

Curriculum Vitae - REMO SANGES, PhD

EDUCATION ACTIVITY

1 October 2006 – 31 January 2007 EBI "European Bioinformatics Institute", Hinxton, UK, - Marie Curie Fellow in the Ensembl Team

Isolation, analysis and characterization of "conserved non-coding sequences" in chordate genomes.

1 May 2004 – 30 June 2004 TLL "Temasek Life Sciences Laboratory", Singapore, - Visiting Fellow in the Fugu Genome Project Team

Parallelization and optimization of the code written for analysis of "conserved non-coding sequences" in vertebrate genomes.

1 November 2002 – 21 December 2006, 2nd University of Naples, Italy - Ph. D. student in "Computational Biology"

Large scale analysis of gene expression during development. Isolation, analysis and characterization of "conserved non-coding sequences" in vertebrate genomes.

1 March 2001 – 30 November 2001, IGB "Adriano Buzzati Traverso", Naples, Italy - post-lauream practice

Proteomic and transcriptomic studies about cellular response to the oxidative stress.

1 November 1996 – 26 February 2001, University "Federico II", Naples, Italy - Biology BSc. Degree magna cum laude

Thesis in Genetics entitled: "DHRXY: identification and characterization of a novel human gene and its murine orthologue" under the supervision of Dr. Michele D'Urso.

EMPLOYMENT

1 March 2010 – ongoing, Stazione Zoologica Anton Dohrn, Naples, Italy – Researcher ("Primo Ricercatore" permanent position)

Principal Investigator of the bioinformatics Lab.

Director of 3 PhD students.

Co-coordinator of 3 funded projects "premiati" about: Metagenomics and the de-novo definition of marine organisms genomes and transcriptomes.

Participant in the "Fragilariopsis cylindrus genome project".

Leader for SZN in the WP3 of the ESFR1 project EMBC: European Marine Biological Resource Centre (<http://www.embrc.eu/>).

Member of the Technical Coordination Committee in the EU project BiMedBridges (<http://www.biomedbridges.eu/>).

1 April 2009 – 28 February 2010, CBM "Cluster in BioMedicine", Trieste, Italy – Head of Bioinformatics (permanent position)

Responsible of the bioinformatics facility and of the bioinformatics research.

Leader for CBM in the FP7 project DOPAMINET; Molecular Networks of Dopaminergic Neurons in Chordates (<http://www.dopaminet.eu>).

Manager of a team of 4 bioinformaticians, of which 3 postdocs.

1 July 2008 – 31 March 2009, CBM "Cluster in BioMedicine", Trieste, Italy - Bioinformatics Specialist (permanent position)

Responsible of the bioinformatics facility. Microarrays, functional genomics, data mining and next generation sequencing data analysis. Lead a bioinformatics team involved in data analysis for services as well as for intramural research. In December 2008 the team obtained the compliance to the requirements of UNI EN ISO 9001 to design and supply bioinformatics analysis.

1 July 2006 – 31 June 2008, CBM "Cluster in BioMedicine", Trieste, Italy - Bioinformatics Postdoc

Analysis and design of pipelines to understand the functions, organization and evolution of non-coding elements. Data analysis and mining of gene expression profiles.

1 December 2004 – 30 June 2006, TIGEM "Telethon Institute of Genetics and Medicine", Naples, Italy - Bioinformatics Scientist

Analysis and design of pipelines to shed light on the functions and organization of "conserved non-coding sequences" and their involvement in transcriptional regulation.

1 December 2001 – 30 November 2004, BioGem "Biotechnology and Molecular Genetics in Southern Italy", Naples, Italy - Bioinformatics Programmer

In the "Gene Expression and Sequencing Core Lab" lead a bioinformatics team involved in the analysis of gene expression data and the analysis and annotation of ESTs libraries.

TEACHING

- December 2002, March 2003, June 2003, December 2003 – Teacher in the "Microarray's Techniques" at Second University of Naples in collaboration with TIGEM and MWG Biotech.
- June and July 2003 – Teacher in the "Microarray data analysis and mining II" at University of Naples Federico II in collaboration with University of Turin, BioGem and Affymetrix.
- September 2003 – Teacher in the "Bioinformatics fundamentals" course at Istituto Superiore di Sanità in Rome in collaboration with Prof. Michele Muscillo.
- October 2003 – Teacher in the "Microarray data analysis course" at University of Turin in collaboration with University of Naples, BioGem and Affymetrix.
- March 2004 – Teacher in the "Microarray data analysis and statistical validation" at University of Turin in collaboration with University of Naples, BioGem and Affymetrix.
- October 2004, October 2005, October 2010 – Teacher in the "Perl for biologists" course at CINECA in Bologna in collaboration with Dr. Andrew Emerson.
- October 2004 – Teacher in the "First Bioperl Workshop" at CEINGE in Naples in collaboration with Dr. Elia Stupka and Dr. Jason Stajich.
- December 2006 – Teacher in the "Data Analysis at Gene Level" course at AFFYMETRIX, High Wycombe, UK, in collaboration with AFFYMETRIX and Stratagene.
- March 2007 – Teacher in the "Data Analysis at Gene Level II" course at AFFYMETRIX, Santa Clara, CA 95051, USA, in collaboration with AFFYMETRIX.
- November 2008, December 2009 – Teacher in the "Practical data EXON 1.0 ST arrays analysis" course at University of Turin in collaboration with Prof. Raffaele Calogero.
- April, May, June 2009 - Assistant Professor of the "Trascrittomics" course inside the "Functional Genomics" degree at the University of Trieste.

SELECTED COMMUNICATIONS

- **Remo Sanges, Pedro Cruz, Vincenza Maselli, Elia Stupka.**
Analysis of long-range interspecies sequences: evidence for inter-phylum conservation of regulatory modules.
Genome Informatics 2004, Joint Cold Spring Harbor Laboratory/Wellcome Trust Conference, Wellcome Trust Genome Campus, Hinxton, UK, September 2004. Selected for oral presentation.
- **Remo Sanges, Elia Stupka.**
The importance of being intron: lessons from conserved non-coding sequences
2nd ESF Functional Genomics Conference, Oslo, Norway, September 2005. Selected for oral presentation.
- **Remo Sanges, Elia Stupka.**
Fragmentation and mobility of conserved non-coding sequences (CNSs) in vertebrate genomes.
Genome Informatics 2005, Joint Cold Spring Harbor Laboratory/Wellcome Trust Conference, Cold Spring Harbor, USA, October 2005. Abstract and poster.
- **Remo Sanges, Eva Kalmar, Pamela Claudiani, Maria D'Amato, Ferenc Mueller and Elia Stupka.**
Identification of shuffled conserved elements (SCEs) reveals much greater extent of functional conservation among vertebrate genomes than previously observed.
System biology: global regulation of gene expression, Cold Spring Harbor, USA, March 2006. Abstract and poster.
- **Remo Sanges, Eva Kalmar, Pamela Claudiani, Maria D'Amato, Ferenc Muller and Elia Stupka**
Shuffling of cis-regulatory elements is a pervasive feature of the vertebrate lineage
Genome Informatics 2006, Cold Spring Harbor Laboratory Meetings - The Wellcome Trust Conference Centre, Hinxton, September 2006. Selected for oral presentation.
- **Daniilo Licastro, Alessandro Gennarino, Remo Sanges, Francesca Petrera, Elia Stupka and Sandro Banfi**
Analysis of ultra-conserved element during mouse development reveals their constitutive strand-specific expression
Genome Informatics 2008, Cold Spring Harbor Laboratory Meetings - The Wellcome Trust Conference Centre, Hinxton, September 2008. Abstract and poster.
- **Remo Sanges, Pasquale De Luca, Graziano Fiorito**
Needs for Genomic Approaches in Cephalopods Research
Euroceph 2011, Naples, Italy, April 2011. Invited oral presentation.
- **Thomas Mock, Chris Bowler, Remo Sanges et al.**
*The *Fragilariopsis cylindrus* Genome Reveals New Insights into Adaptation of Diatoms to Environmental Conditions of the Southern Ocean, Antarctica*
The molecular life of diatoms, Atlanta, USA, June 2011. Oral presentation.

SELECTED COURSES

- June 2004 – Biostat2006: International school on statistical inference in biology and human sciences, Asti, IT.
- June 2009 – CSAMA09: Computational and statistical aspects of microarray analysis, Brixen, IT.

REFERENCES

Dr. Elia Stupka

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University of Birmingham, Institute of Biomedical Research - B15 2TT, Edgbaston, Birmingham - UK
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Prof. Roberto Di Lauro

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phone: +39 081 7461111 - email: roberto.dilauro@unina.it

List of Publications - Remo Sanges, PhD

1. Gianfrancesco F, Sanges R, Esposito T, Tempesta S, Rao E, Rappold G, Archidiacono N, Graves JA, Forabosco A, D'Urso M
Differential divergence of three human pseudoautosomal genes and their mouse homologs: implications for sex chromosome evolution.
Genome Res 2001, 11:2095-100.
2. Quaglino E, Rolla S, Iezzi M, Spadaro M, Musiani P, De Giovanni C, Lollini PL, Lanzardo S, Forni G, Sanges R, Crispi S, De Luca P, Calogero R, Cavallo F
Concordant morphologic and gene expression data show that a vaccine halts HER-2/neu preneoplastic lesions.
J Clin Invest 2004, 113:709-17.
3. Sanges R, Kalmar E, Claudiani P, D'Amato M, Muller F, Stupka E
Shuffling of cis-regulatory elements is a pervasive feature of the vertebrate lineage.
Genome Biol 2006, 7:R56.
4. Ferg M, Sanges R, Gehrig J, Kiss J, Bauer M, Lovas A, Szabo M, Yang L, Straehle U, Pankratz MJ, Olasz F, Stupka E, Müller F
The TATA-binding protein regulates maternal mRNA degradation and differential zygotic transcription in zebrafish.
EMBO J 2007, 26:3945-56.
5. Sanges R, Cordero F, Calogero RA
oneChannelGUI: a graphical interface to Bioconductor tools, designed for life scientists who are not familiar with R language.
Bioinformatics 2007, 23:3406-8.
6. Roma G, Sardiello M, Cobellis G, Cruz P, Lago G, Sanges R, Stupka E
The UniTrap resource: tools for the biologist enabling optimized use of gene trap clones.
Nucleic Acids Res 2008, 36:D741-6.
7. Oliveira C, Senz J, Kaurah P, Pinheiro H, Sanges R, Haegert A, Corso G, Schouten J, Fitzgerald R, Vogelsang H, Keller G, Dwerryhouse S, Grimmer D, Chin S-F, Yang H-K, Jackson CE, Seruca R, Roviello F, Stupka E, Caldas C, Huntsman D
Germline CDH1 deletions in hereditary diffuse gastric cancer families.
Hum. Mol. Genet 2009, 18:1545-1555.
8. Licastro D, Gennarino VA, Petrera F, Sanges R, Banfi S, Stupka E
Promiscuity of enhancer, coding and non-coding transcription functions in ultraconserved elements.
BMC Genomics 2010, 11:151.

9. Amendola E, Sanges R, Galvan A, Dathan N, Manenti G, Ferrandino G, Alvino FM, Di Palma T, Scarfò M, Zannini M, Dragani TA, De Felice M, Di Lauro R
A locus on mouse chromosome 2 is involved in susceptibility to congenital hypothyroidism and contains an essential gene expressed in thyroid.
Endocrinology 2010, 151:1948–1958.
10. Motti D, Le Duigou C, Eugène E, Chemaly N, Wittner L, Lazarevic D, Krmac H, Marstrand T, Valen E, Sanges R, Stupka E, Sandelin A, Cherubini E, Gustincich S, Miles R
Gene expression analysis of the emergence of epileptiform activity after focal injection of kainic acid into mouse hippocampus.
Eur. J. Neurosci 2010, 32:1364–1379.
11. Silberschmidt D, Rodriguez-Mallon A, Mithboakar P, Cali G, Amendola E, Sanges R, Zannini M, Scarfò M, De Luca P, Nitsch L, Di Lauro R, De Felice M
In vivo role of different domains and of phosphorylation in the transcription factor Nkx2-1.
BMC Dev. Biol 2011, 11:9.
12. Lenzken SC, Romeo V, Zolezzi F, Cordero F, Lamorte G, Bonanno D, Biancolini D, Cozzolino M, Pesaresi MG, Maracchioni A, Sanges R, Achsel T, Carrì MT, Calogero RA, Barabino SML
Mutant SOD1 and mitochondrial damage alter expression and splicing of genes controlling neuritogenesis in models of neurodegeneration.
Hum. Mutat 2011, 32:168–182.
13. Perna D, Fagà G, Verrecchia A, Gorski MM, Barozzi I, Narang V, Khng J, Lim KC, Sung W-K, Sanges R, Stupka E, Oskarsson T, Trumpp A, Wei C-L, Müller H, Amati B
Genome-wide mapping of Myc binding and gene regulation in serum-stimulated fibroblasts.
Oncogene 2012, 31:1695–1709.
14. Gennarino VA, D'Angelo G, Dharmalingam G, Fernandez S, Russolillo G, Sanges R, Mutarelli M, Belcastro V, Ballabio A, Verde P, Sardiello M, Banfi S
Identification of microRNA-regulated gene networks by expression analysis of target genes.
Genome Res. 2012, 22:1163–1172.
15. Oliveira P, Sanges R, Huntsman D, Stupka E, Oliveira C
Characterization of the intronic portion of cadherin superfamily members, common cancer orchestrators.
Eur. J. Hum. Genet. 2012, 20:878–883.

16. 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

Transcription initiation arising from E-cadherin/CDH1 intron2: a novel protein isoform that increases gastric cancer cell invasion and angiogenesis.

Hum. Mol. Genet. 2012, 21:4253–4269.

17. Basu S, Sanges R

Discovery of conserved long non-coding RNAs in vertebrates.

EMBNet.journal 2012, 18:pp. 130–131.

18. Basu S, Müller F, Sanges R*

Sequence conservation analyses capture a subset of mouse long non-coding RNAs sharing homology with fish conserved genomic elements.

BMC Bioinformatics ACCEPTED 2013 January.

19. Sanges R*, Hadzhiev Y, Roure A, Ferg M, Meola N, Amore G, Basu S, Brown ER, De Simone M, Petrera F, Licastro D, Strähle U, Banfi S, Lemaire P, Birney E, Müller F, Stupka E

Highly conserved elements discovered in vertebrates are present in non-syntenic loci of tunicates, act as enhancers and can be transcribed during development.

Nucleic Acids Research ACCEPTED 2013 January.

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