REMO SANGES, PhD

Nationality: Italian [redacted]
Associate Professor in BIOS-10/A – International School for Advanced Studies (SISSA), Via Bonomea 265, 34136 Trieste, Italy
[redacted]

Abilitazione Scientifica Nazionale – sector 05/BIOS-10 – I fascia - BIOLOGIA CELLULARE E APPLICATA (BIOS-10/A - ex BIO/13) – from 09/06/2021 to 09/06/2030. I also pass the three thresholds for Commissario ANVUR.

My scientific interests are centered on the function and the evolution of the non-coding portion of the genome (regulatory regions, non-coding RNAs, transposons), 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 20 years of teaching experience.

ISI Publications: 80 – Total IF: 526 – Average IF: 6.6 – H-index: 32 – Citations: ~3700 (Google Scholar, August 2024)

EDUCATION

- 2006 – 2007: European Bioinformatics Institute (EBI), Hinxton, Cambridge, UK, – **Marie Curie Fellow**.
- 2004: Temasek Life Sciences Laboratory (TLL), National University of Singapore – **Visiting Fellow**.
- 2002 – 2006: 2nd University of Naples, Italy – **PhD in Computational Biology**.
- 1996 – 2001: University Federico II, Naples, Italy – **Biology BSc Degree magna cum laude**.

EMPLOYMENT

- 2017–ongoing: International School for Advanced Studies (SISSA), Trieste, Italy – **Associate Professor of Experimental Biology (SSD BIOS-10/A) –** Head of the Computational Genomics Laboratory. Coordinator and professor for the PhD in Functional and Strucutral Genomics.
- 2010–2017: Stazione Zoologica Anton Dohrn, Naples, Italy – **Senior Researcher** – Head of the Computational Genomics Laboratory.
- 2009–2010: Cluster in BioMedicine (CBM), Trieste, Italy – **Head of Bioinformatics** – Responsible of bioinformatics service and research.
- 2008–2009: Cluster in BioMedicine (CBM), Trieste, Italy – **Bioinformatics Specialist** – Responsible of the bioinformatics facility.
- 2006–2008: Cluster in BioMedicine (CBM), Trieste, Italy – **Bioinformatics Postdoc**.
- 2004–2006: Telethon Institute of Genetics and Medicine (TIGEM), Naples, Italy – **Bioinformatics Scientist**.
- 2001–2004: Biotechnology and Molecular Genetics in Southern Italy (BIOGEM), Naples, Italy – **Bioinformatics Programmer**.
- 2001: Adriano Buzzati Traverso (IGB), Naples, Italy – **Post–lauream pratice**.

PROFESSIONAL ACTIVITIES

- **Coordinator of the PhD program** in Functional and Structural Genomics at SISSA, Trieste, Italy, since 2019.
- **Member of the PhD committee** for the PhD program in Theoretical and Scientific Data Science at SISSA, Trieste, Italy, since 2022.
- **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** for the PhD program in Biology at the University of Naples Federico II, Naples, Italy, 2013–2018.
- **Member of the PhD committee** for 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.
- **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, Genes, Genomics, Scientific Data, Evolutionary Bioinformatics, Frontiers in Molecular Neuroscience, Helyon, Plos Genetics, Genome Research, Nature Communications.
- **Grant Reviewer** for: Fondation pour la Recherche Médicale (FRM), France; Italian Ministry of University and Research (MIUR), Italy.
- **Coordinator** of the "Career Development Advisory Plan" offered to SZN PhD students from 2014 to 2018.

GRANTS

- 2005–2008 – 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 in the area of Fundamental knowledge and basic tools for functional genomics in all organisms. Role: Work package leader assistant.
- 2009–2012 – 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. Role: Work package leader.
- 2011–2014 – 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. Role: Work package leader assistant.

- 2012–2015 – 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". Role: Member of the Technical Coordination Committee.
- 2013–2014 – Progetto Premiale MIUR MetaTrac: META–TRAsCrittomica delle fasi di sviluppo e di declino di fioriture algali nel Golfo di Napoli. Role: Co–coordinator.
- 2013–2014 – Progetto Premiale MIUR StarTrEgg: Meccanismi molecolari di controllo della fecondazione nelle uova della stella di mare Astropecten aranciacus. Role: Co–coordinator.
- 2013–2014 – 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). Role: Co–coordinator.
- 2013–2016 – RITMARE: Flagship Project of the National Research Programmes on marine research funded by the Italian MIUR. Role: Coordinator of two operative units.
- 2018–2022 – Gordon and Betty Moore Foundation. Marine Microbiology Initiative. DIsCO: Diatom life cycles, molecular controls and contribution to ecosystem dynamics. Role: Coordinator of bioinformatics.
- 2020–2021 – POR FSE 2014/2020 – Mobility of research fellows within the research centers of the European Commission Joint Research Centers (JRC). Development of a sequence–signatures–fishing bioinformatics pipeline. Role: Coordinator.
- 2024–2025 – Cascade grant within the PNRR National Center for Gene Therapy and Drugs based on RNA Technology: The SINAPPOME – Genomewide identification of SINEUP–like transcripts in the mammalian genome. Role: Coordinator.

ACADEMIC TEACHING

Aligned with the fundamental objectives of BIOS-10/A (ex BIO/13) courses, the focus of the training I give to my students covers the following areas: comparative analysis of genome organization across diverse organisms; bioinformatics; exploration of genome duplication mechanisms and gene expression dynamics; investigation into cellular and viral structural frameworks; elucidation of cellular compartmentalization principles and their functional implications; examination of cellular communication pathways and energy utilization strategies; study of sex determination mechanisms, recombination, and reproductive dynamics; exploration of cellular differentiation and developmental pathways; critical engagement with bibliographic resources. Furthermore, these areas constitute the primary outputs of my scientific research.

- 2013–ongoing: **Professor** of Experimental Biology (SSD BIOS-10/A) in the PhD program on Functional and Structural Genomics at SISSA, Trieste.
- 2019–2023: **Professor** (professore a contratto) of the Bioinformatics course for the Degree in Data Science and Scientific Computing at University of Trieste.
- 2013–2018: **Professor** (professore a contratto) of courses for the students of the PhD program in Biology of The University of Naples Federico II.
- 2010 and 2015: **Professor** of the Bioinformatics course in the PhD program of the SZN Open University.
- 2009–2011: **Cultore della Materia** of the Transcriptomic course in the Functional Genomics laurea degree at University of Trieste.
- 2010–2024: I have **supervised so far 11 PhD students to completion**. Of them, 9 have at least 1 publication with me (minimum 1, maximum 11). I am **currently supervising 4 PhD students**.

TALKS

- 2004 – Talk: 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.
- 2005 – Talk: The importance of being intron: lessons from conserved non–coding sequences. 2nd European Science Foundation Functional Genomics Conference, Oslo, Norway.
- 2006 – Talk: 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.
- 2008 – Invited seminar: Whole Genome Shuffling of Conserved Elements in the Chordate Genomes: Random Sampling or Evolutionary Reality? Stazione Zoologica Anton Dohrn, Naples, Italy.
- 2008 – Invited seminar: Whole Genome Shuffling of Conserved Elements in the Chordate Genomes: Random Sampling or Evolutionary Reality? Columbia University, New York, USA.
- 2011 – Invited seminar: Needs for Genomic Approaches in Cephalopods Research. Cephalopod Biology Research in the 21st Century—A European Perspective. Vico Equense, Naples, Italy.
- 2012 – Invited seminar: 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.
- 2012 – Talk: Transcriptome mining: examples of meta–analysis using gene expression data. EMBO Practical course: Bioinformatics and Comparative Genome Analyses. Stazione Zoologica Anton Dohrn, Naples, Italy.
- 2012 – Invited seminar: 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.
- 2014 – Invited seminar: The Octopus Transcriptome and an Intriguing Convergent Molecular Evolutionary Scenario. ALLBIO Congress – Broadening the Bioinformatics Infrastructure to Unicellular, Animal, and Plant Science. Florence, Italy.
- 2015 – Invited seminar: Transcription, transposons, noncoding and the evolution of organismal complexity. International School for Advanced Studies (SISSA), Trieste, Italy.
- 2015 – Organizer and Chair: Workshop on Metagenomics: Bridging Between Environment and Life. BioMedBridges Symposium. Wellcome Trust Genome Campus, Hinxton, UK.
- 2015 – Invited seminar: Transcription, transposons, non–coding and the evolution of organismal complexity. Università degli Studi del

Piemonte Orientale, Novara, Italy.

- 2016 – Talk: Transcription, Transposons, Noncoding and the Evolution of Organismal Complexity. RNA–Seq Workshop. University of Naples Federico II, Naples, Italy.
- 2013, 2014, 2015, 2016 – Invited seminar: Introduction to Bionformatics. University of Naples Federico II, Naples, Italy.
- 2018 – Invited seminar: Exploring the emerging role of transposable elements in the animal nervous system. University of Udine, Italy.
- 2021 – Invited seminar: Exploration of animal genomes and transcriptomes to understand the impact of transposable elements activity. Columbia University, New York.
- 2022 – Invited seminar: Transposons as a component of non coding RNA. University of Naples Federico II, Italy.
- 2023 – Invited seminar: The Well–Tempered Genome: co–option of transposable elements and the evolution of complexity. University of Turin, Italy.
- 2024 – Invited seminar: The Well–Tempered Genome: co–option of transposable elements and the evolution of complexity. Aachen University, Germany.

SELECTED MEETING CONTRIBUTIONS

- Genetics and genomics in *Pseudo-nitzschia* species. – EMBO Workshop The molecular life of diatoms, Paris, France, 2013.
- Prediction of cis–regulatory constraint in vertebrate lincRNAs by conservation of microsynteny. – The Noncoding Genome, EMBO/EMBL Symposia, EMBL, Heidelberg, Germany, 2013.
- Exploring signaling during sexual reproduction in *Pseudo-nitzschia multistriata*. – 3rd International Conference The Molecular Life of Diatoms, Seattle, USA, 2015.
- Bioinformatic exploration of transposable elements embedded in antisense long non–coding RNAs. – EMBO|EMBL Symposia: The Mobile Genome: Genetic and Physiological Impacts of Transposable Elements, Heidelberg, Germany, 2015.
- Molecular underpinning of diatom response to sexual cues enabled by the genome sequence of *Pseudo-nitzschia multistriata*. – The 17th International Conference On Harmful Algae, Florianópolis, Brazil, 2016.
- Genome–wide analysis of endogenous phospho–H2AX in mouse olfactory epithelium and liver. – EMBO|EMBL Conference From Functional Genomics to Systems Biology, Heidelberg, Germany, 2016.
- SPlinkerette Analysis of Mobile elements reveals extensive somatic variation of full length LINE1 elements in kidney. – EMBO|EMBL Conference From Functional Genomics to Systems Biology, Heidelberg, Germany, 2016.
- Exploratory analysis of retrotransposon activity in the octopus brain. – Genome Informatics, Wellcome Genome Campus, Cambridge, UK, 2018.
- Transposable elements expression in the *C. elegans* early embryo. – Genome Informatics, Wellcome Genome Campus, Cambridge, UK, 2018.
- Identification and prioritization of candidate causal genomic variations from individuals affected by ASD. – Conference on Target Validation Using Genomics and Informatics, EMBL–Wellcome Genome Campus, Cambridge, UK, 2019.
- Transposable element influence on transcriptional dynamics: insights from the murine zygotic genome activation. – 2nd meeting on Transposable Elements, Cold Spring Harbor Laboratory, USA, 2020.
- TEspeX: consensus specific quantification of transposable element expression preventing biases from exonized fragments. – EMBO| EMBL Symposia: The Mobile Genome: Genetic and Physiological Impacts of Transposable Elements, Heidelberg, Germany, 2021.
- Intron retention affect accurate and independent Transposable elements quantification in RNA–seq data. – Italian Bioinformatics Society annual meeting, virtual conference, 2021.
- Transposable elements activation following global DNA demethylation: exploration of transcriptional responses. – Italian Bioinformatics Society annual meeting, virtual conference, 2021.
- A cohort of seven individuals expanding the phenotype of Xia–Gibbs syndrome. – EuroDysmorpho 2023, 33rd European Meeting on Dysmorphology, Lisbon, Portugal, 2023.
- Understanding the function of AHDC1 using in *in-vitro* models. – EMBO Workshop: Epigenetics and condensates in lineage decision, Dresden, Germany, 2023.

PEER REVIEWED PUBLICATIONS

1. Jimenez–Gonzalez A, Ansaloni F, Nebendahl C, Alavioon G, Murray D, Robak W, **Sanges R**, Müller F, Immler S. *Paternal starvation affects metabolic gene expression during zebrafish offspring development and lifelong fitness.* Mol Ecol. 2024 Mar;33(6):e17296. doi: 10.1111/mec.17296.
2. Mangoni D, Simi A, Lau P, Armaos A, Ansaloni F, Codino A, Damiani D, Floreani L, Di Carlo V, Vozzi D, Persichetti F, Santoro C, Pandolfini L, Tartaglia GG, **Sanges R**$^{\$}$, Gustincich S$^{\$}$. *LINE-1 regulates cortical development by acting as long non–coding RNAs*. Nat Commun. 2023 Aug 17;14(1):4974. doi: 10.1038/s41467–023–40743–7.
3. Spirito G, Filosi M, Domenici E, Mangoni D, Gustincich S$^{\$}$, **Sanges R**$^{\$}$. *Exploratory analysis of L1 retrotransposons expression in autism*. Mol Autism. 2023 Jun 28;14(1):22. doi: 10.1186/s13229–023–00554–5.
4. Ansaloni F, Gustincich S$^{\$}$, **Sanges R**$^{\$}$. *In silico characterisation of minor wave genes and LINE-1s transcriptional dynamics at murine zygotic genome activation*. Front Cell Dev Biol. 2023 Jun 14;11:1124266. doi: 10.3389/fcell.2023.1124266.
5. Pierattini B, D'Agostino S, Bon C, Peruzzo O, Alendar A, Codino A, Ros G, Persichetti F, **Sanges R**, Carninci P, Santoro C, Espinoza S, Valentini P, Pandolfini L, Gustincich S. *SINEUP non–coding RNA activity depends on specific N6–methyladenosine nucleotides*. Mol Ther Nucleic Acids. 2023 Apr 7;32:402–414. doi: 10.1016/j.omtn.2023.04.002.
6. Gasperini C, Tuntevski K, Beatini S, Pelizzoli R, Lo Van A, Mangoni D, Cossu RM, Pascarella G, Bianchini P, Bielefeld P, Scarpato M, Pons–Espinal M, **Sanges R**, Diaspro A, Fitzsimons CP, Carninci P, Gustincich S, De Pietri Tonelli D. *Piwil2 (Mili) sustains neurogenesis and prevents cellular senescence in the postnatal hippocampus*. EMBO Rep. 2023 Feb 6;24(2):e53801. doi: 10.15252/embr.202153801.
7. Hadzhiev Y, Wheatley L, Cooper L, Ansaloni F, Whalley C, Chen Z, Finaurini S, Gustincich S, **Sanges R**, Burgess S, Beggs A, Müller F. *The miR-430 locus with extreme promoter density forms a transcription body during the minor wave of zygotic genome activation*. Dev Cell. 2023 Jan 23;58(2):155–170.e8. doi: 10.1016/j.devcel.2022.12.007.

8. Esposito M, Gualandi N, Spirito G, Ansaloni F, Gustincich S, **Sanges R**[$]. *Transposons Acting as Competitive Endogenous RNAs: In-Silico Evidence from Datasets Characterised by L1 Overexpression*. Biomedicines. 2022 Dec 17;10(12):3279. doi: 10.3390/biomedicines10123279.

9. Ansaloni F, Gualandi N, Esposito M, Gustincich S, **Sanges R**[$]. *TEspeX: consensus-specific quantification of transposable element expression preventing biases from exonized fragments*. Bioinformatics. 2022 Sep 15;38(18):4430–4433. doi: 10.1093/bioinformatics/btac526.

10. Pistollato F, Petrillo M, Clerbaux LA, Leoni G, Ponti J, Bogni A, Brogna C, Cristoni S, **Sanges R**, Mendoza-de Gyves E, Fabbri M, Querci M, Soares H, Munoz A, Whelan M, Van de Eede G. *Effects of spike protein and toxin-like peptides found in COVID-19 patients on human 3D neuronal/glial model undergoing differentiation: Possible implications for SARS-CoV-2 impact on brain development*. Reprod Toxicol. 2022 Aug;111:34-48. doi: 10.1016/j.reprotox.2022.04.011.

11. Hernandez-Clavijo A, Gonzalez-Velandia KY, Rangaswamy U, Guarneri G, Boscolo-Rizzo P, Tofanelli M, Gardenal N, **Sanges R**, Dibattista M, Tirelli G, Menini A. *Supporting Cells of the Human Olfactory Epithelium Co-Express the Lipid Scramblase TMEM16F and ACE2 and May Cause Smell Loss by SARS-CoV-2 Spike-Induced Syncytia*. Cell Physiol Biochem. 2022 Jun 7;56(3):254-269. doi: 10.33594/000000531.

12. Gualandi N, Iperi C, Esposito M, Ansaloni F, Gustincich S, **Sanges R**[$]. *Meta-Analysis Suggests That Intron Retention Can Affect Quantification of Transposable Elements from RNA-Seq Data*. Biology (Basel). 2022 May 27;11(6):826. doi: 10.3390/biology11060826.

13. Petrosino G, Ponte G, Volpe M, Zarrella I, Ansaloni F, Langella C, Di Cristina G, Finaurini S, Russo MT, Basu S, Musacchia F, Ristoratore F, Pavlinic D, Benes V, Ferrante MI, Albertin C, Simakov O, Gustincich S, Fiorito G[$], **Sanges R**[$]. *Identification of LINE retrotransposons and long non-coding RNAs expressed in the octopus brain*. BMC Biol. 2022 May 18;20(1):116. doi: 10.1186/s12915-022-01303-5.

14. Annunziata R, Mele BH, Marotta P, Volpe M, Entrambasaguas L, Mager S, Stec K, d'Alcalà MR, **Sanges R**, Finazzi G, Iudicone D, Montresor M, Ferrante MI. *Trade-off between sex and growth in diatoms: Molecular mechanisms and demographic implications.* Sci Adv. 2022 Jan 21;8(3):eabj9466. doi: 10.1126/sciadv.abj9466.

15. Casale AM, Liguori F, Ansaloni F, Cappucci U, Finaurini S, Spirito G, Persichetti F, **Sanges R**, Gustincich S, Piacentini L. *Transposable element activation promotes neurodegeneration in a Drosophila model of Huntington's disease.* iScience. 2021 Dec 28;25(1):103702. doi: 10.1016/j.isci.2021.103702.

16. Floreani L, Ansaloni F, Mangoni D, Agostoni E, **Sanges R**, Persichetti F, Gustincich S. *Analysis of LINE1 Retrotransposons in Huntington's Disease.* Front Cell Neurosci. 2022 Jan 14;15:743797. doi: 10.3389/fncel.2021.743797.

17. Zarantonello G, Arnoldi M, Filosi M, Tebaldi T, Spirito G, Barbieri A, Gustincich S, **Sanges R**, Domenici E, Di Leva F, Biagioli M. *Natural SINEUP RNAs in Autism Spectrum Disorders: RAB11B-AS1 Dysregulation in a Neuronal CHD8 Suppression Model Leads to RAB11B Protein Increase.* Front Genet. 2021 Nov 22;12:745229. doi: 10.3389/fgene.2021.745229.

18. Espinoza S, Bon C, Valentini P, Pierattini B, Matey AT, Damiani D, Pulcrano S, **Sanges R**, Persichetti F, Takahashi H, Carninci P, Santoro C, Cotella D, Gustincich S. *SINEUPs: a novel toolbox for RNA therapeutics.* Essays Biochem. 2021 Oct 27;65(4):775-789. doi: 10.1042/EBC20200114.

19. Papa R, Rusmini M, Schena F, Traggiai E, Coccia MC, Caorsi R, Arrigo S, Pasetti F, Signa S, Barone P, Santamaria G, Spirito G, **Sanges R**, Vozzi D, Cavalli A, Gustincich S, Ravelli A, Gattorno M, Ceccherini I, Volpi S. *Type I interferon activation in RAS-associated autoimmune leukoproliferative disease (RALD).* Clin Immunol. 2021 Oct;231:108837. doi: 10.1016/j.clim.2021.108837.

20. Napoletano F, Ferrari Bravo G, Voto IAP, Santin A, Celora L, Campaner E, Dezi C, Bertossi A, Valentino E, Santorsola M, Rustighi A, Fajner V, Maspero E, Ansaloni F, Cancila V, Valenti CF, Santo M, Artimagnella OB, Finaurini S, Gioia U, Polo S, **Sanges R**, Tripodo C, Mallamaci A, Gustincich S, d'Adda di Fagagna F, Mantovani F, Specchia V, Del Sal G. *The prolyl-isomerase PIN1 is essential for nuclear Lamin-B structure and function and protects heterochromatin under mechanical stress.* Cell Rep. 2021 Sep 14;36(11):109694. doi: 10.1016/j.celrep.2021.109694.

21. Pignata P, Apicella I, Cicatiello V, Puglisi C, Magliacane Trotta S, **Sanges R**, Tarallo V, De Falco S. *Prolyl 3-Hydroxylase 2 Is a Molecular Player of Angiogenesis.* Int J Mol Sci. 2021 Apr 9;22(8):3896. doi: 10.3390/ijms22083896.

22. Cerminara M, Spirito G, Pisciotta L, Squillario M, Servetti M, Divizia MT, Lerone M, Berloco B, Boeri S, Nobili L, Vozzi D, **Sanges R**, Gustincich S, Puliti A. *Case Report: Whole Exome Sequencing Revealed Disease-Causing Variants in Two Genes in a Patient With Autism Spectrum Disorder, Intellectual Disability, Hyperactivity, Sleep and Gastrointestinal Disturbances.* Front Genet. 2021 Feb 18;12:625564. doi: 10.3389/fgene.2021.625564.

23. Asai S, **Sanges R**, Lauritano C, Lindeque PK, Esposito F, Ianora A, Carotenuto Y. *De Novo Transcriptome Assembly and Gene Expression Profiling of the Copepod Calanus helgolandicus Feeding on the PUA-Producing Diatom Skeletonema marinoi.* Mar Drugs. 2020 Jul 27;18(8):392. doi: 10.3390/md18080392.

24. Bertuzzi M, Tang D, Calligaris R, Vlachouli C, Finaurini S, **Sanges R**, Goldwurm S, Catalan M, Antonutti L, Manganotti P, Pizzolato G, Pezzoli G, Persichetti F, Carninci P, Gustincich S. *A human minisatellite hosts an alternative transcription start site for NPRL3 driving its expression in a repeat number-dependent manner*. Hum Mutat. 2020 Apr;41(4):807-824. doi: 10.1002/humu.23974.

25. da Fonseca RR, Couto A, Machado AM, Brejova B, Albertin CB, Silva F, Gardner P, Baril T, Hayward A, Campos A, Ribeiro ÂM, Barrio-Hernandez I, Hoving HJ, Tafur-Jimenez R, Chu C, Frazão B, Petersen B, Peñaloza F, Musacchia F, Alexander GC, Osório H, Winkelmann I, Simakov O, Rasmussen S, Rahman MZ, Pisani D, Vinther J, Jarvis E, Zhang G, Strugnell JM, Castro LFC, Fedrigo O, Patricio M, Li Q, Rocha S, Antunes A, Wu Y, Ma B, **Sanges R**, Vinar T, Blagoev B, Sicheritz-Ponten T, Nielsen R, Gilbert MTP. *A draft genome sequence of the elusive giant squid, Architeuthis dux*. Gigascience. 2020 Jan 1;9(1):giz152. doi: 10.1093/gigascience/giz152.

26. Pargana A, Musacchia F, **Sanges R**, Russo MT, Ferrante MI, Bowler C, Zingone A. *Intraspecific Diversity in the Cold Stress Response of Transposable Elements in the Diatom Leptocylindrus aporus*. Genes (Basel). 2019 Dec 20;11(1):9. doi: 10.3390/genes11010009.

27. Spirito G, Mangoni D, **Sanges R**[$], Gustincich S[$]. *Impact of polymorphic transposable elements on transcription in lymphoblastoid cell lines from public data.* BMC Bioinformatics. 2019 Nov 22;20(Suppl 9):495. doi: 10.1186/s12859-019-3113-x.

28. Ansaloni F, Scarpato M, Di Schiavi E, Gustincich S[$], **Sanges R**[$]. *Exploratory analysis of transposable elements expression in the C. elegans early embryo.* BMC Bioinformatics. 2019 Nov 22;20(Suppl 9):484. doi: 10.1186/s12859-019-3088-7.

29. Fasolo F, Patrucco L, Volpe M, Bon C, Peano C, Mignone F, Carninci P, Persichetti F, Santoro C, Zucchelli S, Sblattero D, **Sanges R**, Cotella D, Gustincich S. *The RNA-binding protein ILF3 binds to transposable element sequences in SINEUP lncRNAs*. FASEB J. 2019 Dec;33(12):13572-13589. doi: 10.1096/fj.201901618RR. Epub 2019 Oct 25.

30. Credendino SC, Bellone ML, Lewin N, Amendola E, **Sanges R**, Basu S, Sepe R, Decaussin-Petrucci M, Tinto N, Fusco A, De Felice M, De Vita G. *A ceRNA Circuitry Involving the Long Noncoding RNA Klhl14-AS, Pax8, and Bcl2 Drives Thyroid Carcinogenesis*. Cancer Res. 2019 Nov 15;79(22):5746-5757. doi: 10.1158/0008-5472.CAN-19-0039. Epub 2019 Sep 26.

31. 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.

32. 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.
33. 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.
34. 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.
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*****: joint first author, [$]: corresponding author

According to law 679/2016 of the Regulation of the European Parliament of 27th April 2016, I hereby express my consent to process and use my data provided in this CV

Trieste, 08.08.2024

[redacted]