technologies: *de novo* bacteria sequencing, amplicon sequencing, target capture resequencing.

From October 1999 to July 2005
Master Degree in Medicine

School of Medicine, Federico II University, Naples, Italy. Thesis: Gene interactions in the development of inherited genetic diseases: the hemophilia case.

Study of a panel of gene candidate as hemophilia modifiers genes.

Molecular biology techniques: DNA/RNA extraction and their qualitative, quantitative evaluation, PCR, amplicon purification, reverse dot blot.

RESEARCH ACTIVITIES

From 2011 to date, Dr. D'Argenio is Principal Investigator (PI) of CEINGE Biotecnologie Avanzate. As PI, Dr. D'Argenio is responsible for and coordinates the research activities of a research group with different professional profiles (undergraduate students, laboratory technicians, PhD students, post-graduate students, post-docs) and characterized by several multidisciplinary collaborations at national and international level, as highlighted also by the scientific production. The research activity of Dr. D'Argenio is in the field of translational research and medical biotechnologies, and is focused on technological innovations in laboratory medicine and their application to the study of the molecular basis of human inherited and acquired diseases, also for diagnostic purposes and in the field of personalized medicine. In this context, the activity of Dr. D'Argenio is aimed, also, at the technological transfer of traditional procedures to advanced "omics" techniques, such as next generation sequencing-based approaches.
Specific research areas:

From 2015 to date	Participation in the activities of a research group devoted to the development and validation of analytical methodologies and biotechnological applications for pre-implantation and pre-natal molecular diagnostics. Dr. D'Argenio, in particular, has dealt with the application and use of whole genome amplification (WGA) protocols on single cell and has contributed to the development and validation of a diagnostic protocol for the optimization of pre-implantation and pre-natal diagnostic workflow.
From 2013 to date	Participation in the activities of a research group aimed at identifying germline mutations associated with an increased risk of breast and ovarian cancer, and their correlation with cancer pathogenesis and therapy. Dr. D'Argenio, in particular, was responsible for the validation of a next generation sequencing protocol for the analysis of the *BRCA1* and *BRCA2* genes, the transfer of the results obtained to routine diagnostics (currently, she is responsible for the diagnostic activity), the study of new identified mutations, as well as the design and validation of a panel of genes associated with a greater risk of hereditary tumors.
From 2012 to date	Participation in the activities of a research group aimed at studying the human microbiome and its possible role in the development of celiac disease. After providing an original contribution to the pathogenesis of celiac disease, through the identification of a bacterial strain in the duodenal mucosa of celiac patients, Dr. D'Argenio is working on the definition of the functional role of this bacterium, as well as of the its possible use as a biomarker.
From 2011 to date	Participation in the activities of research groups aimed at identifying, through the study of the human microbiome in different body areas and starting from different biological samples, qualitative and/or quantitative alterations of the microbial component specifically related to a disease of interest and which can also be used as novel target for the development of new diagnostic and/or therapeutic approaches.

From 2009 to date	Participation in the activities of a research group for the study of the molecular basis of hereditary cardiopathies in order to increase the analytic and diagnostic sensitivity of this type of pathologies featured by high genetic heterogeneity, as well as to improve their differential diagnosis. In particular, Dr. D'Argenio was responsible for the design of a custom panel of over 200 genes for the mutational analysis of subjects suffering from hereditary cardiopathies, as well as their subsequent analysis using next generation sequencing and the interpretation of sequence data. Subsequently, Dr. D'Argenio is dealing with the transfer of the results obtained from the research activity to the diagnostic routine.
From 2006 to date	Participation in the activities of different research groups in order to characterize specific parameters and indicators that are the basis of human diseases, both inherited and acquired, in the perspective of personalized medicine and advanced molecular diagnostics, through the application and validation of next generation sequencing-based approaches. Dr. D'Argenio has been involved in the development and validation of innovative analytical technologies, of biotechnological-applicative aspects (mechanisms of gene expression regulation and possible alterations during illness), and of translational aspects (correlations between genotypic features and the clinical expression of a disease). The results of these multidisciplinary collaborations, shared also with several collaborators (many of clinical area) of other institutions at national level have led to the publication of numerous scientific papers.
From 2009 to 2014	Participation in the activities of a research group aimed at the study and characterization of a bacterium of biotechnological interest for environmental bioremediation, trough the *de novo* sequencing of the entire genome of the bacterium itself, by using next generation sequencing technologies.
From 2006 to 2013	Participation in the activities of a research group aimed at the study and characterization of a microorganism of biotechnological interest (antibiotic producer) and with a large genome (12 Mb). Dr D'Argenio, in particular, was responsible for the *de novo* sequencing of the whole genome and for the RNA-Seq analysis of the bacterium of interest through next generation sequencing technologies.
From 2003 to 2006	Participation in the activities of a research group active in the field of the study of the molecular basis of haemophilia A and B, with particular reference to the identification of phenotype-modifying genes (evaluation of the possible role of polymorphisms associated with thrombophilia in a population of haemophilic patients).

CLINICAL ACTIVITIES

From April 2011 to date — **Responsible for molecular diagnostic activities c/o CEINGE Advanced Biotechnologies.** Dr D'Argenio is Responsible for BRCA1/2 molecular analysis and for the analysis of large panels of genes related to inherited cardiopathies and sudden cardiac death through NGS. In particular, she is Responsible for the development and validation of NGS-based protocols for molecular diagnostics, including multicenter evaluation studies, design and validation of custom multi-genes panels, and exomes analysis.

TEACHING ACTIVITIES

From 2018 — Visiting Professor of Medical Biochemistry at the International University of Gorazde, Department of European Study Jean Monnet (Locarno). Course in English.

From 2015 — Professor of the Master's Degree in Medical Biotechnology at the Federico II University of Naples. Holder of the "Advanced Diagnostics" course, curriculum in English.

July 2014 — Member of the Commissions for the selection and evaluation of the candidates to a II level Master (as part of the MICROMAP project, application code PON01_02589).

July 2013 — Professor of the course "Sequencing techniques with particular reference to the new methods of Next-Generation Sequencing", as part of the training course for "Managers and Expert Researchers of in the biomedical field", Project P.R.I.S.M, PON 2007-2013.

January 2013 — Professor of the MA-09 Molecular Biotechnology-Genomics module, as part of the "PON BIAM EPI- Project - Expert in innovative processes of biomolecular synthesis applied to epigenetic techniques", National Operative Program Research and Competitiveness 2007-2013- PON 01_02512.

From 2012 — Tutor of students of the Master's Degree in Medical Biotechnology, post-graduated student in Clinical Biochemistry and PhD students in related fields.

2012/13 and 2013/14 — Professor of the course "Employment of Biological Markers in Nutritional Evaluation" within the Master's Degree Program in Human Nutrition, LM / 61, Faculty of Medicine and Surgery and Faculty of Biotechnological Sciences, University of Naples Federico II.

From 2011 — Professor of the Postgraduated School in Clinical Biochemistry and Molecular Biology of Federico II University, Naples.

ADDITIONAL INFORMATION

Publications on International Peer-reviewed Journals

1 Labruna G, Nanayakkara M, Pagliuca C, Nunziato M, Iaffaldano L, **D'Argenio V**, Colicchio R, Budelli AL, Nigro R, Salvatore P, Barone MV, Sacchetti L. Celiac disease-associated Neisseria flavescens decreases mitochondrial respiration in CaCo-2 epithelial cells. Impact of Lactobacillus paracasei-CBA L74 on bacterial-induced cellular imbalance. Cell Microbiol. 2019:e13035.

2 Paparo L, Nocerino R, Bruno C, Di Scala C, Cosenza L, Bedogni G, Di Costanzo M, Mennini M, **D'Argenio V**, Salvatore F, Berni Canani R. Randomized controlled trial on the influence of dietary intervention on epigenetic mechanisms in children with cow's milk allergy: the EPICMA study. Sci Rep 2019;9(1):2828.

3 Cariati F, Borrillo F, Shankar V, Nunziato M, **D'Argenio V***, Tomaiuolo R*. Dissecting Intra-Tumor Heterogeneity by the Analysis of Copy Number Variations in Single Cells: The Neuroblastoma Case Study. Int J Mol Sci. 2019;20(4).
***Co-corresponding authors**

4 Nunziato M, Esposito MV, Starnone F, Diroma MA, Calabrese A, Del Monaco V, Buono P, Frasci G, Botti G, D'Aiuto M, Salvatore F, **D'Argenio V**. A multi-gene panel beyond BRCA1/BRCA2 to identify new breast cancer-predisposing mutations by a picodroplet PCR followed by a next-generation sequencing strategy: a pilot study. Analytica Chimica Acta 2019; 1046: 154-162.

5 **D'Argenio V**. The Prenatal Microbiome: A New Player for Human Health. High Throughput 2018; 11: 7(4).

6 **D'Argenio V**, Casaburi G, Precone V, Moccia LG, Postiglione I, Bocchino M, Sanduzzi A. A common microbial signature is present in the lower airways of interstitial lung diseases including sarcoidosis. Sarcoidosis vasculitis and diffuse lung disease 2018; 35:354-62.

7 Iaffaldano L, Granata I, Pagliuca C, Esposito MV, Casaburi G, Salerno G, Colicchio R, Piccirillo M, Ciacci C, Del Vecchio Blanco G, Guarracino MR, Salvatore P, Salvatore F, **D'Argenio V***, Sacchetti L*. Oropharyngeal microbiome evaluation highlights Neisseria abundance in active celiac patients. Sci Rep. 2018;8(1):11047.
***Co-corresponding authors**

8 Ferrucci V, de Antonellis P, Pennino FP, Asadzadeh F, Virgilio A, Montanaro D, Galeone A, Boffa I, Pisano I, Scognamiglio I, Navas L, Diana D, Pedone E, Gargiulo S, Gramanzini M, Brunetti A, Danielson L, Carotenuto M, Liguori L, Verrico A, Quaglietta L, Errico ME, Del Monaco V, **D'Argenio V**, Tirone F, Mastronuzzi A, Donofrio V, Giangaspero F, Picard D, Remke M, Garzia L, Daniels C, Delattre O, Swartling FJ, Weiss WA, Salvatore F, Fattorusso R, Chesler L, Taylor MD, Cinalli G, Zollo M. Metastatic group 3 medulloblastoma is driven by PRUNE1 targeting NME1-TGF-β-OTX2-SNAIL via PTEN inhibition. Brain. 2018;141:1300-1319.

9 Bergougnoux A*, **D'Argenio V***, Sollfrank S*, Verneau F, Telese A, Postiglione I, Lackner KJ, Claustres M, Castaldo G, Rossman H, Salvatore F, Raynal C. Multicenter validation study for the certification of a CFTR gene scanning method using next generation sequencing technology. Clin Chem Lab Med. 2018;56:1046-1053.
***Co-first authors**

10 **D'Argenio V,** Esposito MV, Nunziato M, De Simone A, Buono P, Salvatore F, Frisso G. Molecular diagnosis of Brugada syndrome via next-generation sequencing of a multigene panel in a young athlete. Med Sport 2018;71:27-3.

11 **D'Argenio V.** The High-Throughput Analyses Era: Are We Ready for the Data Struggle? High Throughput. 2018 Mar 2;7(1)

12 **D'Argenio V.** Human Microbiome Acquisition and Bioinformatic Challenges in Metagenomic Studies. Int. J. Mol. Sci. 2018, 19, 383.

13 Iaffaldano L, Nardelli C, D'Alessio F, **D'Argenio V**, Nunziato M, Mauriello L, Procaccini C, Maruotti GM, Martinelli P, Matarese G, Pastore L, Del Vecchio L, Labruna G, Sacchetti L. Altered Bioenergetics Profile in Umbilical Cord and Amniotic Mesenchymal Stem Cells from Newborns of Obese Women. Stem Cells Dev. 2018; 27:199-206.

14 **D'Argenio V**, Del Monaco V, Paparo L, De Palma FDE, Nocerino R, D'Alessio F, Visconte F, Discepolo V, Del Vecchio L, Salvatore F, Berni Canani R. Altered miR-193a-5p expression in children with cow's milk allergy. Allergy 2018; 73: 379-386.

15 Nunziato M, Starnone F, Lombardo B, Pensabene M, Condello C, Verdesca F, Carlomagno C, De Placido S, Pastore L, Salvatore F, **D'Argenio V**. Fast Detection of a BRCA2 Large Genomic Duplication by Next Generation Sequencing as a Single Procedure: A Case Report. Int J Mol Sci. 2017;18(11).

16 Cariati F, Savarese M, **D'Argenio V**, Salvatore F, Tomaiuolo R. The SEeMORE Strategy: Single-tube Electrophoresis analysis-based genotyping to detect MOnogenic diseases Rapidly and Effectively from conception until birth. Clin Chem Lab Med. 2017; 56:40-50.

17 De Palma GD, Colavita I, Zambrano G, Giglio MC, Maione F, Luglio G, Sarnelli G, Rispo A, Schettino P, D'Armiento FP, De Palma FDE, **D'Argenio V**, Salvatore F. Detection of Colonic Dysplasia in Patients With Ulcerative Colitis Using a Targeted Fluorescent Peptide and Confocal Laser Endomicroscopy: A pilot Study. PlosOne. 2017;12:e0180509.

18 **D'Argenio V**, Torino M, Precone V, Casaburi G, Esposito MV, Iaffaldano L, Malapelle U, Troncone G, Coto I, Cavalcanti P, De Rosa G, Salvatore F, Sacchetti L. The Cause of Death of a Child in the 18th Century Solved by Bone Microbiome Typing Using Laser Microdissection and Next Generation Sequencing. Int J Mol Sci. 2017;18.

19 Nardelli C, Granata I, Iaffaldano L, **D'Argenio V**, Del Monaco V, Maruotti GM, Omodei D, Del Vecchio L, Martinelli P, Salvatore F, Guarracino MR, Sacchetti L, Pastore L. MiR-138/miR-222 over-expression characterizes the miRNome of amniotic mesenchymal stem cells in obesity. Stem Cells Dev. 2017;26:4-14.

20 Nardelli C, Granata I, Iaffaldano L, **D'Argenio V**, Del Monaco V, Maruotti GM, Del Vecchio L, Martinelli P, Salvatore F, Guarracino MR, Sacchetti L, Pastore L. Sex-comparative analysis of the miRNome of human amniotic stem cells during obesity. Stem Cells Dev 2017;26:1-3.

21 **D'Argenio V**, Petrillo M, Pasanisi D, Pagliarulo C, Colicchio R, Talà A, de Biase MS, Zanfardino M, Scolamiero E, Pagliuca C, Gaballo A, Cicatiello AG, Cantiello P, Postiglione I, Naso B, Boccia A, Durante M, Cozzuto L, Salvatore P, Paolella G, Salvatore F, Alifano P. The complete 12 Mb genome and transcriptome of Nonomuraea gerenzanensis with new insights into its duplicated "magic" RNA polymerase. Sci Rep. 2016;6:18.

22 Esposito MV, Nunziato M, Starnone F, Telese A, Calabrese A, D'Aiuto G, Pucci P, D'Aiuto M, Baralle F, **D'Argenio V***, Salvatore F*. A Novel Pathogenic BRCA1 Splicing Variant Produces Partial Intron Retention in the Mature Messenger RNA. Int J Mol Sci. 2016;17.
***Co-corresponding authors**

23 **Valeria D'Argenio**, Giorgio Casaburi, Vincenza Precone, Chiara Pagliuca, Roberta Colicchio, Daniela Sarnataro, Valentina Discepolo, Sangman M. Kim, Ilaria Russo, Giovanna Del Vecchio Blanco, David S. Horner, Matteo Chiara, Graziano Pesole, Paola Salvatore, Giovanni Monteleone, Carolina Ciacci, Gregory J. Caporaso, Bana Jabrì, Francesco Salvatore, Lucia Sacchetti. No change in the mucosal gut mycobioma is associated with celiac disease-specific microbioma alteration in adult patients. Am J Gastroenterol 2016;111:1659-1661.

24 Paparo L, Nocerino R, Cosenza L, Aitoro R, **D'Argenio V**, Del Monaco V, Di Scala C, Amoroso A, Di Costanzo M, Salvatore F, Berni Canani R. Epigenetic features of FoxP3 in children with cow's milk allergy. Clin Epigenetics 2016;8:86.

25 **Valeria D'Argenio**, Giorgio Casaburi, Vincenza Precone, Chiara Pagliuca, Roberta Colicchio, Daniela Sarnataro, Valentina Discepolo, Sangman M. Kim, Ilaria Russo, Giovanna Del Vecchio Blanco, David S. Horner, Matteo Chiara, Graziano Pesole, Paola Salvatore, Giovanni Monteleone, Carolina Ciacci, Gregory J. Caporaso, Bana Jabrì, Francesco Salvatore, Lucia Sacchetti. Metagenomics Reveals Dysbiosis and a Potentially Pathogenic N. flavescens Strain in duodenum of Adult Celiac Patients. Am J Gastroenterol 2016;111:879-90.

26 V Precone, V Del Monaco, MV Esposito, F De Palma, A Ruocco, F Salvatore, **V D'Argenio**. Cracking the code of human diseases using next-generation sequencing: applications, challenges and perspectives. Biomed Res Int 2015;2015:161648.

27 **D'Argenio V**, Esposito MV, Telese A, Precone V, Starnone F, Nunziato M, Cantiello P, Iorio M, Evangelista E, D'Aiuto M, Calabrese A, Frisso G, D'Aiuto G, Salvatore F. The molecular analysis of BRCA1 and BRCA2: Next-generation sequencing supersedes conventional approaches. Clin Chim Acta 2015;446:221-5.

28 Berni Canani R, Paparo L, Nocerino R, Cosenza L, Pezzella V, Di Costanzo M, Capasso M, Del Monaco V, **D'Argenio V**, Greco L, Salvatore F. Differences in DNA methylation profile of Th1 and Th2 cytokine genes are associated with tolerance acquisition in children with IgE-mediated cow's milk allergy. Clin Epigenetics 2015;7:38.

29 Conti V, Russomanno G, Corbi G, Toro G, Simeon V, Filippelli W, Ferrara N, Grimaldi M, **D'Argenio V**, Maffulli N, Filippelli A. A polymorphism at the translation start site of the vitamin d receptor gene is associated with the response to anti-osteoporotic therapy in postmenopausal women from southern Italy. Int J Mol Sci 2015;16:5452-5466.

30 Errico F*, **D'Argenio V***, Sforazzini F, Iasevoli F, Squillace M, Guerri G, Napolitano F, Angrisano T, Di Maio A, Keller S, Vitucci D, Galbusera A, Chiariotti L, Bertolino A, de Bartolomeis A, Salvatore F, Gozzi A, Usiello A. A role for D-aspartate oxidase in schizophrenia and in schizophrenia-related symptoms induced by phencyclidine in mice. Transl Psychiatry 2015;5:e512.

***Co-first authors**

31 **D'Argenio V**, Salvatore F. The role of the gut microbiome in the healthy adult status. Clin Chim Acta 2015;451(Pt A):97-102.

32 **Valeria D'Argenio**, Eugenio Notomista, Mauro Petrillo, Piergiuseppe Cantiello, Valeria Cafaro, Viviana Izzo, Barbara Naso, Luca Cozzuto, Lorenzo Durante, Luca Troncone, Giovanni Paolella, Francesco Salvatore, Alberto Di Donato. Complete sequencing of Novosphingobium sp. PP1Y reveals a biotechnologically meaningful metabolic pattern. BMC Genomics 2014. 15:384.

33 Aceto S, Sica M, De Paolo S, **D'Argenio V**, Cantiello P, Salvatore F, Gaudio L. The Analysis of the Inflorescence miRNome of the Orchid Orchis italica Reveals a DEF-Like MADS-Box Gene as a New miRNA Target. PLoS One 2014; 9:e97839.

34 **Valeria D'Argenio**, Giorgio Casaburi, Vincenza Precone, Francesco Salvatore. Comparative Metagenomic Analysis of Human Gut Microbiome Composition Using Two Different Bioinformatic Pipelines. Biomed Res Int 2014; 2014:325340.

35 **Valeria D'Argenio**, Maria Valeria Esposito, Jean Ann Gilder, Giulia Frisso, Francesco Salvatore. Should a BRCA2 Stop Codon Human Variant, Usually Considered a Polymorphism, Be Classified as a Predisposing Mutation? Cancer 2014;120:1594-5.

36 **V D'Argenio**, G Frisso, V Precone, A Boccia, A Fienga, G Pacileo, G Limongelli, G Paolella, Raffaele Calabrò, F Salvatore. DNA sequence capture and next generation sequencing for the molecular diagnosis of genetic cardiomyopathies. J Mol Diagn 2014; 16:32-44.

37 **V D'Argenio**, V Precone, G Casaburi, E Miele, M Martinelli, A Staiano, F Salvatore, L Sacchetti. An Altered Gut Microbiome Profile in a Child Affected by Crohn's Disease Normalized After Nutritional Therapy. American Journal of Gastroenterology 2013;108(5):851-2. doi: 10.1038/ajg.2013.46.

38 **D'Argenio V**, Petrillo M, Cantiello P, Naso B, Cozzuto L, Notomista E, Paolella G, Di Donato A, Salvatore F. De novo sequencing and assembly of the whole genome of Novosphingobium sp.PP1Y. J Bacteriol 2011; 193: 4296.

39 Sanna V, Zarrilli F, Nardiello P, **D'Argenio V**, Rocino A, Coppola A, Di Minno G, Castaldo G. Mutational spectrum of F8 gene and prothrombotic gene variants in haemophilia A patients from Southern Italy. Haemophilia 2008; 14: 796-803.

40 Castaldo G, **D'Argenio V**, Nardiello P, Zarrilli F, Sanna V, Rocino A, Coppola A, Di Minno G, Salvatore F. Haemophilia A: molecular insights. Clin Chem Lab Med 2007; 45: 450–61.

Publications on National Peer-reviewed Journals

1 **V. D'Argenio**, F. Borrillo, F. Cariati, F. Di Maggio, Tomaiuolo R. Glossario di biologia molecolare e biologia molecolare clinica. Parte I: termini generali. Biochimica Clinica 2019; 43(1) 090-105.

2 C. Mazzaccara, **V. D'Argenio**, M. Nunziato, M. V. Esposito, F. Salvatore , G. Frisso. La biologia molecolare clinica nella valutazione e prevenzione del rischio cardiologico nell'attività sportiva e nell'attività motoria intensa. Biochimica Clinica 2019; 43(1) 024-043.

3 F. Starnone, M.V. Esposito, M. Nunziato, F. Di Maggio, **V. D'Argenio**. Role of next generation sequencing technologies for the molecular diagnosis of hereditary breast cancers. Biochimica Clinica 2018; 42: 285-289.

4 F.D.E. De Palma, L. Paparo, R. Nocerino, R. Berni Canani, F. Salvatore, V. **D'Argenio.** Epigenetics and cow's milk allergy: implication for pathogenesis. Biochimica Clinica 2018; 42: 103-111.

5 **V. D'Argenio**, M. Nunziato, N. D'Uonno, F. Borrillo, R. Vallone, A. Conforti, P. De Rosa, R. Tomaiuolo, F. Cariati. Indications and limitations for preimplantation genetic diagnosis. Biochimica Clinica 2017;41:314-321.

6 **D'Argenio V**, Tomaiuolo R, Cariati F. Whole genome amplification on single cell. Biochimica Clinica 2016;40:293-301.

7 **V D'Argenio**, F Salvatore. Psoriasis genetics: State of the art. G Ital Dermatol Venereol 2014;149 (suppl 5):39-41.

8 Fabrizio Stoppoloni, Edoardo Tartaglia, Giancarlo Balbi, Pasquale Pirillo, Sergio Schettini, Alfonso Galderisi, Rocco Paradiso, Mario Passaro, Pasquale Vadalà, Nadia Tinto, **Valeria D'Argenio**, Marina Capuano, Teresa Sena, Pietro Iacobelli, Francesco Prisco, Pasquale Mastrantonio, Lucia Sacchetti, Dario Iafusco. Il Diabete in Gravidanza: dall'Iperglicemia alla Patogenesi. Gyneco AOGOI 2011;2:25-7.

Invited Oral Communications

1. Integrated NGS-based approaches for breast cancer-related germline mutations detection. Developments in NGS Workflows for Human Genetics. Agilent Corporate Satellite Meeting at ESHG2019. Gothenburg, 17 June 2019.
2. BRCA: il test germinale. Attualità e prospettive nel trattamento dei tumori femminili. Napoli, 9 Aprile 2019.
3. One4Two un test genetico per l'infertilità di coppia. SIEOG Regione Toscana, Cuore Fetale & NIPT Arena. Grosseto, 29 Marzo 2019.
4. Celiac Disease and microbiota: possible link. Up dates in autoimmunity 2018. Napoli, 15 Ottobre 2018.
5. One4Two: dall'idea all'impresa. Corso Precongressuale "Trasferimento Tecnologico in Medicina di Laboratorio". 49° Congresso Nazionale SIBioC, Firenze, 16 October 2017.
6. miRNA Libraries and Sequencing Procedures. European Network on Myalgic Encephalomyelitis/Chronic Fatigue Syndrome, COST Action - CA15111 Training School. Pavia, 20 July 2017.
7. Molecular diagnostics of genetic cardiopathies by way of multigene panels. International Society for enzymology (ISE) 2017, Santorini, Grecia, 16-19 June 2017.
8. Human microbiome and its relationship with health and disease status. Bringing Maths to Life 2017, Napoli, Convento di S. Domenico Maggiore, 7-9 June 2017.
9. Applicazione di Next Generation Sequencing in diagnostica. Seminari Magi-Euregio, Bolzano, 20 May 2016.
10. I tumori mammari eredo-familiari: il percorso di diagnostica molecolare. La Senologia nel terzo millennio: nuove acquisizioni diagnostico-terapeutiche, Corso di Formazione residenziale, INT Pascale, Napoli, 16 May 2016
11. La next generation sequencing nella valutazione delle cardiomiopatie: uno strumento irrinunciabile. PLACE Cardiologia, Palazzo Colonna, Roma, 19 November 2015.
12. Il microbioma nella patologia respiratoria. Sorrento breathing – Update and new trends in respiratory medicine. Centro congressi Villa Angelina, Massa Lubrense, 10 April 2015.
13. "Analisi del Microbiota intestinale". Symposium "Le tecnologie di sequenziamento massivo parallelo applicate alla diagnostica molecolare clinica". 46° Congresso Nazionale SIBioc, Roma, 13 October 2014.
14. "Tecniche di Next Generation Sequencing per lo studio del microbioma: applicazioni in patologia umana". I Workshop ARFACID "Le frontiere della microbiologia nella moderna pratica clinica". Napoli, 3 October 2014.
15. "Next generation sequencing as a tool for data acquisition at genomic level: examples in prokaryotes and eukaryotes". EMBO workshop "The Genome: Structure, Expression And Evolution".

Napoli, 22 September 2014.

16. "Ruolo del microbioma nella sarcoidosi polmonare". XII Corso Nazionale di Biologia Cellulare e Molecolare in Pneumologia – BIOCEP. Napoli, Ospedale Monaldi, 23 June 2014.

17. Implementing CFTR diagnostic testing. Multiplicom Corporate Satellite Meeting "Advances of MASTR™ in routine clinical diagnostics". ESHG2014, Milano, 1 June 2014.

18. "Le basi molecolari per un biorisanamento avanzato: tecnologie genomiche per lo studio dei microrganismi". Workshop: "Biotecnologie e risanamento dei suoli". Roma, Senato della Repubblica, Sala Santa Maria in Aquiro, 7 February 2014.

19. "La genetica della psoriasi: stato dell'arte". Le Psoriasi – Convegno multidisciplinare. Napoli, Centro Congressi Federico II, 28-30 November 2013.

20. "Il ruolo del microbioma nelle malattie infiammatorie croniche intestinali". Tecnologia 454: una finestra sulla biodiversità microbica. Milano, Museo della scienza e della tecnologia, 21 November 2013.

21. "Analisi di miRNA attraverso Next Generation Sequencing". Le Giornate Mediterranee di Medicina di Laboratorio. IV Congresso Interregionale SIBioC. Sorrento (NA), Hilton Sorrento Palace, 10 October 2013.

22. "BRCA1 and BRCA2 mutations through Next Generation Sequencing". Breast Cancer – Progress and Controversies. Napoli, Hotel Royal Continental, 14 June 2013.

23. "NGS in the Study of Human Diseases: the Examples of Cardiomyopathies and Ocular Diseases". The Translational Science of Mendelian Disorders from Transomics to Dally Life. BGI Next Generation Sequencing Workshop. Milano, 5 Dicember 2012.

24. "NGS e Medicina: esempi nello studio di cardiomiopatie e patologie oculari". Corso di Aggiornamento professionale F.I.Bio.: Next Generation Sequencing applications and future perspectives. Napoli, CEINGE Biotecnologie Avanzate, 27 April 2012.

25. "Target enrichment strategies for next generation sequencing technologies for the study of human diseases: the example of hypertrophic cardiomyopathies". Cambridge Healthtech Institute: Innovative Sample Prep & Target Enrichment in Clinical Diagnostics. Newport Beach (CA, USA), Hyatt Regency Hotel, 18-19 April 2012.

26. "Next Generation Sequencing in cardiomyopathies". Mediterranean school in cardiovascular sciences. Vietri sul Mare (SA), Lloyd's Baia Hotel, 20 October 2011.

27. "Analisi del DNA attraverso sequenziamento High Throughput". Corso PFA n°261-1821: La genetica nella Pratica Clinica III. San Giovanni Rotondo (Fg), Casa Sollievo della Sofferenza, 30 September 2011.

28. "L'analisi del genoma attraverso il sequenziamento degli acidi nucleici". Aggiornamenti in Medicina e Tecnologia Molecolare. Caserta, Complesso Monumentale di San Leucio, 11 February 2011.

29. Plenary lecture: "Il Microbioma attraverso la Metagenomica in Patologia Umana". 2° Congresso Interregionale SIBioC. Cefalù (PA), Teatro Comunale Salvatore Cicero, 22 September 2010.

Selected Oral Communications

1. Predictive medicine for psoriasis genetic risk using multi-gene panel variant analysis. 50° Congresso Nazionale SIBioC, Napoli, 18 Ottobre 2018.
2. *Detection of BRCA gene mutations and other genetic biomarkers for the prevention of familial breast cancer: a metadata survey. 1° Congresso Young SIBioC, Palermo, 1 Dicember 2017.*
3. *Sudden cardiac death in athletes: a multi-gene panel ameliorate the risk assessment. 49° Congresso Nazionale SIBioC, Firenze, 16-18 October 2017.*
4. "Next generation sequencing in research and diagnostics of genetic cardiomyopathies". EUROMEDLAB Milano 2013. Milano, 22 May 2013.

Communications to National and International meetings

1. M.V. Esposito, **V. D'Argenio**, M. Losi, G. Limongelli, B. Sarubbi, G. Frisso, Salvatore. Large cardiopathy-gene panels enable the identification of previously undiagnosed rare genetic diseases. SIGU 2018; Catania, 24-27 ottobre 2018.
2. M.V. Esposito, **V. D'Argenio**, M. Nunziato, M. D'Aiuto, B. Fosso , G. Casaburi, G. Pesole, G. Botti, F. Salvatore. Breast cancer dysbiosis in paired tumor and normal tissues. SIGU 2018; Catania, 24-27 ottobre 2018.
3. M.V. Esposito, **V. D'Argenio**, G. Limongelli, M. Losi, B. Sarubbi, S. Betocchi, G. Frisso, Salvatore. A large genes panel to improve the diagnosis and predisposition analysis of hereditary cardiomyopathies in a selected population from cardiological health centers. 50° Congresso Nazionale SIBioC, Napoli, 16-18 Ottobre 2018.
4. M.V. Esposito, **V. D'Argenio**, M. Nunziato, M. D'Aiuto, B. Fosso , G. Casaburi, G. Pesole, F. Salvatore. Human microbiome composition in breast cancer tissues as compared to paired normal tissues. 50° Congresso Nazionale SIBioC, Napoli, 16-18 Ottobre 2018.
5. **V. D'Argenio**, M. Nunziato, M.V. Esposito, F. Starnone, F. Di Maggio, M. D'Aiuto, A. Calabrese, M. Pensabene, S. De Placido, F. Salvatore. Beyond BRCA: multi-gene panel testing to define the extent of germline mutations in a number of related genes. 50° Congresso Nazionale SIBioC, Napoli, 16-18 Ottobre 2018.
6. A. Ranieri, F. Verdesca, **V. D'Argenio**, M. Nunziato1, A. Mandarino, F. Errico, A. Usiello, A. Vitale, E. Leggiero, L. Pastore, B. Lombardo. Duplication of D-aspartate oxidase gene in a girl with severe intellectual disability. 50° Congresso Nazionale SIBioC, Napoli, 16-18 Ottobre 2018.
7. C. Nardelli, I. Granata, G. Labruna, L. Iaffaldano, **V. D'Argenio**, V. Pilone, D. Compare, G. Nardone, M.R. Guarracino, F. Salvatore, L. Sacchetti. Characterization of the microbial transcriptome of duodenal mucosa from adult severe obese and control subjects by next generation sequencing. 50° Congresso Nazionale SIBioC, Napoli, 16-18 Ottobre 2018.

8. M. Passarelli, F. Cariati, **V. D'Argenio**, C. Siclari, R. Tomaiuolo. Towards collaborative technology transfer models for life science: the case of "InnovaSIBioC". 50° Congresso Nazionale SIBioC, Napoli, 16-18 Ottobre 2018.
9. M.V. Esposito, M. Nunziato, I. Limongelli, G. Nicora, **V. D'Argenio**. DNA variants interpretation in the next generation sequencing era: the case of EVAI tool. 50° Congresso Nazionale SIBioC, Napoli, 16-18 Ottobre 2018.
10. Maria Valeria Esposito, **D'Argenio Valeria**, Nunziato Marcella, Limongelli Giuseppe, Sarubbi Berardo, Losi Mariangela, Betocchi Sandro, Frisso Giulia, Salvatore Francesco. The genetic heterogeneity of human cardiopathy may be better detected by search of comprehensive of mutational alterations through NGS-based gene panels. XX Congresso Nazionale SIGU, Napoli, 15-18 November 2017.
11. Maria Valeria Esposito, **D'Argenio Valeria**, Nunziato Marcella, Pasqualina Buono, Salvatore Francesco, Frisso Giulia. A pathogenic mutation in the alpha subunit of the sodium channel (SCN5A) gene in an asymptomatic child to became an athlete: a case report. XX Congresso Nazionale SIGU, Napoli, 15-18 November 2017.
12. Flavio Starnone, Marcella Nunziato, Barbara Lombardo, Matilde Pensabene, Caterina Condello, Francesco Verdesca, Chiara Carlomagno, Sabino De Placido, Lucio Pastore, **Valeria D'Argenio**, Francesco Salvatore. Large genomic duplication in BRCA2 gene: a case report using fast detection with a sole NGS approach. XX Congresso Nazionale SIGU, Napoli, 15-18 November 2017.
13. L. Iaffaldano, I. Granata, C. Pagliuca, G. Casaburi, M.V. Esposito, G. Del Vecchio Blanco, C. Ciacci, G. Salerno, P. Salvatore, F. Salvatore, M.R. Guarracino, **V. D'Argenio**, L. Sacchetti. The oropharyngeal microbiome diversity in healthy individuals and in celiac disease patients. 49° Congresso Nazionale SIBioC, Firenze, 16-18 October 2017. Selected as oral communication.
14. M.V. Esposito, **V. D'Argenio**, M. Nunziato, S. Conato, G. Limongelli, B. Sarubbi, M. Losi, S. Betocchi, G. Frisso, F. Salvatore. Implementation of 3 large panels of cardiopathy-related genes for mutational screening in a diagnostic workflow. 49° Congresso Nazionale SIBioC, Firenze, 16-18 October 2017.
15. F. Cimmino, F. Cariati, M. Nunziato, **V. D'Argenio**, M. Capasso, R. Tomaiuolo. Dissecting genetic heterogeneity in tumors using dielectrophoresis (dep) array methodology. 49° Congresso Nazionale SIBioC, Firenze, 16-18 October 2017.
16. F. Cariati, M. Nunziato, L. Di Leo, B. Lombardo, L. Pastore, F. Salvatore, **V. D'Argenio**, R. Tomaiuolo. Improvement in the diagnosis of pathogenic subchromosomal copy number alterations by next-generation sequencing-based preimplantation genetic screening. 49° Congresso Nazionale SIBioC, Firenze, 16-18 October 2017.
17. F. Starnone, **V. D'Argenio**, S. Giordano, M. D'Antonio, M. Nunziato, M.A. Di Tella, D. Scognamiglio, A. Correra, G.

Castaldo, F. Salvatore. A next-generation sequencing-based approach improves and speeds-up the molecular neonatal screening of cystic fibrosis. 49° Congresso Nazionale SIBioC, Firenze, 16-18 October 2017.

18. F.D.E. De Palma, **V. D'Argenio**, M. Nunziato, M. Savarese, P. Buono, G. Esposito, F. Salvatore. Next-generation sequencing-based methodology increases the diagnostic sensitivity of molecular diagnosis and speeds-up Duchenne muscular dystrophy dene analysis. 49° Congresso Nazionale SIBioC, Firenze, 16-18 October 2017.

19. **Valeria D'Argenio**, Valentina del Monaco, Lorella Paparo, Fatima Elisa Domenica De Palma, Rita Nocerino, Francesco Salvatore, Roberto Berni Canani. Small RNA analysis to identify novel diagnostic and therapeutic markers for cow's milk allergy. 48° Congresso Nazionale SIBIOC – Medicina di Laboratorio, Torino, 18-20 October 2016. Awarded as best poster.

20. Marcella Nunziato, Maria Valeria Esposito, Flavio Starnone, Maria Angela Diroma, Alessandra Calabrese, Pasqualina Buono, Massimiliano D'Aiuto, **Valeria D'Argenio**, Francesco Salvatore. Hereditary breast cancer and gene panel analysis – a case report. 48° Congresso Nazionale SIBIOC – Medicina di Laboratorio, Torino, 18-20 October 2016.

21. **Valeria D'Argenio**, Vincenza Precone, Giorgio Casaburi, Livio Gioacchino Moccia, Irene Postiglione, Marialuisa Bocchino, Alessandro Sanduzzi, Francesco Salvatore. Next generation sequencing-based analysis for the complete characterization of the airway microbiome of sarcoidosis. 48° Congresso Nazionale SIBIOC – Medicina di Laboratorio, Torino, 18-20 October 2016.

22. M.V. Esposito, M. Nunziato, B. Fosso, G Casaburi, A. Telese, D. Montanaro, G. Liguori, M. D'Aiuto, G. D'Aiuto, G. Botti, A. Baldi, **V. D'Argenio**, G. Pesole, F. Salvatore. Metagenomic analysis of microbiome composition in breast cancer tissues. 47° Congresso Nazionale SIBIOC – Medicina di Laboratorio, Firenze, 26-27 October 2015.

23. M.V. Esposito, M. Nunziato, F. Starnone, A. Telese, M. D'Aiuto, G. D'Aiuto, **V. D'Argenio**, F. Salvatore. Male and breast cancer: an erroneous underestimation. 47° Congresso Nazionale SIBIOC – Medicina di Laboratorio, Firenze, 26-27 October 2015.

24. M. Nunziato, M.V. Esposito, M.A. Diroma, A. Telese, A. Calabrese , M. D'Aiuto, **V. D'Argenio**, F. Salvatore. Cancer-related genes panel screening in women affected by breast cancer through a coupled NGS-microdroplet PCR approach. 47° Congresso Nazionale SIBIOC – Medicina di Laboratorio, Firenze, 26-27 October 2015.

25. **Valeria D'Argenio**, Giorgio Casaburi, Vincenza Precone, Roberta Colicchio, Chiara Pagliuca, Daniela Sarnataro, Valentina Discepolo, Sangman M. Kim, Ilaria Russo, Giovanna Del Vecchio Blanco, David S. Horner, Matteo Chiara, Graziano Pesole, Paola Salvatore, Giovanni Monteleone, Carolina Ciacci, Gregory J. Caporaso, Bana Jabrì, Francesco Salvatore,

Lucia Sacchetti. Microbial dysbiosis in the gut microbiome of celiac patients revealed through next generation sequencing analysis. GUT MICROBIOME AND DISEASES, Milano 25 June 2015.

26. M.V. Esposito, M. Nunziato, G. Casaburi, A. Telese, M. D'Aiuto, G. D'Aiuto, **V. D'Argenio**, F. Salvatore. Human microbiome composition in breast cancer tissues investigated through 16S rRNA next generation sequencing analysis. GUT MICROBIOME AND DISEASES, Milano 25 June 2015.

27. **Valeria D'Argenio**, Maria Valeria Esposito, Massimiliano D'Aiuto, Antonella Telese, Marcella Nunziato, Flavio Starnone, Alessandra Calabrese, Giulia Frisso, Giuseppe D'Aiuto, Francesco Salvatore. Next generation sequencing screening of the BRCA1 and BRCA2 genes. SIGU 2014, Bologna 30-31 October 2014.

28. Valentina del Monaco, **Valeria D'Argenio**, Massimiliano D'Aiuto, Fatima De Palma, Donatella Montanaro, Giuseppina Liguori, Giuseppe D'Aiuto, Gerardo Botti, Alfonso Baldi, Raffaele Calogero, Francesco Salvatore. Comprehensive transcriptome profiling of breast cancers. ESHG2014, Milan 31Maggio-3 June 2014.

29. Maria Valeria Esposito, Massimiliano D'Aiuto, Antonella Telese, Vincenza Precone, Marcella Nunziato, Alessandra Calabrese, Giulia Frisso, Giuseppe D'Aiuto, **Valeria D'Argenio**, Francesco Salvatore. BRCA1 and BRCA2 mutation detection by a Next Generation Sequencing approach: an epidemiological study conducted in Southern Italy. ESHG2014, Milan 31Maggio-3 June 2014.

30. **Valeria D'Argenio**, Maria Valeria Esposito, Massimiliano D'Aiuto, Alessandra Calabrese, Giuseppe D'Aiuto, Francesco Salvatore. Analysis of a novel BRCA1 splicing mutation in hereditary breast and ovarian cancer woman. ESHG2014, Milan 31Maggio-3 June 2014.

31. Antonella Telese, **Valeria D'Argenio**, Irene Postiglione, Paola Nardiello, Giuseppe Castaldo, Francesco Salvatore. Validation of a next generation sequencing approach for rapid and accurate CFTR mutations screening. ESHG2014, Milan 31Maggio-3 June 2014.

32. **V. D'Argenio**, M.V. Esposito, M. D'Aiuto, V. Precone, P. Cantiello, A. Calabrese, G. Frisso, G. D'Aiuto, F. Salvatore. BRCA1 and BRCA2 mutation detection by a next generation sequencing approach: an epidemiological study in Southern Italy. SIC2013.

33. **V. D'Argenio**, G. Casaburi, V. Precone, C. Ciacci, J.C. Caporaso, L. Sacchetti, F. Salvatore. Characterization of the entire celiac disease intestinal microbiome by Next Generation Sequencing. EUROMEDLAB Milano 2013. Milano, 19-23 May 2013.

34. **V. D'Argenio**, M.V. Esposito, M. D'Aiuto, V. Precone, P. Cantiello, A. Calabrese, G. Frisso, G. D'Aiuto, F. Salvatore. BRCA1 and BRCA2 rapid germline mutations screening by Next Generation Sequencing approach. EUROMEDLAB Milano 2013.

Milano, 19-23 May 2013.

35. G. Esposito, **V. D'Argenio**, G. Guerri, G. Sauchelli, A. Boccia, I.C.M. Tandurella, M. D'Antonio, F. De Falco, G. Paolella, F. Salvatore. A novel mutation in RP1 is a major cause of autosomal dominant retinitis pigmentosa in Southern Italy. EUROMEDLAB Milano 2013. Milano, 19-23 May 2013.

36. **V. D'Argenio**, G. Guerri, A. Telese, A. Palmieri, A. Daniele, F. Salvatore. Long-range PCR and Next Generation Sequencing for the identification of PAH mutation status in HPA italian patients. EUROMEDLAB Milano 2013. Milano, 19-23 May 2013.

37. **D'Argenio V**, Petrillo M, Naso B, Cantiello PG, Pagliarulo C, Cozzuto L, Salvatore P, Alifano P, Paolella G, Salvatore F. New insights about size (12 Mb) and evolution of a "rare actinomycete" by whole genome sequence of Nonomuraea sp. ATCC 39727. 29th Congresso Nazionale SIMGBM. Pisa, 21-23 September 2011.

38. Carata E, Colicchio R, Talà A, Pagliuca C, Pasanisi D, **D'Argenio V**, Paolella G, Salvatore F, Salvatore P, Alifano P. Searching for novel secondary metabolites by genome data mining in Nonomuraea sp. ATCC 39727. 29th Congresso Nazionale SIMGBM. Pisa, 21-23 September 2011.

39. **D'Argenio V**, Frisso G, Boccia A, Fienga A, Limongelli G, Precone V, Pacileo G, Calabrò R, Paolella G, Salvatore F. DNA sequence capture array and next generation sequencing to identify new disease-causing genes: the case of hypertrophic cardiomyopathy. 36th FEBS Congress. Torino, 25-30 June 2011. FEBS JOURNAL 2011; 278SI (Suppl 1): 283.

40. **D'Argenio V**, Frisso G, Boccia A, Fienga A, Limongelli G, Precone V, Pacileo G, Calabrò R, Paolella G, Salvatore F. Next generation sequencing in research and diagnostics of hypertrophic cardiomyopathy. 71° Congresso Nazionale SIC. Roma, Hotel Rome Cavalieri, 11-13 December 2010.

41. **D'Argenio V**, Frisso G, Limongelli G, Precone V, Pacileo G, Fienga A, Boccia A, Calabrò R, Paolella G, Salvatore F. DNA Sequence Capture and High Throughput Sequencing Technology: a novel approach to identify a large number of hypertrophic cardiomyopathy-causing genes. American Heart Association 2010, Chicago 13-17 Novembre 2010. Circulation, 23 November 2010; 122: A19602.

42. **D'Argenio V**, Cantiello P, Naso B, Petrillo M, Cozzuto L, Notomista E, Paolella G, Di Donato A, Salvatore F. *De novo* sequencing and assembly of the whole genome of *Novosphingobium Puteolanum* PP1Y. Congresso Nazionale SIBioC 2010, Roma 5-8 October 2010.

43. Palmieri A, **D'Argenio V**, Guerri G, Sanna V, Daniele A, Salvatore F. Rapid and sensitive assessment of PAH mutation status in HPA italian patients based on DNA high throughput sequencing. Congresso Nazionale SIBioC 2010, Roma 5-8 October 2010.

44. Nardiello P, Zarrilli F, Sanna V, **D'Argenio V,** Rocino A, Coppola A, Di Minno G, Castaldo G. A record of F8 gene mutations and prothrombotic gene variants in Haemophilia A patients from

Campania region. XIII Convegno triennale sui Problemi Clinici e Sociali dell'Emofilia. Milano, 14-16 November 2008. Selected as oral communication. Awarded as best poster. Blood Transfusion (2008) 6 (S3) PO097:s56.

45. **V D'Argenio,** B Naso, A Peluso, F Pane, F Salvatore. Highly sensitive detection of BCR-ABL kinase domain mutations in CML patients by an ultra-deep sequencing approach. Retreat del Dipartimento di Biochimica e Biotecnologie mediche, Napoli 4-5 April 2008.

46. **V D'Argenio**, B Naso, M Petrillo, A Boccia, P Salvatore, G. Paolella, L Pastore, P Alifano, F Salvatore. Sequenziamento de novo del genoma di Nonomuraea ATCC 39727 mediante High-throughput Sequencing (GS20 System). Atti delle Giornate Scientifiche del Polo delle Scienze e delle Tecnologie per la Vita, Napoli 20-21 September 2007.

47. B Naso, **V D'Argenio**, M Petrillo, P Salvatore, G. Paolella, L Pastore, P Alifano, F Salvatore. *De novo* sequencing of the natural antibiotic-producer *Nonomuraea* ATCC 39727. 1st EMEA Genome Sequencer User Meeting, Monaco 28-29 March 2007.

48. V Sanna, P Nardiello**, V D'Argenio**, G Castaldo, A Rocino, A Coppola, G Di Minno, F Salvatore. Analisi molecolare del gene F8C in pazienti con Emofilia A del Sud Italia. SIBioC 2006, Torino 19-22 September 2006.

49. **V D'Argenio**, P Nardiello, F Zarrilli, G Castaldo, A Rocino, A Coppola, G Di Minno, F Salvatore. Interazione tra geni nello sviluppo del fenotipo dell'Emofilia A. SIBioC 2006, Torino 19-22 September 2006.

50. D'Argenio G, Valenti M, Scaglione G, Cosenza V, Mazzone G, Grandone I, Pietrini L, **D'Argenio V**, Sorrentini I, Di Marzo V. Up-regulation af anandamide levels as an endogenous mechanism and a pharmacological strategy to limit colon inflammation. Digestive disease week 2006, Los Angeles 20-25 May 2006.

51. D'Argenio G, Calvani M, Petillo O, Margarucci S, Rienzo M, Torpedine A, Mazzone G, Sorrentini I, **D'Argenio V**, Caporaso N, Peluso G. Influence of carnitine on butyrrate matabolism of colonocytes in a rat model of experimental colitis. Digestive disease week 2006, Los Angeles 20-25 May 2006.

Technological Transfer Activities

From 2015: member of the Project "One4Two: screening dell'infertilità di coppia in next generation sequencing" winner of the competitions Start Cup Campania 2015 (5° classified) and of the Premio Speciale Pari Opportunità, Premio per l'Imprenditoria Femminile to Premio Nazionale per l'Innovazione (PNI), admitted at the acceleration stage of the BioUpper Program (founded by Fondazione Cariplo&Novartis), and winner of the EIT Health INNOSTARS 2016 (Campania Region). The Project has been 1of the 5 selected for the faculty program "Italian Scouts in Silicon Valley" (2017) and won the II edition of the Hack-Merck 2017.

From 2016, is co-founder of the innovative startup KronosDNA.

From July 2017, KronosDNA is a spin off of Federico II University.

In 2018, KronosDNA has obtained Horizon 2020 (EIC-SMEInst-2018-2020) Seal of Excellence (April 2018) and the SME Instrument Phase 1 grant (December 2018).

2018: Member of the Evaluation Committee of the First Edition of InnovaSIBioC.

Honours and Awards

Winner of the Award "Best SIBioC Poster" to the 48° National SIBioC Meeting, Turin, 18-20 October 2016.

Winner of the International Award "N. Pascale", XIII edizione

Scientific Societies Memberships and Editorial Activities

From February 2019, Corresponding Member of the Scientific Committee on Molecular Diagnostics of the International Federation of Clinical Chemistry (IFCC).

From 2019 Editorial Board member of High-Throughput (ISSN 2571-5135) journal.

Author of a chapter in the book "Biochimica Clinica e Medicina di Laboratorio" ed.1 (2017), ed.2 (2018) from EDISES.

Member of the "Società Italiana di Biochimica Clinica (SIBioC)"

Reviewer of international peer-reviewed journals (IJMS, Molecules, Marine Drugs, Molecular Sciences, Genes, BMC bioinformatics, Biomedicine, BMJ Open, Gigasciences, Biochimica Clinica).

Organization of National and International Scientific Conferences

Member of the Scientific Secretariat of the Second SiBioC Young Scientists National Congress, Rome 3 December 2018.

Member of the Scientific Committee of the 50th SIBioC National Congress, Naples, October 16-18, 2018.

Grants and founding

Gennaio 2018 Responsabile di Unità di Ricerca autonoma nel Progetto "Sviluppo di Approcci Terapeutici INnovativi per patologie neoplastiche

	resistenti ai trattamenti (SATIN)", PO FESR 2014-2020, finanziato dalla Regione Campania c/o CEINGE Biotecnologie Avanzate (Responsible Prof. Francesco Salvatore).
December 2017	Admitted to Anvur annual, individual grant for basic research activities.
December 2016	Responsible of the Project "Studio delle basi molecolari dei tumori della mammella eredo-familiari attraverso tecniche di next generation sequencing", POR Campania FSE 2014/2020.
October 2014	Member of the Project "Study of the gut microbiome in the adult celiac disease pathogenesis" granted from FC, call for proposal, 2014.
2011-2015	Scientific referent and member of the Project "Sviluppo di una piattaforma tecnologica multiplex per diagnostica molecolare, portatile ed automatizzata, basata sulla logica strumentale del lab-on-chip, in grado di consentire applicazioni multiparametriche in campo infettivologico" – progetto di formazione" MICROMAP, PON01_02589.

Napoli, July 2019.