

# ALESSANDRO LAGANÀ

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## RESEARCH EXPERIENCE

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**The Ohio State University Comprehensive Cancer Center** 2010 - Present  
*Post-Doctoral Researcher, Prof. Croce's Lab* Columbus, OH

- Development and application of computational tools and databases for the study of microRNAs and other non-coding RNAs in cancer.
- Analysis of microRNA, piRNA and gene expression profiles from RNA-Seq (Illumina and SOLiD), Nanostring and Microarray data.
- Development of a computational tool for the design of multi-site multi-target artificial microRNAs for cancer therapy.
- Discovery and characterization of novel microRNAs and other non-coding RNAs by using deep sequencing data.
- Computational and statistical analysis for the investigation of the incidence of non-coding RNAs in genomic unstable regions such as fragile sites and translocation breakpoints and their involvement in cancer.
- Development of a web based knowledge base for functional analysis and annotation of microRNAs.
- Development of a web database of predicted A-to-I edited microRNA binding sites.

**University of Catania** 2010  
*Post-Doctoral Researcher* Catania, Italy

- Development of a computational tool for microRNA target prediction.
- Computational and statistical analysis for the investigation of the incidence of microRNAs and protein coding genes in fragile sites and the role of repeats and CpG islands in the distribution of genetic material.

## EDUCATION

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**University of Catania, Italy** November 2009  
Ph.D. in Biology, Human Genetics and Bioinformatics  
Thesis: Data Mining on RNA sequence and structure with applications to RNA interference, synthetic biology and viral RNAs

**University of Catania, Italy** July 2004  
M.S. in Computer Science  
Thesis: High-precision multiple sequence alignment and its biological applications

## CONTINUING EDUCATION

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- The Foundation for Advanced Education in the Sciences, Inc. at the National Institutes of Health TRAC45W: *Bioinformatics Analysis of Next Generation Sequencing Data*, July 9-12 2013 (1 Credit, 28 Lecture/Lab Hours).  
Topics covered: DNA-seq and Variation Calling, Transcriptome Analysis, Epigenomics, RNA-seq, CHIP-seq, Downstream analysis of RNA-seq and CHIP-seq Data, The Tuxedo Package for RNA-seq, Galaxy, de Novo Assembly, Hybrid Mapping, The SRA Toolkit, 1000 Genomes, Statistical Analysis of NGS Data.

## PUBLICATIONS

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- F. Russo, S. Di Bella, V. Bonnici, **A. Laganà**, G. Rainaldi, M. Pellegrini, A. Pulvirenti, R. Giugno, A. Ferro. A knowledge base for the discovery of function, diagnostic potential and drug effects on cellular and extracellular miRNAs. *BMC Genomics* 2014; 15(Suppl 3):S4.
- **A. Laganà**, M. Acunzo, G. Romano, A. Pulvirenti, D. Veneziano, L. Cascione, R. Giugno, P. Gasparini, D. Shasha, A. Ferro, C. M. Croce. miR-Synth: a computational resource for the design of multi-site multi-target synthetic miRNAs. *Nucleic Acids Res* 2014; doi:10.1093/nar/gku202.
- P. Nasarre, R. M. Gemmill, V. A. Potiron, J. Roche, X. Lu, A. E. Baron, C. Korch, E. Garrett-Mayer, **A. Laganà**, P. H. Howe, H. A. Drabkin. Neuropilin-2 is upregulated in lung cancer cells during TGF1-induced epithelialmesenchymal transition. *Cancer Res* 2013; 73(23):7111-7121.
- **A. Laganà**, F. Russo, D. Veneziano, S. Di Bella, A. Pulvirenti, R. Giugno, C. M. Croce, A. Ferro. Extracellular circulating viral microRNAs: current knowledge and perspectives. *Frontiers in Genetics* 2013; 4:120.
- M. Acunzo, G. Romano, D. Palmieri, **A. Laganà**, M. Garofalo, V. Balatti, A. Drusco, M. Chiariello, P. Nana-Sinkam, C. M. Croce. Cross-talk between MET and EGFR in non-small cell lung cancer involves miR-27a and Sprouty2. *Proc Natl Acad Sci U S A* 2013; 110(21):8573-8578.
- F. Pichiorri, D. Palmieri, L. De Luca, J. Consiglio, J. You, A. Rocci, T. Talabere, C. Piovan, **A. Laganà**, L. Cascione, J. Guan, P. Gasparini, V. Balatti, G. Nuovo, V. Coppola, C. C. Hofmeister, G. Marcucci, J. C. Byrd, S. Volinia, C. L. Shapiro, M. A. Freitas, C. M. Croce. In vivo NCL targeting affects breast cancer aggressiveness through miRNA regulation. *J Exp Med* 2013; 210(5):951-68.
- N. Zanesi, V. Balatti, J. Riordan, A. Burch, L. Rizzotto, A. Palamarchuk, L. Cascione, **A. Laganà**, A. J. Dupuy, C. M. Croce, Y. Pekarsky. A Sleeping Beauty screen reveals NF-kB activation in CLL mouse model. *Blood* 2013; 121(21):4355-4358.
- V. Manfé, E. Biskup, A. Willumsgaard, A. G. Skov, D. Palmieri, P. Gasparini, **A. Laganà**, A. Woetmann, N. Odum, C. M. Croce, R. Gniadecki. cMyc/miR-125b-5p Signalling Determines Sensitivity to Bortezomib in Preclinical Model of Cutaneous T-Cell Lymphomas. *PLoS ONE* 2013; 8(3): e59390.
- R. Distefano, G. Nigita, V. Macca, **A. Laganà**, R. Giugno, A. Pulvirenti, A. Ferro. VIRGO: visualization of A-to-I RNA editing sites in genomic sequences. *BMC Bioinformatics* 2013; 14(Suppl 7): S5.
- L. Cascione, A. Ferro, R. Giugno, **A. Laganà**, G. Pigola, A. Pulvirenti, D. Veneziano. Elucidating the Role of microRNAs in Cancer Through Data Mining Techniques. *Adv Exp Med Biol* 2013; 774: 291-315.
- **A. Laganà**, R. Giugno, A. Pulvirenti, A. Ferro. Computational Approaches to RNAi and Gene Silencing. In *From Linear Operators to Computational Biology: Essays in Memory of Jacob T. Schwartz* 2013; 169-194. Editors: Martin Davis, Edmond Schonberg.
- F. Russo, S. Di Bella, G. Nigita, V. Macca, **A. Laganà**, R. Giugno, A. Pulvirenti, A. Ferro. miRandola: Extracellular Circulating MicroRNAs Database. *PLoS ONE* 2012; 7(10): e47786.
- **A. Laganà**, A. Paone, D. Veneziano, L. Cascione, P. Gasparini, S. Carasi, F. Russo, G. Nigita, V. Macca, R. Giugno, A. Pulvirenti, D. Shasha, A. Ferro, C. M. Croce. miR-EdiTar: A database of predicted A-to-I edited miRNA target sites. *Bioinformatics* 2012; 28(23): 3166-3168.
- P. Ranganathan, C. E. Heaphy, S. Costinean, N. Stauffer, C. Na, M. Hamadani, R. Santhanam, C. Mao, P. A. Taylor, S. Sandhu, G. He, A. Shana'ah, G. J. Nuovo, **A. Laganà**, L. Cascione, S. Obad, O. Broom, S. Kauppinen, J. C. Byrd, M. Caligiuri, D. Perrotti, G. A. Hadley, G. Marcucci, S. M. Devine, B. R. Blazar, C. M. Croce, R. Garzon. Regulation of acute graft-versus-host disease by microRNA-155. *Blood* 2012; 119(20): 4786-4797.

- **A. Laganà**, F. Russo, C. Sismeiro, R. Giugno, A. Pulvirenti, A. Ferro. Variability in the Incidence of miRNAs and Genes in Fragile Sites and the Role of Repeats and CpG Islands in the Distribution of Genetic Material. *PLoS ONE* 2010; 5(6): e11166.
- **A. Laganà**, S. Forte, F. Russo, R. Giugno, A. Pulvirenti, A. Ferro. Prediction of human targets for viral-encoded microRNAs by thermodynamics and empirical constraints. *Journal of RNAi and Gene Silencing* 2010; 6(1): 379-385.
- **A. Laganà**, S. Forte, A. Giudice, M. R. Arena, P. L. Puglisi, R. Giugno, A. Pulvirenti, D. Shasha, A. Ferro. miRò: a miRNA knowledge base. *Database* 2009; Vol. 2009, bap008.
- V. Svicher, C. Alteri, R. D'Arrigo, **A. Laganà**, M. Trignetti, S. Lo Caputo, A. P. Callegaro, F. Maggiolo, F. Mazzotta, A. Ferro, S. Dimonte, S. Aquaro, G. di Perri, S. Bonora, C. Tommasi, M. P. Trotta, P. Narciso, A. Antinori, C. F. Perno, F. Ceccherini-Silberstein. The Treatment with the Fusion Inhibitor Enfuvirtide Influences the Appearance of Mutations in the HIV-1 Regulatory Protein Rev. *Antimicrobial Agents and Chemotherapy* 2009; 53(7): 2816-2823.
- C. Di Pietro, M. Ragusa, D. Barbagallo, L. R. Duro, M. R. Guglielmino, A. Majorana V. Giunta, A. Rapisarda, E. Tricarichi, M. Miceli, R. Angelica, A. Grillo, B. Banelli, I. Defferari, S. Forte, **A. Laganà**, C. Bosco, R. Giugno, A. Pulvirenti, A. Ferro, K. H. Grzeschik, A. Di Cataldo, G. P. Tonini, M. Romani, M. Purrello. Involvement of GTA protein NC2beta in Neuroblastoma pathogenesis suggests that it physiologically participates in the regulation of cell proliferation. *Molecular Cancer* 2008; 7:52.
- S. Forte, S. Scarpulla, **A. Laganà**, L. Memeo, M. Gulisano. Gene Expression Analysis for the Identification of Genes Involved in Early Tumour Development. *Proceedings of the 15th International Workshops on Conceptual Structures ICCS 2007*. Sheffield Hallam University, Sheffield UK, July 22-27, 2007; 62-68. Ed. Springer-Verlag.
- C. Di Pietro, M. Ragusa, L. Duro, M. R. Guglielmino, D. Barbagallo, A. Carnemolla, **A. Laganà**, P. Buffa, R. Angelica, A. Rinaldi, M. S. Calafato, I. Milicia, C. Caserta, R. Giugno, A. Pulvirenti, V. Giunta, A. Rapisarda, V. Di Pietro, A. Grillo, A. Messina, A. Ferro, K. H. Grzeschik, M. Purrello. Genomics, Evolution and Expression of TBPL2, a Member of the TBP Family. *DNA and Cell Biology* 2007; 26(6): 369-385.

## SPEAKING ENGAGEMENTS AND TEACHING EXPERIENCE

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- Speaker, BITS 2010 - Bioinformatics Italian Society Meeting. Bari, Italy, April 14-16 2010.
- Teaching assistant, Course: Bioinformatics, Master's Degree Program in Computer Science, University of Catania, Italy, 2004-2010.
- Teaching assistant, Course: Biological Basis of Bioinformatics, Master's Degree Program in Computer Science, University of Catania, Italy, 2007-2008.
- Teaching assistant, Course: Introduction to Bioinformatics, Bachelor's Degree Program in Computer Science, University of Catania, Italy, 2004-2008.
- Co-Advisor, Master's and Bachelor's Degree Theses in Computer Science. University of Catania, Italy, 2004-2010.
- Speaker, NETTAB 2009 Ninth Annual Workshop *Network Tools and Applications in Biology*, Department of Mathematics and Computer Science, University of Catania, June 10-12 2009.
- Speaker, Lipari International School on Bioinformatics and Computational Biology. Lipari, Italy, July 2009.
- Speaker, BITS 2007 - Bioinformatics Italian Society Meeting. Napoli, Italy, April 26-28 2007.

## CONFERENCE ORGANIZATION

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- Member of the organizing committee, *NETTAB 2009 Ninth Annual Workshop Network Tools and Applications in Biology*, University of Catania, Department of Mathematics and Computer Science, June 10-12 2009.

## **ASSOCIATION MEMBERSHIP**

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- Member, Bioinformatics Italian Society (BITS).
- Member, Social Committee, The Ohio State University Post Doctoral Association.

## **JOURNAL REVIEWER**

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Bioinformatics, Briefings in Bioinformatics, Chromosome Research, Journal of Computational Science, Nucleic Acids Research, PLoS ONE.

## **TECHNICAL SKILLS**

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### **Operating Systems**

Linux, Mac OS X, Windows

### **Programming Languages**

C, C++, Java, Python, Perl, Ruby, R

### **Web Languages and Technologies**

HTML, CSS, Javascript, ASP.NET, JSP, PHP, Ruby on Rails

### **Databases**

MySQL

### **NGS Analysis Tools**

BWA, samtools, vcftools, bedtools, tabix, Picard tools, GATK, CASAVA, Bowtie, Tophat, Cufflinks, IGV, FastQC, MACS, muTect, VarScan, SomaticSniper

### **Other Analysis Tools**

WEKA, T-Mev, GenePattern, Ingenuity Pathway Analyzer

## **LANGUAGES**

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- Italian: Native
- English: Fluent, spoken and written