

CURRICULUM VITAE

December, 2013

NAME Danilo Licastro

Italian Citizen

Born March 11, 1979, **Vibo Valentia**, Italy

Cluster in Biomedicine - CBM S.c.r.l.

AREA Science Park, s.s. 14 km 163.5 –

Basovizza - 34149 Trieste (Italy)

Phone +39 040 3757720; mobile +39 348 0105567

Email: danilo.licastro@cbm.fvg.it; danilo.licastro@gmail.com

EDUCATION

2003 Master Degree in Biotechnology Sciences, *Summa Cum Laude*
University of Bologna *Alma Mater Studiorum*

2008 PhD in Molecular Medicine,
University of Trieste (Italy) Department of Biochemistry,
Biophysics and Macromolecular Chemistry Jointly with Burlo
Garofolo Hospital, Trieste, Italy

RESEARCH AND PROFESSIONAL EXPERIENCE

2002-2003 **Internship** at the LNCIB Laboratory, Trieste, Italy Italy.
Research in cDNA library production and cDNA spotted slide.
Thesis title (translated from Italian): “Human transcriptome
analysis: Genes Discovery of new un-annotated genes”
Supervisor: Prof Giuliano Della Valle (University of Bologna).
Co-Supervisor: Prof Claudio Schneider (University of Udine).

2003-2004 **Pre-doctoral Fellow** at the Functional and Structural Genomics
Unit of LNCIB Laboratory, AREA Science Park, Trieste, Italy.
Research topic: Molecular Biology and gene expression study;
Construction and analysis of human cDNA library; Gene
expression study with Microarray Analysis.
Supervisor: Prof Claudio Schneider (University of Udine)

2005-2008 **PhD student** at the Department of Biochemistry, Biophysics and
Macromolecular Chemistry of the University of Trieste (Italy),
Jointly with Burlo Garofolo Hospital, Trieste, Italy. Research
activities: Study of the gene expression with multiple platforms;
Development of primary culture from mouse embryo inner ear.
Supervisor: Prof. Paolo Gasparini

- 2008- 2009 **Genomics Specialist**, Cluster in Biomedicine (CBM), AREA Science Park, Trieste, Italy. Main activity: Illumina and Combimatrix Gene Expression service.
- 2009-2011 **Genomics Specialist**, Cluster in Biomedicine (CBM), AREA Science Park, Trieste, Italy. Main activity: Illumina and SOLiD High-throughput sequencing service
- 2012-present **Genomic Core Facility Manager**, Cluster in Biomedicine (CBM), AREA Science Park, Trieste, Italy. Main activity: High-throughput sequencing and Genotyping services.
- 2009-2013 **Lecturer** at the University of Trieste. Teaching activity: course of “Transcriptomics” (24 hrs) for the master degree in Functional Genomics.

TRAINING AND COURSES

Attendance to the following courses and meetings:

- May 2005 Microarrays Agilent Demo training
Agilent Technologies, Waldbronn, Germany
- July 2006 CombiMatrix Technology Symposium
CombiMatrix Corporation, Mukilteo, WA, USA
- Sept 2006 Genome Informatics Meeting
Cold Spring Harbor Laboratory/Wellcome Trust Joint Meeting on
Genome Informatics, Hinxton, UK
- Oct 2006 Affimetrix Gene Expression Training
Cluster in Biomedicine (CBM), AREA Science Park, Trieste, Italy
- August 2006, February 2007, April 2007
Illumina Genotyping Goldengate and Infinium Training; Illumina
Gene Expression Direct Hyb and DASL Training
Cluster in Biomedicine (CBM), AREA Science Park, Trieste, Italy
- Dec 2007 CustomArray Synthesizer operator training and quality control
testing. CombiMatrix Corporation
Burlo Garofolo Hospital, Trieste, Italy
- Feb 2009 Application workshop SOLiD in Action
Applied Biosystems, European Training Center, Darmstadt,
Germany
- June 2010 SOLiD Instrument and software Training

Applied Biosystems, European Training Center, Darmstadt, Germany

July 2012 Bioinformatics and biostatistic course
CSAMA 2012 (Computational Statistics for Genome Biology)
Brixen-Bressanone, Italy

2008, 2009, 2010, 2011
Illumina User Meetings, Illumina Inc.

SKILLS AND COMPETENCES

Scientific background: molecular and cell biology, human genetics, genomics, gene expression and next-generation sequencing analyses.

Technical competences: PCR, RT-PCR, qPCR; RNA/DNA Extraction and purification, Bioanalyzer RNA/DNA quality control; Southern, Northern and Western blotting; Plasmids preparation and cloning; Sequencing with ABI PRISM 3700 Sanger Sequence Analysis; Production of cDNA Microarrays slides, Hybridization; Embryo tissue dissection, Primary Cell culture, Transient Transfections, Immunofluorescence, RNA In situ Hybridization; Illumina gene expression and genotyping protocols, Affymetrix gene expression protocols, Combimatrix array protocols; SOLiD fragment library preparation, sequencing and analyses; Illumina Pair-end library preparation (TrueSeq protocol with or without exome-enrichment, Nextera protocol), sequencing and analyses. NGS Bioinformatic analyses: mapping, variant calling, splice-junction finding, CNV detection, RNAseq analysis.

Computer skills: Competent with PC and Macintosh computer
Operative Systems: Linux (Debian and Ubuntu distro), Windows, MacOS9.x, MacOSX.
Languages, Servers and Databases: Perl, BASH, R, MySQL, PostgreSQL.
API: BioPerl, Ensembl, DBI.
Microarray Analysis Software: BioConductor, BeadArray Studio, TMEV.
Sequence Analysis Software: BioConductor, Bioscope Suite, Casava, Bowtie, BWA, MAQ, Rsubread, GATK.

EDUCATIONAL ACTIVITIES

Lecturer at the University of Trieste, Italy, from 2009.
Course of “Transcriptomics” (24 hrs) for the Master Degree in Functional Genomics.

Instructor at the Burlo Garofolo Hospital, Trieste, Italy.

“Corso teorico-pratico di Microarray”, September 2009

PUBLICATIONS

1. LNCIB human full-length cDNAs collection: towards a better comprehension of the human transcriptome.
Dalla E, Verardo R, Lazarević D, Marchionni L, Reid JF, Bahar N, Klarić E, Marcuzzi G, Marzio R, Belgrano A, **Licastro D**, Schneider C.
C R Biol. 2003 Oct-Nov;326(10-11):967-70.
2. Discovery of 342 putative new genes from the analysis of 5'-end-sequenced full-length-enriched cDNA human transcripts.
Dalla E, Mignone F, Verardo R, Marchionni L, Marzinotto S, Lazarević D, Reid JF, Marzio R, Klarić E, **Licastro D**, Marcuzzi G, Gambetta R, Pierotti MA, Pesole G, Schneider C.
Genomics. 2005 Jun;85(6):739-51.
3. Vezatin, an integral membrane protein of adherens junctions, is required for the sound resilience of cochlear hair cells.
Bahloul A, Simmler MC, Michel V, Leibovici M, Perfettini I, Roux I, Weil D, Nouaille S, Zuo J, Zadro C, **Licastro D**, Gasparini P, Avan P, Hardelin JP, Petit C.
EMBO Mol Med. 2009 May;1(2):125-38.
4. Mixed lineage kinase 3 gene mutations in mismatch repair deficient gastrointestinal tumours.
Velho S, Oliveira C, Paredes J, Sousa S, Leite M, Matos P, Milanezi F, Ribeiro AS, Mendes N, **Licastro D**, Karhu A, Oliveira MJ, Ligtenberg M, Hamelin R, Carneiro F, Lindblom A, Peltomaki P, Castedo S, Schwartz S Jr, Jordan P, Aaltonen LA, Hofstra RM, Suriano G, Stupka E, Fialho AM, Seruca R.
Hum Mol Genet. 2010 Feb 15;19(4):697-706.
5. Promiscuity of enhancer, coding and non-coding transcription functions in ultraconserved elements.
Licastro D, Gennarino VA, Petrera F, Sanges R, Banfi S, Stupka E.
BMC Genomics. 2010 Mar 4;11:151.
6. Molecular epidemiology of Usher syndrome in Italy.
Vozzi D, Aaspõllu A, Athanasakis E, Berto A, Fabretto A, **Licastro D**, Külm M, Testa F, Trevisi P, Vahter M, Ziviello C, Martini A, Simonelli F, Banfi S, Gasparini P.
Mol Vis. 2011;17:1662-8. Epub 2011 Jun 22.

7. Transcription initiation arising from E-cadherin/CDH1 intron2: a novel protein isoform that increases gastric cancer cell invasion and angiogenesis. Pinheiro H, Carvalho J, Oliveira P, Ferreira D, Pinto MT, Osório H, **Licastro D**, Bordeira-Carriço R, Jordan P, Lazarevic D, Sanges R, Stupka E, Huntsman D, Seruca R, Oliveira C. Hum Mol Genet. 2012 Jul 11.
8. Molecular diagnosis of usher syndrome: application of two different next generation sequencing-based procedures. **Licastro D**, Mutarelli M, Peluso I, Neveling K, Wieskamp N, Rispoli R, Vozzi D, Athanasakis E, D'Eustacchio A, Pizzo M, D'Amico F, Ziviello C, Simonelli F, Fabretto A, Scheffer H, Gasparini P, Banfi S, Nigro V. PLoS One. 2012;7(8):e43799. Epub 2012 Aug 29.
9. Epigenetic Regulation of Survivin by Bmi1 is Cell Type Specific During Corticogenesis and in Gliomas. Acquati S, Greco A, **Licastro D**, Bhagat H, Ceric D, Rossini Z, Grieve J, Shaked-Rabi M, Henriquez NV, Brandner S, Stupka E, Marino S. Stem Cells. 2012 Nov 6.
10. Alagille Syndrome: a new missense mutation detected by whole-exome sequencing in a case previously found to be negative by dHPLC and MLPA. Vozzi D, **Licastro D**, Martellosi S, Athanasakis E, Gasparini P, Fabretto A. Molecular Syndromology, 2013 Apr 4.
11. Highly conserved elements discovered in vertebrates are present in non-syntenic loci of tunicates, act as enhancers and can be transcribed during development. Sanges R, Hadzhiev Y, Roure A, Ferg M, Meola N, Amore G, Basu S, Brown E, De Simone M, Petrera F, **Licastro D**, Strähle U, Banfi S, Lemaire P, Birney E, Müller F, Stupka E. NAR, 2013 Feb 7.
12. Overexpression of facioscapulohumeral muscular dystrophy region gene 1 causes primary defects in myogenic stem cells. Xynos A, Neguembor MV, Onorati MC, **Licastro D**, Picozzi P, Bortolanza S, Caccia R, Godio C, Pistoni M, Cabianca DS, Stupka E, Corona DF, Schotta G, Gabellini D. J of Cell Science, 2013 May 15.
13. Next Generation Sequencing in Nonsyndromic Intellectual Disability: from a Negative Molecular Karyotype to a Possible Causative Mutation Detection. Athanasakis E*, **Licastro D***, Faletra F, Fabretto A, Dipresa S, Vozzi D, D'Adamo P, Pecile V, Gasparini P.
*These authors contributed equally to the work
American Journal of Medical Genetics, Accepted August 30, 2013.

14. Treatment of cultured cells with serum collected from humans on long-term calorie restriction enhances stress resistance in vitro
Daniela Omodei^{1,2*}, **Danilo Licastro**^{3*}, Franco Salvatore², Seth D. Crosby⁴, Luigi Fontana.
*These authors contributed equally to the work
AGING. Accepted July 22, 2013.
15. Linkage study and Exome sequencing identify BDP1 as a new gene causing Hereditary Hearing Loss. Giorgia Giroto; Khalid Abdulhadi; Annalisa Buniello; Diego Vozzi; **Danilo Licastro**; Angela d'Eustacchio; Dragana Vuckovic; Moza Khalifa Alkowari; Karen P. Steel; Ramin Badii; Paolo Gasparini.
PLoS One, Accepted October 10, 2013.
16. Dissecting the signaling pathways associated with the oncogenic activity of MLK3 P252H mutation. Velho S, Pinto A, **Licastro D**, Oliveira M, Sousa F, Stupka E, Seruca R.
BMC Cancer, *submitted*
17. Bmi1 enhances skeletal muscle regeneration through Mt1 mediated oxidative stress protection. Valentina Di Foggia, Xinyu Zhang, Rahul Phadke, Francesco Muntoni, **Danilo Licastro**, Sharagim Tajbakhsh, Giulio Cossu, Lesley G. Robson and Silvia Marino.
Developmental Cell, *submitted*

References

Sandro Banfi, MD

Associate Investigator

TIGEM

Telethon Institute of Genetics and Medicine

Via Pietro Castellino 111

80131 Naples

Italy

E-mail: banfi@tigem.it

Elia Stupka, B.Sc. M.Res. Ph.D.

Co-Director and Head of Unit

Center for Translational Genomics and Bioinformatics

San Raffaele Scientific Institute

Via Olgettina 58

20132 Milano

Italy

E-mail: stupka.elia@hsr.it

Luigi Fontana, MD, PhD

Professor of Nutritional Sciences

Department of Medicine
Salerno University School of Medicine
Via Allende 84081 Baronissi (SA) Italy
E-mail: lufontana@unisa.it

and

Department of Internal Medicine
Division of Geriatrics and Nutritional Sciences
Center of Human Nutrition
Washington University
660 S.Euclid Ave. - Campus Box 8113
St.Louis, MO 63110-1093
E-mail: lfontana@dom.wustl.edu

Germana Meroni

Group leader of Functional Genomics Lab.
Cluster in Biomedicine CBM S.c.r.l.
AREA SCIENCE PARK
Basovizza - SS 14, Km. 163,5
34012 TRIESTE (ITALY)
E-mail: germana.meroni@cbm.fvg.it