

REMO SANGES, PhD

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My scientific interests are centered on the function and the evolution of the noncoding portion of the genome (regulatory regions, noncoding RNAs, repeats), how these features shaped the genomes of living organisms, the way in which they affect transcription and their impact in the establishment of complexity, with a strong focus on health, disease and cognitive capabilities. 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.

ISI Publications: 35 - Total IF: 250 - Average IF: 7 - H-index: 16 - Citations: 944 (Google Scholar, February 2017)

EDUCATION

- 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 - PhD 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 AND GRANTS

- **March 2010 – ongoing, Stazione Zoologica Anton Dohrn, Naples, Italy – Principal Investigator (Primo Ricercatore, permanent position)** - Principal Investigator and responsible of the Computational Genomics Laboratory. Director of PhD students and postdocs. Co-coordinator of 3 Nationally funded projects (total funding 900K euros). 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 postdoc bioinformaticians and 2 technicians). 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

1. Mock T, Otilar RP, Strauss J, McMullan M, Paaanen P, Schmutz J, Salamov A, Sanges R, Toseland A, Ward BJ, Allen AE, Dupont CL, Frickenhaus S, Maumus F, Veluchamy A, Wu T, Barry KW, Falciatore A, Ferrante MI, Fortunato AE, Glöckner G, Gruber A, Hipkin R, Janech MG, Kroth PG, Leese F, Lindquist EA, Lyon BR, Martin J, Mayer C, Parker M, Quesneville H, Raymond JA, Uhlig C, Valas RE, Valentin KU, Worden AZ, Armbrust EV, Clark MD, Bowler C, Green BR, Moulton V, van Oosterhout C, Grigoriev IV. *Evolutionary genomics of the cold-adapted diatom *Fragilariopsis cylindrus**. *Nature* 2017 Jan 26;541(7638):536-540.
2. Basu S, Hadzhiev Y, Petrosino G, Nepal C, Gehrig J, Armant O, Ferg M, Strahle U, Sanges R¹, Müller F². *The Tetraodon nigroviridis reference transcriptome: developmental transition, length retention and microsynteny of long non-coding RNAs in a compact vertebrate genome*. *Sci Rep* 2016 Sep 15;6:33210.
3. Taddei L, Stella GR, Rogato A, Bailleul B, Fortunato AE, Annunziata R, Sanges R, Thaler M, Lepetit B, Lavaud J, Jaubert M, Finazzi G, Bouly JP, Falciatore A. *Multisignal control of expression of the LHCX protein family in the marine diatom *Phaeodactylum tricornutum**. *J Exp Bot* 2016 Jun;67(13):3939-51.

4. Tarallo A, Angelini C, Sanges R, Yagi M, Agnisola C, D'Onofrio G. *On the genome base composition of teleosts: the effect of environment and lifestyle.* BMC Genomics 2016 Mar 2;17:173.
5. Patil S, Moeys S, von Dassow P, Huysman MJ, Mapleson D, De Veylder L, Sanges R, Vyverman W, Montresor M, Ferrante MI. *Identification of the meiotic toolkit in diatoms and exploration of meiosis-specific SPO11 and RAD51 homologs in the sexual species Pseudo-nitzschia multistriata and Seminavis robusta.* BMC Genomics 2015 Nov 14;16(1):930.
6. Di Dato V, Musacchia F, Petrosino G, Patil S, Montresor M, Sanges R, Ferrante MI. *Comparison of three Pseudo-nitzschia species through transcriptome sequencing reveals the existence of Nitric Oxide Synthase genes in diatoms.* Sci Rep 2015 Jul 20;5:12329.
7. Zucchelli S, Cotella D, Takahashi H, Carrieri C, Cimatti L, Fasolo F, Jones MH, Sblattero D, Sanges R, Santoro C, Persichetti F, Carninci P, Gustincich S. *SINEUPs: a new class of natural and synthetic antisense long non-coding RNAs that activate translation.* RNA Biol 2015;12(8):771-9.
8. Russo MT, Annunziata R, Sanges R, Ferrante MI, Falciatore A. *The upstream regulatory sequence of the Light Harvesting Complex Lhcf2 gene of the marine diatom Phaeodactylum tricornutum enhances transcription in an orientation- and distance-independent fashion.* Mar Genomics 2015 Dec;24P1:69-79.
9. Musacchia F, Basu S, Petrosino G, Salvemini M, Sanges R. *Annocript: a flexible pipeline for the annotation of transcriptomes also able to identify putative long noncoding RNAs.* Bioinformatics 2015 Jul 1;31(13):2199-201.
10. 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.* PlosONE 2014 Dec 4;9(12):e114191.
11. Dvořák P, Casamatta DA, Pouličková A, Hašler P, Ondřej V, Sanges R. *Synechococcus: 3 billion years of global dominance.* Mol Ecol 2014 Nov;23(22):5538-51.
12. 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 Oct;101:225-36.
13. Racioppi C, Kamal AK, Razy-Krajka F, Gambardella G, Zanetti I, Di Bernardo D, Sanges R, Christiaen IA 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.
14. 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 Jul;42(12):7793-806.
15. 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 Feb;141(3):715-24.
16. 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.
17. 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 Jan;31:153-162.
18. Sanges R⁵, 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 E⁵. *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 Apr 1;41(6):3600-18.
19. Basu S, Müller F, Sanges R⁵. *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.
20. 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 Oct 1;21(19):4253-69.
21. 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 Jun;22(6):1163-72.
22. 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 Aug;20(8):878-83.
23. 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 Mar 29;31(13):1695-709.
24. 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 Feb 23;11:9.
25. Lenzen SC, Romeo V, Zolezzi F, Cordero F, Lamorte G, Bonanno D, Biancolini D, Cozzolino M, Pesaresi MG, Maracchioni A, Sanges R, Achsel T, Carri MT, Calogero RA, Barabino SML. *Mutant SOD1 and mitochondrial damage alter expression and*

splicing of genes controlling neurogenesis in models of neurodegeneration. *Hum Mutat* 2011 Feb;32(2):168-82.

26. 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 Oct;32(8):1364-79.
27. 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 Apr;151(4):1948-58.
28. Licastro D, Gennarino VA, Petrerà F, Sanges R, Banfi S, Stupka E. *Promiscuity of enhancer, coding and non-coding transcription functions in ultraconserved elements*. *BMC Genomics* 2010 Mar 4;11:151.
29. 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 May 1;18(9):1545-55.
30. 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 Jan;36(Database issue):D741-6.
31. 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 Dec 15;23(24):3406-8.
32. 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 Sep 5;26(17):3945-56.
33. 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.
34. 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 Mar;113(5):709-17.
35. 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 Dec;11(12):2095-100.

*: joint first author, †: corresponding author

TEACHING

- December 2002, March 2003, June 2003, December 2003 – Instructor in the “Microarray’s Techniques” course.
- June, July and October 2003 – Instructor in the “Microarray data analysis and mining II” course.
- September 2003 – Instructor in the “Bioinformatics fundamentals” course.
- March 2004 – Instructor in the “Microarray data analysis and statistical validation” course.
- October 2004, October 2005, October 2010 – Instructor in the “Perl for biologists” course.
- October 2004 – Instructor in the “First BioPerl Workshop”.
- December 2006 – Instructor in the “Data Analysis at Gene Level” course.
- March 2007 – Instructor in the “Data Analysis at Gene Level II” course.
- November 2008, December 2009 – Instructor in the “Practical data EXON 1.0 ST arrays analysis”.
- 2009/2011 - “Cultore della Materia” of the Transcriptomic course in the Functional Genomics degree at University of Trieste.
- Since 2013 – Teaching assignments for the “Data Analysis at Gene Level and Transcriptomics” course in the PhD program on “Functional and Structural Genomics” at SISSA, Trieste.
- 2010/2015 – Organizer and Professor of the “Bioinformatics course” in the PhD program of the SZN Open University.

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 Scientific Council SZN 2014.
- Member of the Technical Coordination Committee in the EU project BioMedBridges (<http://www.biomedbridges.eu/>).
- Member of Program Committee for the Italian Bioinformatics Society Annual Meeting since 2012.

- Reviewer for: Bioinformatics, BMC Bioinformatics, BMC Genomics, Neuroscience, Briefing in Functional Genomics, Marine Genomics, Journal of Molecular Evolution, PlosOne, Genome Biology and Evolution, Molecular Ecology, Journal of Experimental Botany.
- Grant Reviewer for FRM: Fondation pour la Recherche Médicale, France.

POSTDOC AND PHD STUDENTS

- **Post-doctoral fellows:** Francesco Musacchia (2012-present), Swaraj Basu (2014-2015), Simeone Dal Monego (2008-2010), Paolo Sonogo (2008-2010), Warren Emmet (2008-2010).
- **PhD Students, PhD successfully completed in 3 years:** Swaraj Basu, Open University PhD student, completed on 05/2014. Giuseppe Petrosino, University of Naples, PhD in Bioinformatics, completed on 04/2015. Veerendra Gadekar Open University PhD student, completed on 09/2016.
- **PhD Students, Ongoing:** Massimiliano Volpe, 2nd year Open University PhD student, 2016-2018, Guglielmo Roma, 2nd year University of Naples Biology PhD student.
- **Co-supervision:** Kumari Richa, OU PhD student; Sneha Asai, OU PhD student; Greta Bussemi, OU PhD student.
- **Master students:** Luca Roma, University of Rome, master in Bioinformatics, 2014-2015. Massimiliano Volpe, University of Rome, master in Bioinformatics, 2015-2016.

REFERENCES

Dr. Elia Stupka

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16/2/2017

Elia Stupka