

REMO SANGES, PhD

Nationality: Italian - Birth date: 11/07/1976

Stazione Zoologica Anton Dohrn - Villa Comunale - 80121 Napoli - Italy

Tel.: +39 081 5833428 - Mobile: +39 340 2789194 - e-mail: remo.sanges@szn.it

My scientific interest is focused on the function and the evolution of the noncoding portion of the genome (regulatory regions, noncoding RNAs, repeats), how these features have shaped the genomes of living organisms and the way in which they affect transcriptions during development and disease. I have extensive experience in development and usage of bioinformatics pipelines, data integration and harmonization, tools, methods and databases for large-scale functional genomics data analysis.

EDUCATION ACTIVITY

September 2006 - January 2007 EBI “European Bioinformatics Institute”, Hinxton, UK, - Marie Curie Fellow in the Ensembl Team

May 2004 - June 2004 TLL “Temasek Life Sciences Laboratory”, Singapore, - Visiting Fellow in the Fugu Genome Project Team

November 2002 - December 2006, 2nd University of Naples, Italy - Ph. D. student in “Computational Biology”

March 2001 - November 2001, IGB “Adriano Buzzati Traverso”, Naples, Italy - post-lauream practice

November 1996 - February 2001, University “Federico II”, Naples, Italy - Biology BSc. Degree magna cum laude

EMPLOYMENT

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 and 1 postdoc. Co-coordinator of 3 Nationally funded projects. Leader for SZN in the WP3 of the ESFRI project EMBRC: European Marine Biological Resource Centre (<http://www.embrc.eu/>). Member of the Technical Coordination Committee in the EU project BioMedBridges (<http://www.biomedbridges.eu/>).

April 2009 - February 2010, CBM “Cluster in BioMedicine”, Trieste, Italy - Head of Bioinformatics (permanent position)

Responsible of the bioinformatics facility and research (4 bioinformaticians). Leader for CBM in the FP7 project DOPAMINET: Molecular Networks of Dopaminergic Neurons in Chordates (<http://www.dopaminet.eu/>).

July 2008 - March 2009, CBM “Cluster in BioMedicine”, Trieste, Italy - Bioinformatics Specialist (permanent position)

Responsible of the bioinformatics facility. Leader of a bioinformatics team involved in data analysis for services as well as for intramural research. The team obtained the UNI EN ISO 9001:2000 compliance to design and supply bioinformatics services.

July 2006 - June 2008, CBM “Cluster in BioMedicine”, Trieste, Italy - Bioinformatics Postdoc

Evolution of non-coding elements. Data analysis of gene expression profiles.

December 2004 - June 2006, TIGEM “Telethon Institute of Genetics and Medicine”, Naples, Italy - Bioinformatics Scientist

Analysis and design of bioinformatics comparative genomics pipeline.

December 2001 - November 2004, BioGeM “Biotechnology and Molecular Genetics in Southern Italy”, Naples, Italy - Bioinformatics Programmer

Lead a bioinformatics team involved in the analysis of gene expression data.

PUBLICATIONS (ISI indexed)

Total Impact Factor: 176 - Average: 6.8 - H-index: 12 - Citation: 579

- 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(12):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(5):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(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(17):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(24):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(Database issue):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, Yang H, 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(9):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(4):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(8):1364-1379.
- 11) 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(2):168-182.
- 12) Silberschmidt D, Rodriguez-Mallon A, Mithboakar P, Cali G, Amendola E, **Sanges R**, Zannini MS, 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.

- 13) Perna D, Fagà G, Verrecchia A, Gorski MM, Barozzi I, Narang V, Khng J, Lim KC, Sung WK, **Sanges R**, Stupka E, Oskarsson T, Trumpp A, Wei CL, Müller H, Amati B. *Genome-wide mapping of Myc binding and gene regulation in serum-stimulated fibroblasts*. Oncogene 2012;31(13):1695-709.
- 14) Oliveira P, **Sanges R**, Huntsman D, Stupka E, Oliveira C. *Characterization of the intronic portion of cadherin superfamily members, common cancer orchestrators*. Eur J Human Gen 2012;20(8):878-83.
- 15) 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(6):1163-72.
- 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(19):4253-69.
- 17) 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 2013; 14(Suppl 7):S14.
- 18) **Sanges R**[§], Hadzhiev Y, Roure A, Ferg M, Meola N, Amore G, Basu S, Brown ER, De Simone M, Petrerà 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 Res 2013;41(6):3600-3618.
- 19) Carotenuto Y, Dattolo E, Lauritano C, Pisano F, **Sanges R**, Miralto A, Procaccini G, Ianora A. *Insights into the transcriptome of the marine copepod Calanus helgolandicus feeding on the oxylipin-producing diatom Skeletonema marinoi*. Harmful Algae 2014, 31:153-162.
- 20) Adelfi MG, Borra M, **Sanges R**, Montresor M, Fontana A, Ferrante MI. *Selection and validation of reference genes for qPCR analysis in the pennate diatoms Pseudo-nitzschia multistriata and P. arenysensis*. Journal of Exp Marine Biol and Ecol 2014, 451:74-81.
- 21) Roberts JA, Miguel-Escalada I, Slovik KJ, Walsh KT, Hadzhiev Y, **Sanges R**, Stupka E, Marsh EK, Balciuniene J, Balciunas D, Müller F. *Targeted transgene integration overcomes variability of position effects in zebrafish*. Development 2014, 141:715-724.
- 22) Conte I, Merella S, Garcia-Manteiga JM, Migliore C, Lazarevic D, Carrella S, Marco-Ferreres R, Avellino R, Davidson NP, Emmett W, **Sanges R**, Bockett N, Van Heel D, Meroni G, Bovolenta P, Stupka E, Banfi S. *The combination of transcriptomics and informatics identifies pathways targeted by miR-204 during neurogenesis and axon guidance*. Nucleic Acids Res 2014, 10.1093/nar/gku498.
- 23) Racioppi C, Kamal AK, Razy-Krajka F, Gambardella G, Zanetti L, Di Bernardo D, **Sanges R**, Christiaen LA and Ristoratore F. *Fibroblast growth factors sequentially govern nervous system patterning and pigment cell specification in Ciona intestinalis*. Nature Comm 2014 Sep 5;5:4830.
- 24) Dattolo E, Ruocco M, Brunet C, Lorenti M, Lauritano C, D'Esposito D, De Luca P, **Sanges R**, Mazzuca S, Procaccini G. *Response of the seagrass Posidonia oceanica to different light environments: Insights from a combined molecular and photo-physiological study*. Mar Environ Res 2014 Aug 1. pii: S0141-1136(14)00137-8.
- 25) Dvořák P, Casamatta DA, Poulíčková A, Hašler P, Ondřej V, **Sanges R**. *Synechococcus: 3 billion years of global dominance*. Mol Ecol 2014 Oct 5. doi: 10.1111/mec.12948.
- 26) Salvemini M, Arunkumar KP, Nagaraju J, **Sanges R**, Petrella V, Tomar A, Zhang H, Zheng W, Saccone G. *De Novo Assembly and Transcriptome Analysis of the Mediterranean Fruit fly Ceratitis capitata Early Embryos*. Accepted for publication in PlosONE (13 November 2014).

*: joint first author, §: corresponding author

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, Cold Spring Harbor/Wellcome Trust Conference, Hinxton, UK, 2004.
- **Remo Sanges**, Elia Stupka.
Fragmentation and mobility of conserved non-coding sequences (CNSs) in vertebrate genomes. Genome Informatics 2005, Cold Spring Harbor /Wellcome Trust Conference, Cold Spring Harbor, USA, 2005.
- **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, 2006.

- **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/Wellcome Trust Conference, Hinxton, UK, 2006.
- 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, 2011.
- Swaraj Basu, Ferenc Muller, **Remo Sanges**
Prediction of cis-regulatory constraint in vertebrate lincRNAs by conservation of microsynteny.
The Noncoding Genome, EMBO/EMBL Symposia, EMBL, Heidelberg, Germany, 2013.
- Francesco Musacchia, Swaraj Basu, Marco Salvemini, **Remo Sanges**
Annocript: a flexible pipeline for transcriptome annotation that can also identify putative long non-coding RNAs.
European Conference on Computational Biology, Strasbourg, France, 2014,

TEACHING

- December 2002, March 2003, June 2003, December 2003 - Instructor in the "Microarray's Techniques" at Second University of Naples in collaboration with TIGEM and MWG Biotech.
- June, July and October 2003 - Instructor in the "Microarray data analysis and mining II" at University of Naples Federico II and at University of Turin in collaboration with BioGeM and Affymetrix.
- September 2003 - Instructor in the "Bioinformatics fundamentals" course at Istituto Superiore di Sanità in Rome in collaboration with Prof. Michele Muscillo.
- March 2004 - Instructor 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 - Instructor in the "Perl for biologists" course at CINECA in Bologna in collaboration with Dr. Andrew Emerson.
- October 2004 - Instructor in the "First Bioperl Workshop" at CEINGE in Naples in collaboration with Dr. Elia Stupka and Dr. Jason Stajich.
- December 2006 - Instructor in the "Data Analysis at Gene Level" course at AFFYMETRIX, High Wycombe, UK, in collaboration with AFFYMETRIX and Stratagene.
- March 2007 - Instructor in the "Data Analysis at Gene Level II" course at AFFYMETRIX, Santa Clara, CA 95051, USA, in collaboration with AFFYMETRIX.
- November 2008, December 2009 - Instructor 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 - "Cultore della materia" of the "Trascrittomics" course in the "Functional Genomics" degree at the University of Trieste.
- April 2013, January 2014 - Visiting teacher of the "Data Analysis at Gene Level and Transcriptomics" course in the PhD program on Functional and Structural Genomics" at SISSA, Trieste.

APPOINTMENTS AND AWARDS

- Member of the PhD committee of the Open University (UK) at the Affiliate Research Center Stazione Zoologica Anton Dohrn, Naples, Italy, since 2012.
- Member of the PhD committee of the PhD program in Biology at the University of Naples Federico II, Naples, Italy, since 2013.
- Winner of the Best Poster Award at the Bioinformatics Italian Society Meeting in 2013 and 2014.
- Winner of the Best Presentation Award and the Best Poster Award at Consiglio Scientifico SZN 2014.

REFERENCES

Dr. Elia Stupka

Co-Director and Head of Unit Center for Translational Genomics and Bioinformatics
San Raffaele Scientific Institute, Milano, Italy - phone: +39 02 26439137 - email: stupka.elia@hsr.it

Dr. Ferenc Müller

Department of Medical and Molecular Genetics - School of Clinical and Experimental Medicine
University of Birmingham, UK - phone: +44 121 414 2895 - email: f.mueller@bham.ac.uk

Dr. Ewan Birney

Associate Director, European Bioinformatics Institute, EMBL-EBI, Hinxton, UK
Direct email birney@ebi.ac.uk Email for scheduling, diary, reminders : birney-request@ebi.ac.uk