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Stefano Cagnin

Personal data

Marital status: married

Nationality at birth: Italian

Residence: Massanzago (Pd) via Marconi, 19 - 35010

Born data: 13th January 1974

Born city: Camposampiero (Pd)

Tax code: CGNSFN74A13B563C

Education

- 23th April 2007. Phd in Biotechnology at the University of Padova. Title of the thesis: “Gene expression profiles of dystrophic muscles and improvements on DNA microarray technique”.
Tutor: Prof. G. Lanfranchi.

- 10th July 2003. Master in Biology from the University of Padova. Final grade: 110/110 cum laude.
Title of the thesis: “cDNA micorarray production and their application to determine gene expression profiles of patients affected by limb girdle muscular distrophy type 2B”
Supervisor: Prof. G. Lanfranchi.

- December 2000. Thesis internship in the functional genomics laboratory supervised by Prof G. Lanfranchi and G. Valle. The laboratory is located in the CRIBI Biotechnology Centre. I spent my time to develop microarray technology.

- July 1993. Scientific high school degree.

Informatic abilities

Usage of biological databases at the NCBI and EMBL repositories.

Bioinformatic analyses of DNA and RNA sequences.

Usage of bioinformatics tools to analyse microarray data.

Usage of R statistical tool.

Working experiences

- 14th May 2012 – today. Assistant professor of Genetics at the Department of Biology of the University of Padova – Italy.

- January 2009 – today. Coordinator of Gene expression microcribi service at the CRIBI Biotechnology Center of the University of Padova - Italy.

- February 2011 – 31th January 2012. Research fellowship at the Depertment of Anatomy and Human Physiology of the University of Padova - Italy.

- January 2008 – 31th December 2010. Research fellowship at the Department of Biology of the University of Padova - Italy.

- January 2007 – 31th December 2008. Research fellowship at the Depertment of Biology of the University of Padova - Italy.

- January 2004 – January 2007. PhD student at the CRIBI Biotechnology Center of the University of Padova - Italy.

- July 2003. Telethon fellowship in the B 57_2 project financed by Telethon foundation.

- 2000 – 2003. Internship for master's degree.

Awards/Grants

- December 2017. FFABRR - finanziamento delle attività base di ricerca 3,000 euros.

- March 2017. Fondazione CARIPLO 55,000 euros to identify miRNAs involved in metabolic cell modulation. Title of the project: "Multicomponent Analysis of phYsical frailty BiomarkErs: focus on mitochondrial health: MAYBE". I am a component of the Unit of the University of Padova.

- July 2014. National project for three years of 353,800 euros to identify gene variation involved in dyslipidemia. Title of the project: "Towards the prediction of dyslipidemia from next generation sequencing data". Project code: GR-2011-02346845. I am the responsible of the Operative Unit of the Department of Biology that has 120,000 euros as budget.

- March 2014. International project for two years of 100,000 euros

to identify miRNAs involved in redox response in diabetic cardiomyopathy. Project founded by European Foundation for the Study of Diabetes (EFSD). Title of the project: “Monoamine oxidase inhibition as a new therapeutic strategy for the treatment of diabetic cardiomyopathy”. I am responsible of the Operative Unit to dissect miRNA expression with 35,000 euros as budget.

- January 2014. National project for two years (“Progetto di Ateneo”) of 53,000 euros to dissect the role of long non-coding RNAs in skeletal musle differentiation. Title of the project: “The role of non-coding RNA in pathophysiological conditions of skeletal muscle.” Project code: CPDA139317/13.

- June 2009. Award for the publication in the atherosclerosis field: “Identification of genetic networks involved in the atherosclerosis”

Teaching activity

- Co-supervisor for Doctorate in Genetics and Molecular Biology of Development Cycle XXVIII. Title of the thesis “The role of long non-coding RNAs in pathophysiological conditions of skeletal muscle”.
- Supervisor for Master’s degree in Industrial Biotechnology. Title of the thesis “The role of EGFR and AGD3 in skeletal muscle fibre type and metabolism”. University of Padova in collaboration with Imperial College – Italy Academic Year 2016/2017.
- Supervisor for Master’s degree in Industrial Biotechnology. Title of the thesis “Establishing a multi-well plate reader system for high-throughput imaging and analysis of fluorescent zebrafish larvae to investigate the central nervous system”. University of Padova in collaboration with University of Bonn – Italy Academic Year 2016/2017.
- Supervisor for Master’s degree in Industrial Biotechnology. Title of the thesis “Alteration of miRNA expression in ALS: involvement of miRNAs in the maintenance of NMJ”. University of Padova – Italy Academic Year 2016/2017.
- Supervisor for Master’s degree in Industrial Biotechnology. Title of the thesis “miRNAs in the cluster miR17-92 influences metastatic progression in melanoma through the regulation of OPA1”. University of Padova – Italy Academic Year 2016/2017.
- Supervisor for Bachelor’s degree in Biotechnology. Title of the thesis: “miRNAs as candidate biomarkers in ALS”. University of Padova – Italy. Academic Year 2016/2017.
- Supervisor for Master’s degree in Molecular Biology. Title of the thesis “Long non-coding RNAs in ALS: the gene *Plasmacytoma variant translocation 1* (Pvt1) influences

mitochondria function in skeletal muscle". University of Padova – Italy Academic Year 2015/2016.

- Supervisor for Master's degree in Molecular Biology. Title of the thesis "Gene expression analysis of long non-coding RNAs (lncRNAs): their role in skeletal muscle physiopathology". University of Padova – Italy Academic Year 2015/2016.
- Supervisor for Bachelor's degree in Biotechnology. Title of the thesis: "Characterization of Pl*asmacytoma variant translocation 1* (Pvt1) in diabetic patients". University of Padova – Italy. Academic Year 2015/2016.
- Supervisor for for Bachelor's degree in Biotechnology. Title of the thesis: "qRT-PCR for the determination of gene expression". University of Padova – Italy. Academic Year 2012/2013.
- Supervisor for Master's degree in Molecular Biology. Title of the thesis "The role of miR-27a in Rhabdomyosarcoma". University of Padova – Italy Academic Year 2013/2014.
- Teacher of Structural and functional genomics course included in the training for Master's degree in Industrial Biotechnology at the University of Padova – Italy. Academic Years from 2012/2013 to 2017/2018.
- Teacher of Genetic ingegnering course included in the training for Bachelor's degree in Biotechnology at the University of Padova – Italy. Academic Year 2011/2012.
- Assistant supervisor for Bachelor's degree in Biotechnology. Title of the thesis: "Sinthesis of miRNA library for Ion Torrent sequencer". University of Padova – Italy. Academic Year 2011/2012.
- Assistant supervisor for Bachelor's degree in Biotechnology. Title of the thesis: "miRNA expression through RAKE technology". University of Padova – Italy. Academic Year 2009/2010.
- Assistant supervisor for Master's degree in Industrial Biotechnology. Title of the thesis: "Development of a new technique for the identification of microRNAs and its use for the analysis on the genome regulation in different pig (*Sus scrofa*) tissues". University of Padova - Italy. Academic Year 2009/2010.
- Supervisor for educational workshop of Genetics course included in the training for Bachelor's degree in Biotechnology at the University of Padova – Italy. Academic Year 2009/2010.
- Supervisor for educational workshop of Genomics, bioinformatics and statistics course included in the training for Master's degree in Industrial Biotechnology at the University of Padova – Italy. Academic Year 2009/2010.

- Supervisor for educational workshop of Bioinformatics 2 course included in the training for Master's degree in Industrial Biotechnology the the University of Padova – Italy. Academic Year 2008/2009.
- Supervisor for educational workshop of Methods of functional genomics course included in the training for Master's degree in Industrial Biotechnology at the University of Padova – Italy. Academic Year 2008/2009.
- Assistant supervisor for Bachelor's degree in Biotechnology. Title of the thesis: "Phage libraries to analyze inflammation in skeletal muscle". University of Padova – Italy. Academic Year 2007/2008.
- Assistant supervisor for Master's degree in Industrial Biotechnology. Title of the thesis: "miRNA expression in cell lines of Rhabdomyosarcoma through xMAP technique". University of Padova – Italy. Academic Year 2007/2008.
- Assistant supervisor for Master's degree in Industrial Biotechnology. Title of the thesis: "Meta analysis of gene expression of patients affected by inflammatory myopathies: gene network reconstruction". University of Padova – Italy. Academic Year 2007/2008.
- Assistant supervisor for Master's degree in Industrial Biotechnology. Title of the thesis: "Gene expression alteration in inflammatory myopathies". University of Padova – Italy. Academic Year 2007/2008.
- Supervisor for educational workshop of Methods of functional genomics course included in the training for Master's degree in Industrial Biotechnology at the University of Padova – Italy. Academic Year 2007/2007.
- Assistant supervisor for bachelor's degree in Molecular Biology. Title of the thesis: "Gene expression in LGMD2B". University of Padova – Italy. Academic Year 2006/2007.
- Assistant supervisor for master degree in Industrial Biotechnology. Title of the thesis: "A new quantitative method to analyze microarray gene expression". University of Padova - Italy. Academic Year 2006/2007.
- Supervisor for educational workshop of Methods of functional genomics course included in the training for Master's degree in Industrial Biotechnology at the University of Padova – Italy. Academic Year 2006/2007.
- Supervisor for educational workshop of Methods of functional genomics course included in the training for Master's degree in Industrial Biotechnology at the University of Padova – Italy. Academic Year 2005/2006.
- Supervisor for educational workshop of Methods of functional

genomics course included in the training for Master's degree in Industrial Biotechnology at the University of Padova – Italy. Academic Year 2004/2005.

Reviewer and Editorial activity

Reviewer

- *BMC Genomics; PlosOne; Biology Open*
- *AFM Association Française contre les Myopathies*
- *MIUR "Ministero dell'Istruzione dell'Università e della Ricerca"*

Editorial

- Leader Guest Editor for a Special Issue titled "Mediators of Heart Failure and Metabolic Consequences: Improvements in the Prevention or Treatment of Heart Failure" in BioMed Research International
- Leader Guest Editor for a special Issue titled "Improvements in the comprhension of multicellular organisms by the analysis of single cells" in International Journal of Genomics

Scientific activity

My scientific activity is focused on transcriptional analysis in *H. sapiens*, different model organisms (*M. musculus, D. melanogaster, S. scrofa*) and cell cultures. I applied new bioinformatic approaches, molecular biology, enginering biology and genomics techniques to dissect transcriptional regulation in different pathologies. Analyses performed requested setting up of new methods and follow are summarized principal themes of my present and past research:

1) Development of Human Array 1.0

Sistematic sequencing of ESTs (Expressed Sequence Tags), from cDNA libraries of skeletal muscle, allowed producing a phisical-sequenced library that was used to produce the first muscle specific microarray. It was used to analyze gene expression profiles of patients with different muscular dystrophies (*Campanaro S. et al., Minerva Biotec., 2002*).

2) Gene expression profiles of patients affected by limphoblastic leukemia and facio scapulo humeral dystrophy and proteomic data integration

After the cDNA sequencing derived from bone marrow the Human array 1.0 was expanded to the Human array 2.0 including 4,801 transcripts. It was applied to evaluate gene expression in pathients affected by leukemia. We identified 30 genes able to discriminate between T-ALL, B-ALL and B-ALL (*Campanaro S. et*

al., Minerva Biotec., 2003).
Gene expression analysis is based on assumption that gene expression alterations are associated to protein expression alterations. This is not always true because post-transcriptional and post-transductional mechanisms. It was demonstrated that these mechanisms are particularly important in pathogenetic processes. The integration of transcriptional and proteomic profiles affected by facio scapulo humeral dystrophy evidenced a fiber switching regulated by MYOD network (*Celegato B. et al., Proteomics, 2006*).

3) Gene expression profiles in cardiocirculatory system.
After the human genome was finished, microarray technology was widely used to evaluate gene expression profiles in human pathologies. Different platforms based on oligonucleotides probes (different from cDNA probes) were developed. Using oligonucleotide microarrays I analyzed gene expression of atherosclerotic plaques evidencing the under-expression of transcripts involved in the smooth muscle modification (*Cagnin S. et al., Medimond, 2007*). Because the complexity of atherosclerosis and the peculiar localization of plaques that are localized preferentially in coronaries, carotids, iliac aorta it was evaluated the relationship between gene expression of cells in the plaque and transcriptional factors and cytokines released in blood torrent. We evidenced, performing a meta analysis, that JAK/STAT pathway and caveole system, involved in smooth muscle differentiation, are involved in the atherosclerosis (*Cagnin S. et al., BMC Genomics, 2009*). Cardiocirculatory system is fundamental for the maintenance of organisms' homeostasis and for life. Many efforts were done to understand how it operates and molecular mechanisms involved in tissue function maintenance. We used *Sus scrofa* as model organism to understand networks involved in the maintenance of different tissues of cardiocirculatory system (*Martini P. et al., Int J Mol Sci., 2013*). Moreover, we demonstrated the ability of in vivo regeneration of cardiac valve evidencing molecular pathway involved in this proces (*Iop L. et al., PlosOne, 2014*).

4) Meta analysis and pathway analysis techniques applied to gene expression.
Public repositories for gene expression data allow the analysis of a specific pathology withouth performing in house experiments. Meta analysis is a research tool, based on statistic-matemetic methods, that allows comparing data from different studies or laboratories to extrapolate conclusions to be tested. Using a meta analysis approach we evidenced that in all muscle atrophy

conditions energetic mechanisms are impaired while are activated processes involved in the protein degradation where SMAD3/4, GNB2LI/RACKI, MYC, MAX and JUN transcription factors play a central role (*Calura E. et al., BMC Genomics, 2008*). Meta analysis techniques do not take in account chromatin reorganization that is a central process in the gene expression regulation. We implemented an algorithm that takes in account chromatin reorganization to describe gene expression and we applied it in the analysis of acute leukemia gene expression identifying the importance of HOX genes (*Martini P. et al., BMC Bioinformatics, 2011*). The same algorithm demonstred the ability to separate gene expression profiles from different muscular dystrophies maintaing those correlated strongly clustered. Gene expression analysis using genome wide approaches allows the identification of altered genes as a simple gene list that has to be interpreted. If we have the ability to map genes in pathways involved in cell biology genome wide expreiments become more informative. We developed a new algorithm to identify altered pathways in time series experiments (*Martini P. et al., BMC Bioinformatics, 2014*).

5) Evaluation of genetic modifiers in Duchenne muscular dystrophy

Duchenne muscular dystrophy is associated with early patients die because cardiac and respiratory problems. Today Duchenne muscular dystrophy is treated with glucocorticoids with variable effects on patients. Using transcriptional analysis comparing a group of patients evidencing strong response to glucocorticoids against those presenting a mild response we identified SPP1 as the gene most activacted in patients with a poor response. Genotype analysis of SPP1 evidenced the presence of a SNP that can be associated to the treatment efficacy (*Pegoraro E. et al., Neurology, 2011*).

6) Improvement of methods to evaluate nucleic acid hybridization.

Microarray technology is based on target labeling with fluorescent dyes. It is interesting and it is an improvement to measuere nucleic acid hybridization without labeling because the use in diagnostic tools. In collaboration with the Department of Engineriing and Electronics of the University of Padova we deeloped a tool that is able to identify DNA hybridization also evaluating the hybridization kinetics (*Bandiera L. et al., Biosens Bioelectron., 2007*). DNA sensors technology has been improved during years and we discussed it in a recent work (Cagnin S. et al., Sensors, 2009).

7) Cell culture miniaturization.

In the pharmacology field it is indispensable to evaluate the response of cells to different compounds. Parallelization speeds up essays. Using photolitography and polimerization techniques we developed an elastic matrix where print different proteins to allow cell growth. Device allows mimiking fluids dynamic as we have in nature (blood circulation). C2C12 analysis evidenced that cells cultured in dynamic maintain proliferative and differenziative ability (*Cimetta E.*, Cagnin S.* et al., Biotechnol Prog., 2010 and Cagnin S. et al., Sensors, 2012*).

8) Role of microRNAs and long non-coding RNAs in gene expression and metabolism regulation.

MiRNAs are short non-coding transcripts that, during last years, acqured more and more importance in biology and human pathology because their ability of post-transcriptional transcripts regulation.

I am involved in different projects to determine miRNA expression and to integrate their expression with mRNA and long non-coding RNA expression:

1. We developed a new method for the analysis of single miRNAs through x-MAP technology (Luminex) using micorbeads and cytofluorimeter. Comparing our method with different established methods we demonstrated that our method is more sensitive, precise and economically advantageous (Biscontin A. et al., BMC Molecular Biology, 2010).
2. Usage of pig heart valves to substitute pathological human heart valves is a surgical routine. Even if a wide usage of pig heart valves to substitute the human ones, molecular mechanisms at the base of cardiocirculatory system biology are not well known. The end of the pig genome sequencing in 2009 allowed miRNA prediction and their experimental validation. We identified 777 miRNAs expressed from the pig genome in different tissues and we reconstructed their interaction networks. Regarding to regenerative processes of cardiac valves we evaluated molecular mechanisms and miRNAs involved in (*Martini P. et al., Int J Mol Sci., 2013; Martini P. et al., PlosOne, 2014; Iop L. et al., PlosOne, 2014*).
3. Skeletal muscle is the most abundant and plastic tissue of the human body and is involved in different processes such as metabolism regulation. Skeletal muscle atrophy is a condition related with pathologies and aging therfore understanding molecular mechanisms related with atrophy

could improve its treatment. We evidenced miRNAs altered in different skeletal muscular atrophies and in vivo characterized the ability of miR-21 and miR-206 to induce skeletal muscle atrophy (*Soares RJ. et al., JBC, 2014*). ALS is a pathology associated to skeletal muscle for which is not present treatments. As a final result of the pathology there is the lack of NMJ and muscle atrophy. We evaluated which miRNAs are involved in the maintenance of NMJ components determining their function in vivo (manuscript in preparation). Importantly, several cell types, not all directly involved in its contraction compose skeletal muscle. The functional units of skeletal muscle are myofibers and understanding how they regulate their metabolism could improve diseases treatment. In fact, many diseases are associated to fiber switch associated with a modification in its metabolism. We conducted a cohompriensive analysis of coding and non-coding RNAs in single myofibers demonstrating the importance of both miRNAs and long non-coding RNAs in the regulation of muscle metabolism in vivo. We evidenced the ability of a specific long non-coding RNA to interact with peculiar genomic regions to regulate mitochondrial function (manuscripts in preparation). Adipose tissue is associated to muscle function because usually its increases induce muscle atrophy. It would be interesting understanding mechanisms involved in this cohoperation expecially those related with miRNAs. I am involved in two projects (CARIPLO and GR-2011-02346845 projects) to understand relationship between these tissues and their metabolism modulation. Metabolic alterations occure also in hearth of diabetic patients. Modulating cell oxidative stress can have a therapeutic effect in the treatment of diabetic cardiomyopathy. I am involved in a project to identify miRNAs that can be used as drugs for this purpose (EFSD project).

4. MiRNAs are involved in cancer pathogenesis and progression. We used malignant melanoma to understand which miRNAs are involved in metastatization processes and which are their real targets. Applying the Ago immunoprecipitation associated to RNA sequencing we identified miRNA-targets physical interactions evidencing pathways altered during metastatization processes (*Cagnin S. Ion World Tour Bologna – Italy, 2014* and manuscript in preparation).
5. Inflammation is an important state that also leads to chronic diseases or tumors (e.g. gastric tumors). It causes

also muscle diseases that are treatable if it will be identified antigens against whom the immune system reacts. We developed a Phage Display library from skeletal muscle to identify antigens associated to chronic inflammations of this tissue (manuscript in preparation). During inflammatory state macrophages are involved in the presentation of antigen to produce a response. We demonstrated that miRNAs are important modulators for the ability of macrophages to present antigens (Pagliari M. et al., Front. In Immunol., 2017).

Pubblications

Pagliari M, Munari F, Toffoletto M, Lonardi S, Chemello F, Codolo G, Millino C, Della Bella C, Pacchioni B, Vermi W, Fassan M, de Bernard M*, Cagnin S.* (2017) **Helicobacter pylori Affects the Antigen Presentation Activity of Macrophages Modulating the Expression of the Immune Receptor CD300E through miR-4270.** Front Immunol.; 8:1288. [ISSN: 1664-3224 - I.F. 6.429] * co-corresponding author

Martini P, Paracchini L, Caratti G, Mello-Grand M, Fruscio R, Beltrame L, Calura E, Sales G, Ravaggi A, Bignotti E, Odicino FE, Sartori E, Perego P, Katsaros D, Craparotta I, Chiorino G, Cagnin S, Mannarino L, Ceppi L, Mangioni C, Ghimenti C, D'Incalci M, Marchini S, Romualdi C. (2016) **lncRNAs as Novel Indicators of Patients' Prognosis in Stage I Epithelial Ovarian Cancer: A Retrospective and Multicentric Study**. Clin Cancer Res.; 23(9):2356-2366. [ISSN: 1078-0432 – I.F. 9.619].

Chemello F, Mammucari C, Gherardi G, Rizzuto R, Lanfranchi G, Cagnin S.* (2015) **Gene expression changes of single skeletal muscle fibers in response to modulation of the mitochondrial calcium uniporter (MCU)** Genomics Data; 5:64-67. [ISSN: 2213-5960]. * corresponding author.

Mammucari C, Gherardi G, Zamparo I, Raffaello A, Boncompagni S, Chemello F, Cagnin S, Braga A, Zanin S, Pallafacchina G, Zentilin L, Sandri M, De Stefani D, Protasi F, Lanfranchi G, Rizzuto R. (2015) **The mitochondrial calcium uniporter controls skeletal muscle trophism in vivo.** Cell Rep.;10(8):1269-79. [ISSN: 2211-1247 – I.F.: 8.358].

Fede C, Millino C, Pacchioni B, Celegato B, Compagnin C, Martini P, Selvestrel F, Mancin F, Celotti L, Lanfranchi G, Mognato M, Cagnin S*. (2014) **Altered gene transcription in human cells treated with Ludox® silica nanoparticles.** Int J Environ Res

Public Health. 28;11(9):8867-90. [ISSN 1660- 4601 – I.F.: 1.993]. * corresponding author.

Martini P, Sales G, Calura E, Cagnin S, Chiogna M, Romualdi C. (2014) **timeClip: pathway analysis for time course data without replicates.** BMC Bioinformatics.15 Suppl 5:S3. [ISSN 1460-2059 - I.F.: 4.621].

Iop L, Bonetti A, Naso F, Rizzo S, Cagnin S, Bianco R, Dal Lin C, Martini P, Poser H, Franci P, Lanfranchi G, Busetto R, Spina M, Basso C, Marchini M, Gandaglia A, Ortolani F, Gerosa G. (2014) **Decellularized allogeneic heart valves demonstrate self-regeneration potential after a long-term preclinical evaluation.** PLoS One. 18;9(6):e99593. [ISSN 1932-6203 – I.F.: 3.534].

Soares RJ, Cagnin S, Chemello F, Silvestrin M, Musaro A, De Pitta C, Lanfranchi G, Sandri M. (2014) **Involvement of microRNAs in the regulation of muscle wasting during catabolic conditions.** J Biol Chem. 8;289(32):21909-25. [ISSN 0021-9258 – I.F.: 4.6].

Martini P, Sales G, Brugiolo M, Gandaglia A, Naso F, De Pittà C, Spina M, Gerosa G, Chemello F, Romualdi C, Cagnin S*, Lanfranchi G. (2014) **Tissue-specific expression and regulatory networks of pig microRNAome.** PLoS One. 3;9(4):e89755. [ISSN 1932-6203 – I.F.: 3.534]. * corresponding author.

Martini P, Sales G, Calura E, Brugiolo M, Lanfranchi G, Romualdi C, Cagnin S*. (2013) **Systems biology approach to the dissection of the complexity of regulatory networks in the S. scrofa cardiocirculatory system.** Int J Mol Sci. 14(11):23160-87. [ISSN 1422-0067 - I.F.: 2.339]. * corresponding author.

Cagnin S., Cimetta E., Guiducci C., Martini P., Lanfranchi G. (2012) **Overview of Micro- and Nano-Technology Tools for Stem Cell Applications: Micropatterned and Microelectronic Devices.** Sensors 12, 15947-15982 [ISSN 1424-8220 – I.F.: 1,739].

Trainotti L., Cagnin S., Forcato C., Bonghi C., Dhingra A., Koepke T., Prat L., Maldonado J., Silv H. (2012) **Functional Genomics: Transcriptomics** in Genetics, Genomics and Breeding of Stone Fruits Ed. by CRC Press Editor(s): Chittaranjan Kole, *Clemson University, South Carolina, USA*; Albert G. Abbott, *Clemson University, South Carolina, USA* [ISBN 9781578088010].

Kyriakides T., Pegoraro E., Hoffman EP., Piva L., Cagnin S. S Lanfranchi G., Griggs RC., Nelson SF. (2011) **SPP1 genotype is determinant of disease severity in Duchenne muscul dystrophy: predicting the severity of Duchenne muscul dystrophy: implications for treatment.** Neurology. 77: 1858-185 [ISSN: 0028-3878 - I.F.: 8,17].

Martini P., Risso D., Sales G., Romualdi C., Lanfranchi G.*, Cagnin S.* (2011) **Statistical test of Expression Pattern (STEPath): a new strategy to integrate different genomic information in gene expression and meta-analysis studies** BMC Bioinformatics 12:92. * Co-corresponding author. [ISSN 1471-2105 – I.F.: 3,43].

Pegoraro E, Hoffman E.P., Piva L, Gavassini B.F., Cagnin S., Ermani M., Bello L., Soraru G., Pacchioni B., Lanfranchi G., Angelini C., Kesari A., Lee I., Devaney J.M., Gordish-Dressman H., McDonald C. (2011) **SPP1 genotype is a determinant of disease severity in Duchenne muscular dystrophy** Neurology 76(3): 219-226. [ISSN: 0028-3878 - I.F.: 8,17]

Biscontin A., Casara S., Cagnin S., Tombolan L., Rosolen A., Lanfranchi G., De Pittà C. (2010) **New miRNA labeling method for bead-based quantification** BMC Mol Biol. 16;11:44. [ISSN 1471-2199 - I.F.: 2,85].

Cimetta E.*, Cagnin S.*, Volpatti A., Lanfranchi G., Elvassore N. (2010) **Dynamic culture of bubble-confined cell arrays** Biotechnol Prog. 26(1):220-31. *Equally contributed [E- ISSN: 1520-6033 - I.F.: 2,398].

Cagnin S., Caraballo M., Guiducci C., Martini P., Ross M., SantAna M., Danley D., West T., Lanfranchi G. (2009) **Overview of electrochemical DNA biosensors: new approaches to detect the expression of life** Sensors 9(4): 3122-3148. [ISSN 1424-8220 - I.F.: 1,903].

Cagnin S., Biscuola M., Patuzzo C., Trabetti E., Pasquali A., Faggian G., Iafrancesco M., Mazzucco A., Pignatta P.F., Lanfranchi G. (2009) **Reconstruction and functional analysis of altered molecular pathways in atherosclerotic arteries** BMC Genomics; 10(1):13. [ISSN 1471-2164 - I.F.: 4,18].

Calura E., Cagnin S., Raffaello A., Lanfranchi G., Romualdi C. (2008) **Meta-analysis of expression signatures of muscle atrophy: gene interaction networks in early and late stages** BMC Genomics;9(1):630. [ISSN 1471-2164 - I.F.: 4,18].

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Millino C., Celegato B., Campanaro S., Romualdi C., Bellin M., **Cagnin S.**, Valle G., Ricci E., Angelini C., Lanfranchi G. (2003). **Expression profiling of neuromuscular disorders with a dedicated muscle microarray platform.** Journal of Muscle Research and Cell Motility. [P-ISSN: 0142-4319 – I.F.: 1,657].

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MANUSCRIPTS IN PREPARATION

Chemello F, Grespi F, Zulian A, Cancellara P, Hebert-Chatelain E, Martini P, Bean C, Alessio E, Ferrazza R, Laveder P, Guella G, Reggiani C, Romualdi C, Bernardi P, Scorrano L, Cagnin S*, and Lanfranchi G*
miR-27a-3p and -142-3p control fuel utilization by skeletal muscle mitochondria. * co-corresponding author

Alessio E, Buson L, Chemello F, Grespi F, Martini P, Millino C, Pacchioni B, Cancellara P, Reggiani C, Massimino M, Scorrano L,

Romualdi C, Bertoli A, Sandri M, Lanfranchi G, and Cagnin S
The long non-coding RNA Pvt1 influences mitochondria function during skeletal muscle atrophy

Zampini M, Martini P, Chemello F, Romualdi C, Taverna D, De Pitta' C, Lanfranchi G, Cagnin S
Argonaute immunoprecipitation approach and miRNA expression profiling identify the miR-130a-SLC7A5 couple as a putative molecular switch in melanoma metastasis development

Castoldi E, Cagnin S, Sartorello F, Simioni P. **A specific genomic duplication in F8 gene is responsible for its overexpression.**

Martini P, De Palma S, Borsato C, Sales G, Vasso M, Salarioli R, Raffaello T, Romualdi C, Fanin M, Cenacchi G, Gelfi C, Angelini C, Lanfranchi G*, Cagnin S*.
Altered processes and protein modifications in patients affected by inflammatory myopathies: identification of ISG15 target proteins. * co-corresponding author

Contribution for a chapter of a Book titled "**Single-cell omics: technological advances and applications**" publised by Elsevier.

Communications

Alessio E, Chemello F, Grespi F, Buson L, Martini P, Pacchioni B, Millino C, Romualdi C, Massimino M, Bertoli A, Sandri M, Lanfranchi G, **Cagnin S Long non-coding RNAs modulate mitochondria morphology and functionality in skeletal muscle** (2017) Advances in Skeletal Muscle Biology in Health and Disease, Gainesville, FL, USA.

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