Curriculum Vitae Prof. Raffaele A. Calogero

CONTACT INFORMATION

Name: Raffaele A. Calogero
Date and place of birth: March 3, 1960, Torino (Italy).
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H-index: 36
Total citations (Scopus): 4967

EDUCATION

1984: Laurea in Biological Sciences summa cum laude from Naples University "Federico II" (Italy).
1984-1985: Post-degree training at Institute of Genetics, General and Molecular Biology (Naples University "Federico II").
1985-1988: Fellowship at Max Plank Institute fuer Molekulare Genetik, Berlin (Germany).

PROFESSIONAL EXPERIENCES

1989-1992: Researcher at SORIN Biomedica S.p.A. (I).
1992-1998: Associate Professor of Molecular Biology, at Naples University "Federico II".
1998-present: Associate Professor of Molecular Biology at University of Torino.

CONSULTANCY ACTIVITIES

2004-2008: Consultant for the microarray program (AXXAM S.r.l, Milano, I)
2005-2009: Consultant for the microarray program (Nerviano Medical Sciences S.r.l, Nerviano, MI, I)
2010-2013: Consultant for Next generation sequencing application in QC (RBM SERONO, IVREA, I)
2016-2019: Consultant for Next generation sequencing application Galderma R&D, France.
2017: Consultant for Next generation sequencing application S. Raffaele Hospital (Milan,I).

OTHER ACTIVITIES

2000-present Part of the Faculty of the PhD Program in Complex Systems, University of Torino.
2009-present Associated editor for BMC Bioinformatics.
2012-present Associated editor for PLOS ONE.
2017-present Member of the steering committee of the HPC C3S (c3s.unito.it) University of Torino.
2018-present: Representative for University of Torino at the General Assembly of Elixir Italian Node.
2019-present: Co-coordinator of Elixir IT single cell community.

INTERNATIONAL TRAINING COURSES

2002-2010: Introductory course on Microarray data analysis, supported by Affymetrix (University of Torino, Italy).
2013-present: Introductory and Advance course on RNAseq data Analysis, sponsored by Illumina (University of Torino, Italy).
2010-present: Whole transcriptome data analysis course (EMBL – Heidelberg, Germany). Since 2016 the course doubled for high requests and it is run in spring and autumn.
2014: RNAseq data analysis course (Jagiellonian University Medical College, Krakow, Poland)
2015-present: Analysis and Integration of Transcriptome and Proteome Data course (EMBL – Heidelberg, Germany)
2015-present: Whole transcriptome data analysis course (DUKE-NUS – Singapore, Singapore)
2018: Whole transcriptome data analysis course (IIT – Genova, Italy)
2019: Single-cell Omics EMBO course (EMBL – Heidelberg, Germany)

RESEARCH INTERESTS

My research experience was devoted to the development and optimization of analysis workflows and in mining transcription-based experiments, mainly in the oncology framework. An important aspect of my past and present work was the constant focus on new technologies (e.g. today single-cell and single-molecule sequencing) and their integration in our analysis workflows.

I started my journey in Bioinformatics in latest 90's when I developed a tool to simulate, for windows-based PCs, a molecular biology laboratory (Iazzetti, et al., 1998). My tool was used for at least a decade at University of Naples "Federico II" first and then in high schools to train students in the basic concepts of molecular biology laboratory practice.

In 1998 I established at University of Torino the Genomics and Bioinformatics unit (B&Gu). B&Gu is an interdisciplinary group devoted to the study of multifactorial diseases by mean of high throughput technologies - i.e. microarray, Next Generation Sequencing – and bioinformatics. Since then my interests moved to research topics in which computational approaches could be used to mine biological data (Accardo, et al., 2004; Iazzetti, et al., 1998; Lazzarato, et al., 2004; Olivero, et al., 2003; Ruggiero, et al., 2003). Those years were the period in which expression microarrays started to be an effective tool to investigate genes involved in diseases and general biological processes. I was involved in various studies in which microarray data analysis played an important role (Astolfi, et al., 2005; Calogero, et al., 2004; Cicatiello, et al., 2004; Quaglino, et al., 2004). In collaboration with the group of cancer immunologists leaded by Prof. Forni at University of Torino, I focused the work of my group on the identification of new targets for anti-tumor vaccination protocols (Calogero, et al., 2007; Calogero, et al., 2008; Cavallo, et al., 2005; Cavallo, et al., 2007). Because of my experience in microarray data analysis, my group was involved in a large number of collaborations in Italy and abroad (Berkofsky-Fessler, et al., 2010; Bosotti, et al., 2007; Murphy, et al., 2007; Sassano, et al., 2009; Saviozzi, et al., 2009; Spugnini, et al., 2006; Volante, et al., 2007). It is notable that, using gene expression microarrays, we were able to identify for the first time the presence of coding transcripts in circulating blood vesicles (Bruno, et al., 2009; Deregibus, et al., 2007; Herrera, et al., 2010), today a very hot topic in the field of biomarker discovery.

Since I started my research career as molecular biologist, I am convinced that genomics/transcriptomics data analysis, at least to some extent, should be placed back in the hands of wet biologists, thus it is more than a decade that I am involved in training of PhD and Post-docs in the transcriptomics field, running courses at University of Naples first, then at University of Turin (Sponsored by Affimetrix first and later by Illumina), at EMBL-Heidelberg, DUKE-NUS in Singapore and Italian Institute of Technology in Genova. Thus, with my group I have developed tools to simplify data analysis for microarray first (Sanges, et al., 2007) and then for Next generation sequencing (Beccuti, et al., 2017; Beccuti, et al., 2018). I am also the cofounder of the Reproducible Bioinformatics Project, a community of bioinformaticians aiming to the creation of easy to use and reproducible bioinformatics workflows (http://www.reproducible-bioinformatics.org/).

GRANTS

2012-2018 EPIGEN project, Bioinformatics work package. Research unit PI (200,000€).

2013-2015 Next Generation Sequencing platform for targeted Personalized Therapy of Leukemia (FP7-HEALTH-2012-INNOVATION-1) Responsible of work package (540,000 €).

2008-2010 Oncoantigens and microenvironment perturbation as a new antitumor vaccine strategy for inhibition of cancer (Italian Research program PRIN 2008) Research unit PI (64,000€).

2006-2009 Pipeline for Rapid Evaluation and Scoring of Targets in Oncology (Piedmont Region industrial research call CIPE 2006) Research unit PI (80,000€).

2006-2009 Innovative approaches to anticipate the diagnosis and to target therapies of colorectal cancer (AIRC Regione Piemonte 2006) Research unit PI (45,000€).

2006-2008 An integrated Bioinformatics and Genomics approach for oncoantigens identification (PRIN 2006) Research unit PI (65,000€).

2004-2006 Identification of new targets for the immunoprevention of cancer (Piedmont Region industrial research call CIPE 2004) Responsible of work package (80,000€).

2003-2005 Definition of gene expression profiles and prognostic predictors of response to endocrine therapy for breast cancer (Program for Health Science Italy 2003) Research unit PI (25,000€).

2002-2003 Isolation and functional characterization of p63 ligands involved in Hay-Wells Syndrome (AEC). (PRIN 2002) Research unit PI (35,000€).

2001-2002 Identification of p63 specific target genes by p63 isoforms-mediated transcriptional profiling. (PRIN 2001) Research unit PI (52,000€).

2001-2003 Design and construction of expression vectors based on the translational reinitiation process (Progetto Finalizzato CNR 2001) Research unit PI (10,000€).

2001-2003 Improvement of the quality and quantity of production in horticulture and fruit: contribution of parthenocarpic fruit development and improvement of fertility, with genetic engineering techniques, a variety

cultivated tomato, eggplant, strawberry, raspberry, table grape, tangerine and lemon (FIRB 2001) Research unit PI (60,000€).

PATENT	TITLE	TYPE	YEAR	ROLE
TO2015000088.978	Molecole di acidi nucleici codificanti proteine chimeriche CSPG4 e relativi usi terapeutici	Italian/filed to Europe 2018	2015	coauthor
TO20100020	Costrutto di acido nucleico, vettore e vaccino a DNA includenti detto costrutto	Italian	2011	coauthor
TO20100028	Costrutto di acido nucleico, vettore e vaccino a DNA includenti detto costrutto	Italian	2011	coauthor
EP0571337 B1	Process to purify proteins from cell systems	European	1993	coauthor
EP0485347 A3	Recombinant hepatitis delta antigen, process for the purification and use thereof	European	1992	coauthor

HOBBIES
Kendo 4th Dan.
Kendo blogger (http://kendodream.blogspot.it/ ; http://www.youtube.com/user/kendomaniac)
Learning Japanese language: level beginner.