

## REMO SANGES, PhD

Nationality: Italian - Birth date: 11.07.1976

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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, the nervous system and somatic variations. 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 and more than 10 years of teaching experience.*

**ISI Publications: 50 - Total IF: 337 - Average IF: 6.7 - H-index: 23 - Citations: 1667 (Google Scholar, Jul. 2019)**

### EDUCATION

- November 2002 – December 2006: 2nd University of Naples, Italy - **PhD student** in “Computational Biology” under the supervision of Elia Stupka.
- November 1996 – February 2001: University “Federico II”, Naples, Italy - **Biology BSc Degree magna cum laude** under the supervision of Michele D’Urso.

### EMPLOYMENT

- **December 2017 – ongoing, SISSA “International School for Advanced Studies”, Trieste, Italy – Associate Professor (permanent position)** – Professor of Applied Biology in the Neuroscience department. Head of the Computational Genomics Laboratory. Deputy director and professor for the PhD in Functional and Structural Genomics.
- **March 2010 – December 2017, Stazione Zoologica Anton Dohrn, Naples, Italy – Principal Investigator (Primo Ricercatore a tempo indeterminato, 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 (3 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** – Research on the evolution of non-coding elements and data analysis of gene expression profiles under the supervision of Elia Stupka.
- **May 2004 – June 2004, TLL “Temasek Life Sciences Laboratory”, Singapore - Visiting Fellow** in the Fugu Genome Project Team under the supervision of Elia Stupka.
- **December 2004 – June 2006, TIGEM “Telethon Institute of Genetics and Medicine”, Naples, Italy - Bioinformatics Scientist** – Research on the evolution of vertebrate genomes and design of bioinformatics comparative genomics pipeline under the supervision of Elia Stupka.
- **December 2001 – November 2004, BioGeM “Biotechnology and Molecular Genetics in Southern Italy”, Naples, Italy - Bioinformatics Programmer** – Contribution to the establishment of a bioinformatics team and involvement in several research projects on the analysis of gene expression data in development and disease under the supervision of Roberto Di Lauro and Pasquale De Luca.
- **March 2001 – November 2001, IGB “Adriano Buzzati Traverso”, Naples, Italy - Post-lauream practice** – Molecular biology and proteomics of cellular stress response under the supervision of Michele D’Urso and Pasquale De Luca.

### AWARDS

- Italian national scientific qualification (**Abilitazione Scientifica Nazionale**), sector 05/F1 - II fascia - Biologia applicata (BIO/13) - from 04/04/2017 to 04/04/2023.
- **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.
- September 2006 – January 2007: EBI “European Bioinformatics Institute”, Hinxton, Cambridge, UK, - **Marie Curie Fellow** in the Ensembl Team under the supervision of Ewan Birney.
- **Exonerated** by the civil service for scientific merits in 2002.

### PROFESSIONAL ACTIVITIES

- **Member of the PhD committee** for the Open University (OU), UK, at the Affiliate Research Center Stazione Zoologica Anton Dohrn, Naples, Italy, 2012-2017.
- **Member of the PhD committee** of the PhD program in Biology at the University of Naples Federico II, Naples, Italy, 2013-2018.
- **Member of the PhD committee** of the PhD program in Functional and Structural Genomics at SISSA, Trieste, Italy, since 2018.
- **Member of the Technical Coordination Committee** in the EU project BioMedBridges (<http://www.biomedbridges.eu/>).

- **Ordinary member** of the Bioinformatics Italian Society since 2012.
- **Member of the 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, Scientific Reports, Nucleic Acids Research, Neuroscience.
- **Grant Reviewer** for: FRM: Fondation pour la Recherche Médicale, France; MIUR: Italian Ministry of University and Research, Italy.
- **Coordinator** of the “Career Development Advisory Plan” offered to SZN PhD students from 2014 to 2017.
- **Examiner** of 1 Open University PhD thesis, 7 SISSA PhD in Functional and Structural Genomics thesis and 1 University of Turin PhD in Complex Systems thesis and several degree thesis at University of Trieste.

## ACADEMIC TEACHING

- 2009/2011 – “**Cultore della Materia**” of the Transcriptomic course in the Functional Genomics laurea degree at University of Trieste. Performed lessons, practical exercises and final course exams.
- 2010 and 2015 – **Organizer and Professor** of the “Bioinformatics course” in the PhD program of the SZN Open University. Performed a course of 18 hours per year.
- Since 2013 – **Organizer and Professor** of one day of lessons per year with the researchers of SZN for the students of the PhD program in Biology of The University of Naples Federico II.
- 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. Perform a course of 35 hours per year.

## MENTORING

- **Post-doctoral fellows:** Francesco Musacchia (2012-2016) - Swaraj Basu (2014-2015) - Simeone Dal Monego (2008-2010) - Paolo Sonego (2008-2010) - Warren Emmet (2008-2010) - Massimiliano Volpe (2019-) - Chiara Agnoletto (2019-).
- **PhD Students, PhD successfully completed:** Swaraj Basu, Open University PhD student, completed in 2014 - Giuseppe Petrosino, University of Naples, PhD in Bioinformatics, completed in 2015 - Veerendra Gadekar Open University PhD student, completed in 2016. Massimiliano Volpe, Open University PhD student, completed in 2019. Guglielmo Roma, University of Naples, PhD in Biology, completed in 2019.
- **PhD Students, Ongoing:** Gabriele Leoni, 3<sup>rd</sup> year SISSA PhD student in Genomics - Federico Ansaloni, 2<sup>nd</sup> year SISSA PhD student in Genomics - Giovanni Spirito, 2<sup>nd</sup> year SISSA PhD student in Genomics. Mauro Esposito, 1<sup>st</sup> year SISSA PhD student in Genomics - Nicolò Gualandi, 1<sup>st</sup> year SISSA PhD student in Genomics.
- **Co-supervision:** Erik Garrison, Cambridge University PhD student - 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.

## OTHER TEACHING

- December 2002, March 2003, June 2003, December 2003 – Instructor in the “Microarray’s Techniques” course at the University of Naples Federico II.
- June, July and October 2003 – Instructor in the “Microarray data analysis and mining II” course at the University of Naples Federico II.
- September 2003 – Instructor in the “Bioinformatics fundamentals” course at the Istituto Superiore di Sanita’ in Rome.
- March 2004 – Instructor in the “Microarray data analysis and statistical validation” course at the University of Turin.
- October 2004, October 2005, October 2010 – Instructor in the “Perl for biologists” course at the CINECA in Bologna.
- October 2004 – Instructor in the “First BioPerl Workshop” at the University of Naples Federico II.
- December 2006 – Instructor in the “Data Analysis at Gene Level” course at Affymetrix UK in High Wycombe, UK.
- March 2007 – Instructor in the “Data Analysis at Gene Level II” course at Affymetrix USA in California, USA.
- November 2008, December 2009 – Instructor in the “Practical data EXON 1.0 ST arrays analysis” at the University of Turin.

## GRANTS AND FUNDING

- 01-01-2005 - 31-03-2008 - TRANSCODE: Novel tool for high-throughput characterization of genomic elements regulating gene expression in chordates.  
Project id: 511990 - Call: FP6-2003-LIFESCIHEALTH-I  
Topic: LSH-2002-1.1.0-1 - Topics for Specific Targeted Research Project/CA in the area of Fundamental knowledge and basic tools for functional genomics in all organisms.  
Contribution to different work packages with tasks related to: the identification of conserved non-coding sequences among vertebrates and their evolution; the study of the mechanisms at the basis of the evolution and regulation of the initiation of transcription; the study of the gene expression dynamics using cellular and non-human animal models. Part of my PhD and postdoc was funded by the project.
- 01-02-2009 - 31-07-2012 - DOPAMINET: Molecular Networks of Dopaminergic Neurons in Chordates.  
Project id: 223744 - Call: FP7-HEALTH-2007-B  
Topic: HEALTH-2007-2.1.2-5 - Multidisciplinary fundamental genomics and molecular biology approaches to study basic biological processes relevant to health and diseases.  
Contribution to different work packages, with tasks mainly related to: the coordination of WP3; the identification, analysis and evolutionary study of regulatory regions conserved among chordates and involved in the regulation of transcription during development of the nervous system; analysis of developmental gene expression dynamics.

- 02-01-2011 - 31-01-2014 - EMBRC: European marine biological resource centre - preparatory phase.  
Project id: 262280 - Call: FP7-INFRASTRUCTURES-2010-1  
Topic: INFRA-2010-2.2.5 - European marine biological resource centre.  
Work package leader assistant in the WP3, “Planning e-Infrastructure”, with specific tasks on the identification and description of current high performance computer clusters used in bioinformatics research and the design of a distributed bioinformatics infrastructure for an European research hub.
- 01-01-2012 - 31-12-2015 - BioMedBridges: Building data bridges between biological and medical infrastructures in Europe.  
Project id: 284209 - Call: FP7-INFRASTRUCTURES-2011-1  
Topic: INFRA-2011-2.3.2. - Implementation of common solutions for a cluster of ESFRI infrastructures in the field of “Life sciences”.  
Member of the Technical Coordination Committee with tasks regarding: the technical directions and choices to be taken by the consortium; the identification and collection of the main bioinformatics tools adopted in marine research; the establishment of specific analysis for marine metagenomics data and the organization of an international workshop.
- 01-01-2013 - 31-12-2013 - Progetto Premiale MIUR MetaTrac: META-TRASCrittomica delle fasi di sviluppo e di declino di fioriture algali nel Golfo di Napoli.  
Co-coordinator responsible of metagenomics analysis.
- 01-01-2013 - 31-12-2013 - Progetto Premiale MIUR StarTrEgg: Meccanismi molecolari di controllo della fecondazione nelle uova della stella di mare *Astropecten aranciacus*.  
Co-coordinator responsible for the generation, functional and evolutionary analysis of the reference transcriptome of the starfish aiming at understanding the molecular mechanisms at the basis of the fertilization.
- 01-01-2013 - 31-12-2013 - Progetto Premiale MIUR MolEcOC: Approaching inter- and intra-individual variability by molecular ecology for the technology transfer of basic research on marine model organisms (*Octopus vulgaris* and *Caretta caretta*).  
Co-coordinator responsible for the functional genomics analysis mainly related to the establishment of reference transcriptomes, developmental gene expression studies and identification of neural bio-markers.
- 01-01-2013 - 31-12-2016 - RITMARE: Flagship Project of the National Research Programmes on marine research funded by the Italian MIUR.  
Coordinator of two operative units aiming at the development of bioinformatics pipelines for the analysis of sequence data and the design and prototypization of an infrastructure for the bioinformatics research.
- 01-02-2014 - 31-01-2016 - Comparative Population Transcriptomics To Uncover Sex Determination of *Aedes albopictus* and *Phlebotomus perniciosus*, Two Emerging Haematophagous Insect Species.  
STAR Project supported by the University of Naples Federico II and by the Fondazione San Paolo through the STAR 2013 programme (Sostegno Territoriale alle Attività di Ricerca). I was member of the research team and contributed to the design and supervision of the experiments and analysis. The project was ranked first out of 88 selected projects and evaluated as top priority by the evaluating panel of the European Science Foundation.

## OTHER PROJECTS COORDINATION AND COLLABORATION

- 01/01/2011 - 31/05/2013 - **Direction** of the “Fish Long Non-coding RNAs (lncRNAs) Conservation Group”, aiming at studying the level of conservation, the evolution and the expression of fish long non-coding RNAs with respect to mammals. The study was in collaboration with Prof. Ferenc Muller, University of Birmingham, UK.
- 01/01/2011 - Ongoing - **Member** of the “*Fragilariopsis cylindrus* Genome Consortium”, aiming at the assembly, annotation functional and evolutionary analysis of the genome of the diatom *Fragilariopsis cylindrus*. The Consortium is coordinated by Prof. Thomas Mock of the University of East Anglia, Norwich, UK. Other members are from Germany, France, USA and Canada. My role is the analysis of promoters and their evolution in diatom’s genomes with special focus on adaptation to life in extreme environments.
- 01/01/2013 - 30/09/2016 - **Co-direction** of the “Tetraodon Nigroviridis Reference Transcriptome Project”, aiming at the establishment of the first experimentally generated reference transcriptome for the fish *Tetraodon nigroviridis*, the identification of long non-coding RNAs and the analysis of their evolution in vertebrates. My role has been the design of the project and the coordination of all the bioinformatics analysis. The other co-director was Prof. Ferenc Muller, University of Birmingham, UK, which took care of the wet-lab part of the project. Other collaborators were from Germany and Denmark.
- 01/01/2013 - Ongoing - **Participation** to the “*Pseudo-nitzschia Multistriata* Genome Project”, aiming at the assembly, analysis, annotation and data-mining of the genome and the transcriptome of the diatom *Pseudo-nitzschia multistriata* with a strong focus on the evolution of sexual reproduction in this species. The project is lead by Dr. Mariella Ferrante of the Stazione Zoologica Anton Dohrn, Naples, Italy, and involves research groups mainly from UK and France. My role is the design and coordination of all the bioinformatics analysis.
- 01/01/2014 - Ongoing - **Participation** to the “Ascidian Genomes Project”, aiming at the assembly and transcriptional and evolutionary analysis of different ascidians genomes, mainly to understand how very divergent genomes can give birth to morphologically similar embryos. The project is led by Dr. Patrick Lemaire, CRBM, France, and involves research groups from France, Spain, Italy and Japan. The project is currently ongoing and my role is to identify, annotate and analyze putative regulatory regions involved in the regulation of transcription during development.
- 01/01/2009 - 01/07/2012 - **Participation** to a study on the identification of gene expression networks regulated by microRNAs in collaboration with TIGEM, Italy. My role was the development of a specific tool capable to identify microRNA targets using sequence and gene expression information from Affymetrix microarray.
- 01/01/2008 - 01/05/2009 - **Participation** to a study aiming at identifying the genetic causes of hereditary gastric cancer. The study was in collaboration with groups from Canada, Portugal, Denmark, UK, Germany, Korea and USA. My role was the analysis and the identification of the molecular causes of the identified mutations and the reconstruction of their origins.
- 01/01/2012 - 31/12/2014 - **Co-direction** of a study aiming at the assembly, annotation and evolutionary analysis of the genome of a *Synechococcus* cyanobacteria. The study was in collaboration with groups from Czech Republic and USA. My role has been contribution to the design of the study and the direction of the bioinformatics analysis.
- 01/04/2012 - Ongoing - **Direction** of the research group on “Active transposons in the nervous system of *Octopus vulgaris*: biological and molecular mechanisms at the basis of cellular complexity”. The project aims at understanding the biological, molecular and

developmental features at the basis of the evolution of complexity by studying the activity of putative transposable elements in the *Octopus vulgaris* nervous system. The project exploits cellular biology and functional genomics techniques. It is in collaboration with groups from Italy (SZN, Federico II) and Germany (EMBL).

- 04/07/2012 - Ongoing - **Participation** to a study on cellular motility in cancer. The study aims at understanding the mechanisms at the basis of cellular motility in cancer using animal models and is coordinated by Prof. Roberto Di Lauro and Gabriella De Vita, Federico II, Naples. It is in collaboration with groups from Bari and Naples.

## SELECTED CONFERENCES, SEMINARS AND LECTURES

- October 2004 - **Selected oral presentation**: “The importance of being intron: lessons from conserved non-coding sequences”. Genome Informatics 2004, Joint Cold Spring Harbor Laboratory/Wellcome Trust Conference, Wellcome Trust Genome Campus, Hinxton, UK.
- October 2005 - **Selected oral presentation**: “The importance of being intron: lessons from conserved non-coding sequences”. 2nd European Science Foundation Functional Genomics Conference, Oslo, Norway.
- October 2006 - **Selected oral presentation**: “Shuffling of cis-regulatory elements is a pervasive feature of the vertebrate lineage”. Genome Informatics 2006, Joint Cold Spring Harbor Laboratory/Wellcome Trust Conference, Wellcome Trust Genome Campus, UK.
- February 2008 - **Invited seminar**: “Whole Genome Shuffling of Conserved Elements in the Chordate Genomes: Random Sampling or Evolutionary Reality?”. Stazione Zoologica Anton Dohrn, Naples, Italy.
- August 2008 - **Invited seminar**: “Whole Genome Shuffling of Conserved Elements in the Chordate Genomes: Random Sampling or Evolutionary Reality?”. Columbia University, New York, USA.
- April 2011 - **Invited lecture**: “Needs for Genomic Approaches in Cephalopods Research”. Cephalopod Biology Research in the 21st Century—A European Perspective. Vico Equense, Naples, Italy.
- April 2012 - **Invited lecture**: “Insights into the Octopus Transcriptome”. EuroCeph 2012 - Meeting for an European Proposal of a Consortium for genome sequencing of *Octopus vulgaris*. Vico Equense, Naples, Italy.
- May 2012 - **Contribution to the organization and invited lecture**: “Transcriptome mining: examples of meta-analysis using gene expression data”. EMBO Practical course: Bioinformatics and Comparative Genome Analyses. Stazione Zoologica Anton Dohrn, Naples, Italy.
- July 2012 - **Invited lecture**: “De-novo Assembly of the Octopus Transcriptome Integrating Custom and Public Sequencing Data”. DAAD program German-Italian Dialogue 2012, Next Generation Sequencing - Application cases and bioinformatics development. Naples, Italy.
- June 2014 - **Invited lecture**: “The Octopus Transcriptome and an Intriguing Convergent Molecular Evolutionary Scenario”. ALLBIO Congress - Broadening the Bioinformatics Infrastructure to Unicellular, Animal, and Plant Science. Florence, Italy.
- March 2015 - **Invited seminar**: “Transcription, transposons, noncoding and the evolution of organismal complexity”. International School for Advanced Studies (SISSA), Trieste, Italy.
- November 2015 - **Organizer and Chair**: “Workshop on Metagenomics: Bridging Between Environment and Life”. BioMedBridges Symposium. Wellcome Trust Genome Campus, Hinxton, UK.
- December 2015 - **Invited seminar**: “Transcription, transposons, non-coding and the evolution of organismal complexity”. Università degli Studi del Piemonte Orientale, Novara, Italy.
- July 2016 - **Contribution to the organization and invited lecture**: “Transcription, Transposons, Noncoding and the Evolution of Organismal Complexity”. RNA-Seq Workshop. University of Naples Federico II, Naples, Italy.
- December 2013, 2014, 2015, 2016 - **Invited lecture**: “Introduction to Bioinformatics”. University of Naples Federico II, Naples, Italy.
- December 2018 - **Invited seminar**: “Exploring the emerging role of transposable elements in the animal nervous system”. University of Udine, Italy.

## PEER REVIEWED PUBLICATIONS

1. Busseni G, Vieira FRJ, Amato A, Pelletier E, Pierella Karlusich JJ, Ferrante MI, Wincker P, Rogato A, Bowler C, **Sanges R**, Maiorano L, Chiurazzi M, d'Alcalà MR, Caputi L, Iudicone D. *Meta-omics reveals genetic flexibility of diatom nitrogen transporters in response to environmental changes*. *Mol Biol Evol*. 2019 Jul 1. pii: msz157. doi: 10.1093/molbev/msz157.
2. Petrella V, Aceto S, Colonna V, Saccone G, **Sanges R**, Polanska N, Volf P, Gradoni L, Bongiorno G, Salvemini M. *Identification of sex determination genes and their evolution in Phlebotominae sand flies (Diptera, Nematocera)*. *BMC Genomics*. 2019 Jun 25;20(1):522. doi: 10.1186/s12864-019-5898-4.
3. Zarrella I, Herten K, Maes GE, Tai S, Yang M, Seuntjens E, Ritschard EA, Zach M, Styfhals R, **Sanges R**, Simakov O, Ponte G, Fiorito G. *The survey and reference assisted assembly of the Octopus vulgaris genome*. *Sci Data*. 2019 Apr 1;6(1):13. doi: 10.1038/s41597-019-0017-6.
4. Styfhals R, Seuntjens E, Simakov O, **Sanges R**, Fiorito G. *In silico Identification and Expression of Protocadherin Gene Family in Octopus vulgaris*. *Front Physiol*. 2019 Jan 14;9:1905. doi: 10.3389/fphys.2018.01905.
5. Russo MT, Vitale L, Entrambasaguas L, Anestis K, Fattorini N, Romano F, Minucci C, De Luca P, Biffali E, Vyverman W, **Sanges R**, Montresor M, Ferrante MI. *MRP3 is a sex determining gene in the diatom Pseudo-nitzschia multistriata*. *Nature Comm*. 2018 Nov 28;9(1):5050. doi: 10.1038/s41467-018-07496-0.
6. Volpe M, Miralto M, Gustincich S, **Sanges R**<sup>5</sup>. *ClusterScan: simple and generalistic identification of genomic clusters*. *Bioinformatics*. 2018 Jun 15. doi: 10.1093/bioinformatics/bty486.
7. Amato A, Sabatino V, Nylund GM, Bergkvist J, Basu S, Andersson MX, **Sanges R**, Godhe A, Kjørboe T, Selander E, Ferrante MI. *Grazer-induced transcriptomic and metabolomic response of the chain-forming diatom Skeletonema marinoi*. *ISME J*. 2018 Jun;12(6):1594-1604.
8. Nanjappa D, **Sanges R**, Ferrante MI, Zingone A. *Diatom flagellar genes and their expression during sexual reproduction in Leptocylindrus danicus*. *BMC Genomics*. 2017 Oct 23;18(1):813.
9. Musacchia F, Vasilev F, Borra M, Biffali E, **Sanges R**, Santella L, Chun JT. *De novo assembly of a transcriptome from the eggs and early embryos of Astropecten aranciacus*. *PLoS One*. 2017 Sep 5;12(9):e0184090.
10. Richa K, Balestra C, Piredda R, Benes V, Borra M, Passarelli A, Margiotta F, Saggiomo M, Biffali E, **Sanges R**, Scanlan DJ, Casotti R. *Distribution, Community Composition, and Potential Metabolic Activity of Bacterioplankton in an Urbanized Mediterranean Sea Coastal Zone*. *Appl Environ Microbiol*. 2017 Aug 17;83(17).

11. Credendino SC, Lewin N, de Oliveira M, Basu S, D'Andrea B, Amendola E, Di Guida L, Nardone A, **Sanges R**, De Felice M, De Vita G. *Tissue- and Cell Type-Specific Expression of the Long Noncoding RNA Klhl14-AS in Mouse*. [Int J Genomics](#). 2017;2017:9769171.
12. Basu S, Patil S, Mapleson D, Russo MT, Vitale L, Fevola C, Maumus F, CasottiR, Mock T, Caccamo M, Montresor M, **Sanges R**<sup>5</sup>, Ferrante MI<sup>5</sup>. *Finding a partner in the ocean: molecular and evolutionary bases of the response to sexual cues in a planktonic diatom*. [New Phyt](#) 2017 Jul;215(1):140-156.
13. Amato A, Dell'Aquila G, Musacchia F, Annunziata R, Ugarte A, Maillet N, Carbone A, Ribera d'Alcalà M, **Sanges R**, Iudicone D, Ferrante MI. *Marine diatoms change their gene expression profile when exposed to microscale turbulence under nutrient replete conditions*. [Sci Rep](#) 2017 Jun 19;7(1):3826.
14. Ruocco M, Musacchia F, Olivé I, Costa MM, Barrote I, Santos R, **Sanges R**, Procaccini G, Silva J. *Genome-wide transcriptional reprogramming in the seagrass *Cymodocea nodosa* under experimental ocean acidification*. [Mol Ecol](#) 2017 Jun 14.
15. Entrambasaguas L, Jahnke M, Biffali E, Borra M, **Sanges R**, Marín-Guirao L, Procaccini G. *Tissue-specific transcriptomic profiling provides new insights into the reproductive ecology and biology of the iconic seagrass species *Posidonia oceanica**. [Mar Genomics](#) 2017 May 26. pii: S1874-7787(17)30059-4.
16. Mock T, Otillar RP, Strauss J, McMullan M, Paajanen 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.
17. Basu S, Hadzhiev Y, Petrosino G, Nepal C, Gehrig J, Armant O, Ferg M, Strahle U, **Sanges R**<sup>5</sup>, Müller F<sup>5</sup>. *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.
18. 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.
19. 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.
20. 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.
21. 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.
22. 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.
23. 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.
24. Musacchia F, Basu S, Petrosino G, Salvemini M, **Sanges R**<sup>5</sup>. *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.
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