

PERSONAL INFORMATION

Luca Ambrosino



- ✉ [luca.bioinfo@gmail.com](mailto:luca.bioinfo@gmail.com) - [luca.ambrosino@szn.it](mailto:luca.ambrosino@szn.it)
- ☎ 3398496090
- 🌐 [www.linkedin.com/in/luca-ambrosino](https://www.linkedin.com/in/luca-ambrosino) - <https://orcid.org/0000-0003-1756-9538>

Sex Male | Date of birth 08/07/1979 | Nationality Italian

FIELD OF EXPERTISE

Computational Biology and Bioinformatics, Molecular Biotechnology

WORK EXPERIENCE

April 2022 – Today

**Technician**

Stazione Zoologica Anton Dohrn di Napoli (SZN) – Research Infrastructure for Marine Biological Resources (RIMAR) Department

- Member of the Bioinformatics, Computational Analysis & Data management (BAC) unit
- Bioinformatics services on behalf of SZN for structural and functional genomics, comparative genomics, molecular evolution of marine species
- Contact person for genomics, transcriptomics, proteomics and metabolomics within the “BAC” unit
- Prediction of ortholog and paralog genes
- RNA-seq analysis
- Differential expression analysis and co-expression networks identification
- Functional annotation
- Protein structure prediction and investigation

**Research areas** Computational Biology and Bioinformatics, Marine Biotechnology

November 2017 – March 2017

**Postdoctoral Researcher**

Stazione Zoologica Anton Dohrn di Napoli (SZN) – Research Infrastructure for Marine Biological Resources (RIMAR) Department

- Member of BIONforMA group (Bioinformatics for Marine Biology)
- Bioinformatics services on behalf of SZN for structural and functional genomics, comparative genomics, molecular evolution of marine species
- Contact person for genomics, transcriptomics, proteomics and metabolomics within “BIONforMA” group
- Prediction of ortholog and paralog genes
- RNA-seq analysis
- Differential expression analysis and co-expression networks identification
- Functional annotation
- Metabolic pathways investigation
- Protein structure prediction and investigation

**Research areas** Computational Biology and Bioinformatics, Marine Biotechnology

December 2016 – October 2017

**Scientific Collaboration**

Università degli Studi di Napoli “Federico II” – Agricultural Department

- Functional genomics analyses
- Prediction of ortholog and paralog genes

**Research areas** Computational Biology and Bioinformatics, Functional biology of yeasts

June 2016 – November 2016

**Postdoctoral Researcher**

Università degli Studi di Napoli “Federico II” – Agricultural Department

- Development of pipelines for the prediction of ortholog, paralog and species-specific genes in *Solanum lycopersicum* (tomato) and *Solanum tuberosum* (potato)

**Research areas** Computational Biology and Bioinformatics , Agricultural biotechnology

May 2016 – June 2016

### Contract for Occasional Work

NO SELF s.r.l. di Napoli

- Bioinformatics analyses of sequencing data from yeasts

**Research areas** Computational Biology and Bioinformatics, Functional biology of yeasts

December 2015 – April 2016

### Scientific Collaboration

Università degli Studi di Napoli “Federico II” – Agricultural Department

- Prediction of ortholog and paralog networks in *Solanum lycopersicum* (tomato) and *Vitis vinifera* (grape)

**Research areas** Computational Biology and Bioinformatics, Agricultural biotechnology

February 2015 – November 2015

### Research fellowship

Università degli Studi di Napoli “Federico II” – Agricultural Department

- Development of a bioinformatics platform for comparative genomics in Solanaceae
- Development of a pipeline for the comparison of ortholog and paralog networks
- Species-specific genes identification
- Functional domains prediction
- Metabolic network analyses

**Research areas** Computational Biology and Bioinformatics, Agricultural biotechnology

October 2013 – February 2015

### Research Grant

National Research Council (CNR) – Institute of Biosciences and BioResources (IBBR) di Portici

- Development of a database of paralog genes in *Arabidopsis thaliana*
- Development of a comparative approach based on the comparison of mRNA sequences of *Arabidopsis thaliana* and *Sorghum bicolor*
- Development of bioinformatics platform for functional and comparative genomics of species. Of agronomic interest

**Research areas** Computational Biology and Bioinformatics, Agricultural biotechnology

December 2012 - May 2013

### Post-graduate training

National Research Council (CNR) – Protein Biochemistry Institute (IBP) di Napoli

- Functional and structural characterization of extremophile enzymes with a biotechnological potential
- Extraction of metabolites from Antarctic bacteria

**Research areas** Computational Biology and Bioinformatics, Microbial biotechnology

## EDUCATION AND TRAINING

May 2013 – May 2016

### Ph.D. in Computational Biology and Bioinformatics

Università degli Studi di Napoli “Federico II” – Agricultural Department

- Development of a database of paralog genes in *Arabidopsis thaliana*
- Development of a software for the prediction of ortholog mRNA sequences
- Comparative analysis of *Solanum lycopersicum* (tomato) and *Vitis vinifera* (grape): prediction of ortholog, paralog and species-specific genes
- Prediction of protein domains, enzymatic class and metabolic pathways for *Solanum lycopersicum* (tomato), *Vitis vinifera* (grape) e *Solanum tuberosum* (potato)

**Thesis Title** Comparative Approaches for Plant Genomes: Unraveling “Intra” and “Inter” Species Relationships from Preliminary Gene Annotations

December 2009 – March 2012

**Master Degree in Molecular and Industrial Biotechnology**

Università degli Studi di Napoli “Federico II” – Biotechnology Department

**Thesis Title** A Structural Analysis of Four Novel Disease-Causing PAH Mutants

September 2006–December 2009

**Bachelor Degree in Molecular and Industrial Biotechnology**

Università degli Studi di Napoli “Federico II” – Biotechnology Department

**Thesis Title** Time-resolved fluorescence of coenzyme FAD**Publications**

- Pazzaglia, J., Santillán-Sarmiento, A., Ruocco, M., Dattolo, E., **Ambrosino, L.**, Marín-Guirao, L., & Procaccini, G. (2022). Local environment modulates whole-transcriptome expression in the seagrass *Posidonia oceanica* under warming and nutrients excess. *Environmental Pollution*, 119077. DOI: 10.1016/j.envpol.2022.119077
- Sabatino, V., Orefice, I., Marotta, P., **Ambrosino, L.**, Chiusano, M. L., d’ Ippolito, G., ... & Ferrante, M. I. (2022). Silencing of a *Pseudo-nitzschia arenysensis* lipoxygenase transcript leads to reduced oxylipin production and impaired growth. *New Phytologist*. DOI: <https://doi.org/10.1111/nph.17739>
- Esposito, A., **Ambrosino, L.**, Piazza, S., D’Aniello, S., Chiusano, M.L., Locascio, A. (2021). Evolutionary Adaptation of the Thyroid Hormone Signaling Toolkit in Chordates. *Cells* 10(12), 3391. DOI: <https://doi.org/10.3390/cells10123391>
- Sañé, E., Del Mondo, A., **Ambrosino, L.**, Smerilli, A., Sansone, C., & Brunet, C. (2021). The Recent Advanced in Microalgal Phytosterols: Bioactive Ingredients Along With Human-Health Driven Potential Applications. *Food Reviews International*, 1-20. DOI: <https://doi.org/10.1080/87559129.2021.1938115>
- Marotta, P., Salatiello, F., **Ambrosino, L.**, Berruto, F., Chiusano, M. L., & Locascio, A. (2021). The ascidia *Ciona robusta* provides novel insights on the evolution of the AP-1 transcriptional complex. *Frontiers in Cell and Developmental Biology*, 2093. DOI: <https://doi.org/10.3389/fcell.2021.709696>
- Del Mondo, A., Smerilli, A., **Ambrosino, L.**, Albini, A., Noonan, D. M., Sansone, C., & Brunet, C. (2021). Insights into phenolic compounds from microalgae: structural variety and complex beneficial activities from health to nutraceuticals. *Critical Reviews in Biotechnology*, 41(2), 155-171. DOI: <https://doi.org/10.1080/07388551.2021.1874284>
- Ruocco, M., **Ambrosino, L.**, Jahnke, M., Chiusano, M. L., Barrote, I., Procaccini, G., Silva, J, and Dattolo, E. (2020). m6A RNA Methylation in Marine Plants: First Insights and Relevance for Biological Rhythms. *International Journal of Molecular Sciences*, 21(20), 7508. DOI: <https://doi.org/10.3390/ijms21207508>
- Ambrosino, L.**, Colantuono, C., Diretto, G., Fiore, A., and Chiusano, M. L. (2020). Bioinformatics Resources for Plant Abiotic Stress Responses: State of the Art and Opportunities in the Fast Evolving-Omics Era. *Plants*, 9(5), 591. DOI: <https://doi.org/10.3390/plants9050591>
- Lauritano, C., Roncalli, V., **Ambrosino, L.**, Cieslak, M. C., and Ianora, A. (2020). First De Novo Transcriptome of the Copepod *Rhincalanus gigas* from Antarctic Waters. *Biology*, 9(11), 410. DOI: <https://doi.org/10.3390/biology9110410>
- Elagoz, Ali M., **Ambrosino, L.**, and Lauritano, C. (2020) "De novo transcriptome of the diatom *Cylindrotheca closterium* identifies genes involved in the metabolism of anti-inflammatory compounds." *Scientific reports* 10.1: 1-9. DOI: <https://doi.org/10.1038/s41598-020-61007-0>
- Ambrosino, L.**; Tangherlini, M.; Colantuono, C.; Esposito, A.; Sangiovanni, M., Miralto, M., Sansone, C., and Chiusano, M.L. (2019). "Bioinformatics for Marine Products: An Overview of Resources, Bottlenecks, and Perspectives." *Marine drugs* 17, (10). DOI: 10.3390/md17100576
- Esposito, A.; Tamburini, S.; Triboli, L.; **Ambrosino, L.**; Chiusano, M. L., and Jousson, O. (2019) "Insights into the genome structure of four acetogenic bacteria with specific reference to the Wood-Ljungdahl pathway." *MicrobiologyOpen* 2019, e938. DOI: 10.1002/mbo3.938.
- Ambrosino, L.**, Vassalli, Q. A., D’Agostino, Y., Esposito, R., Cetrangolo, V., Caputi, L., Amoroso, A., Aniello, F., D’Aniello, S., Chatzigeorgiou, M., Chiusano, M.L., and Locascio, A. (2019). "Functional conserved non-coding elements among tunicates and chordates." *Dev Biol* 448(2): 101-110. DOI: 10.1016/j.ydbio.2018.12.012
- Ambrosino, L.**, Ruggieri, V., Bostan H., Miralto, M., Vitulo, N., Zouine, M., Barone, A., Bouzayen, M., Frusciante, L., Pezzotti, M., Valle, G., Chiusano, M.L. (2018) "Multilevel comparative bioinformatics to investigate evolutionary relationships and specificities in gene annotations", *BMC Bioinformatics* 19(15): 435. DOI: 10.1186/s12859-018-2420-y
- Ambrosino, L.**, Colantuono, C., Monticcolo, F., and Chiusano, M. L. (2018). "Bioinformatics resources for plant genomics: bottlenecks and opportunities in the -omics era." in "Next-generation Sequencing and Bioinformatics for Plant Science" *Current Issues in Molecular Biology* 71-88 DOI: 10.21775/cimb.027.071
- Ambrosino, L.**, Chiusano, M.L. (2017). "Transcriptologs: a transcriptome-based approach to predict orthology relationships." *Bioinformatics and Biology Insights* 11 DOI:

10.1177/1177932217690136

17. **Ambrosino, L.**, Bostan, H., Ruggieri, V., and Chiusano, M. L. (2016). "Bioinformatics resources for pollen." *Plant reproduction* 29 (1-2), 133-147 DOI: 10.1007/s00497-016-0284-8
18. De Santi, C., B. Altermark, M. M. Pierechod, **L. Ambrosino**, D. de Pascale and N. P. Willassen (2016). "Characterization of a cold-active and salt tolerant esterase identified by functional screening of Arctic metagenomic libraries." *BMC Biochem* 17(1): 1 DOI: 10.1186/s12858-016-0057-x
19. **Ambrosino, L.**, H. Bostan, P. di Salle, M. Sangiovanni, A. Vigilante and M. L. Chiusano (2016). "pATsi: Paralogs and Singleton Genes from Arabidopsis thaliana." *Evol Bioinform Online* 12: 1-7 DOI: 10.4137/EBO.S32536
20. De Santi, C., **L. Ambrosino**, P. Tedesco, L. Zhai, C. Zhou, Y. Xue, Y. Ma and D. de Pascale (2015). "Identification and characterization of a novel salt-tolerant esterase from a Tibetan glacier metagenomic library." *Biotechnol Prog* 31(4): 890-899 DOI: 10.1002/btpr.2096
21. Maiorano, F., **L. Ambrosino** and M. R. Guarracino (2015). The MetaboX Library: Building Metabolic Networks from KEGG Database. *Bioinformatics and Biomedical Engineering: Third International Conference, IWBBIO 2015, Granada, Spain, April 15-17, 2015, Proceedings, Part I.* F. Ortuño and I. Rojas. Cham, Springer International Publishing: 565-576 DOI: 10.1007/978-3-319-16483-0\_55
22. De Santi, C., P. Tedesco, **L. Ambrosino**, B. Altermark, N. P. Willassen and D. de Pascale (2014). "A New Alkaliphilic Cold-Active Esterase from the Psychrophilic Marine Bacterium *Rhodococcus* sp.: Functional and Structural Studies and Biotechnological Potential." *Appl Biochem Biotechnol.* DOI: 10.1007/s12010-013-0713-1 t

#### Scientometric indices (April, 2022)

- Number of ISI publications with Impact Factor: 21
- H index: 8
- Numero citations: 193

#### Awards

- Winner of a Grant to present the research activity related to the comparative analysis between tomato and grapevine based on the comparison of sequences and of expression data, entitled: "Characterization of derivative relationship between tomato and grapevine: a key step to investigate fruit development in the two species" to the international Congress "Quality Fruit 2014, 3rd Annual Conference of the Cost Action FA1106" 21-24 Settembre 2014 Chania, Greece

#### Speaker at Conferences

1. L. Ambrosino, C. Colantuono, M. Miralto, M. Sangiovanni, M.L. Chiusano (2017). "A multilevel comparative genomics approach to check for inter and intra species relationships and gene predictions" - 12th BBCC - Bioinformatics and Computational Biology International Conference, Naples, Italy, 18-20 December 2017
2. L. Ambrosino, H. Bostan, V. Ruggieri, M.L. Chiusano (2016). "An integrated multi-level comparison highlights common aspects and specific features between distantly-related species: Tomato and Grapevine" - BITS 2016, 13th Annual Meeting of the Bioinformatics Italian Society, June 15-17, 2016, University of Salerno, Italy
3. L. Ambrosino, H. Bostan, V. Ruggieri, L. Frusciantè, M.L. Chiusano (2015). "Solanum lycopersicum versus Vitis vinifera: a multilevel gene comparison from fleshy fruit species" – joint Congress SIBV-SIGA 2015, Feeding the planet: plant science and breeding for the future, September 8-11th Milano, Italy
4. L. Ambrosino, H. Bostan, V. Ruggieri, M.L. Chiusano – "Characterization of derivative relationship between tomato and grapevine: a key step to investigate fruit development in the two species" – Quality Fruit 2014, 3rd Annual Conference of the Cost Action FA1106, September 21-24th Chania, Greece

#### Seminars, organization of courses and supervision

- Speaker of the introductory tutorial "BLAST service at SZN – an example for TARA data", 18 September 2020, Stazione Zoologica Anton Dohm, about the use of BLAST-based platforms developed by the bioinformatics unit of SZN.
- Co-organizer of the international course "Metabarcoding And Metagenomic Data Processing And Analyses", 3-7 February 2020, Stazione Zoologica Anton Dohm, Assemble+ course (Co-funded by EMBRC)
- Lecturer of the theoretical lesson "Introduction to bioinformatics" to the students of the University of Rome "La Sapienza" visiting the Stazione Zoologica Anton Dohm of Naples, 10 January 2020
- Lecturer of the practical lesson "Protein function and evolution: Databases and tools to predict and visualize protein structures", PhD Programme Course (Curriculum BEOM), 9 December 2019, Stazione Zoologica Anton Dohm of Naples
- Lecturer of the PhD course of Stazione Zoologica Anton Dohm "Basic course in Bioinformatics" 15-

18 July 2019, Stazione Zoologica Anton Dohrn of Naples, with two theoretical and practical lessons “Sequence alignments (global, local, multiple)” and “Functional annotation (Interpro, GO, KEGG)” (<https://bioinfo.szn.it/basic-course-in-bioinformatics/>)

- Co-organizer of the course “1st International Summer School on Marine Ecotoxicology” 1-5 July 2019, Stazione Zoologica Anton Dohrn of Naples
- Co-organizer of the course “Data Carpentry for Ecologist” 6-7 February 2019, Stazione Zoologica Anton Dohrn di Napoli (<https://alevigi.github.io/2019-2-6-SZN/>)
- Speaker of the internal seminary “Comparative genomics and Structural proteomics: sequence and structural similarities to unveil hidden features”, during the “BIOINforMA meets SZN” meeting, 19 July 2018, Stazione Zoologica Anton Dohrn of Naples
- Tutor to MD thesis activity in Bioinformatics “Development of strategies to analyze biological data” of grad student in Informatics Daniele Del Monaco (2016)
- Tutor to MD thesis activity in Bioinformatics “Comparative genomics of plant species: Reconciliation and gene annotations analyses” of grad student in Biology Carlo Impradice
- Tutor to BD thesis activity in Bioinformatics “Characterization of EST sequences from *Solanum lycopersicum*” of General and Applied Biology grad student Noemi Di Bernardo (2013)

#### Participation to Projects

Participation to the following projects carrying out bioinformatics activities supporting experimental analyses:

- 2022: SEA-Stress (Israeli-Italian Scientific and Technological Cooperation, MAECI, Italy)
- 2021: European Union’s Horizon 2020 (grant agreements No. 654008 e 730984)
- 2021: Antitumor Drugs and Vaccines from the Sea (ADVISE) (PG/2018/0494374)
- 2020: Marine Hazard (PON03PE\_00203\_1) of Ministero dell’Istruzione, dell’Università e della Ricerca (MIUR)
- 2020: COST Action CA15136 - European network to advance carotenoid research and applications in agro-food and health (EUROCAROTEN)
- 2020: COST Action CA18210 - Oxygen sensing a novel mean for biology and technology of fruit quality
- 2019: Partecipazione alla stesura della proposta di associatura che ha permesso alla Stazione Zoologica Anton Dohrn di entrare a far parte del nodo italiano di “ELIXIR” ([https://elixir-italy.org/member/stazione\\_zoologica\\_anton\\_dohrn/](https://elixir-italy.org/member/stazione_zoologica_anton_dohrn/))
- 2017: Italian Flagship project “Bioinformatica per la Biologia Marina”
- 2016: AIB 2011 Parco Nazionale del Cilento e Vallo di Diano
- 2016: Solanaceae Pollen Thermotolerance – Marie Curie Initial Training Network project (grant agreement no. 289220)
- 2016: Molecules for the future Novel enzyme activities from environmental libraries – MARZymes (grant No. 219710 finanziato dal “Research Council of Norway”)
- 2016: Bioprospecting for drug and enzymes discovery from Antarctic and Arctic sub-sea sediments (grant No. 192123 finanziato dal “Research Council of Norway”)
- 2015-2017: GENHORT - Valorizzazione di produzioni ortive campane di eccellenza con strumenti di genomica avanzata (PON02\_00395\_3215002)
- 2015-2017: GENOPOM PRO Potenziamento della filiera pomodoro attraverso l’uso di piattaforme integrate di post-genomica (PON02\_00395\_3082360)
- 2015: MIUR project PON02 00619
- 2015: Italian Flagship project “Interomics”
- 2015: CNR-CAS Cooperation Agreement 2011–2013 “Discovery of new extremozymes and their potential use in biotechnology”
- 2014-2017: COST Action FA1106 - An integrated systems approach to determine the developmental mechanisms controlling fleshy fruit quality in tomato and grapevine
- 2014: P.N.R.A. (Italian National Antarctic Research Programme) 2009–2011
- 2013: C.A.R.I.N.A. – Sicurezza, sostenibilità e competitività delle produzioni agroalimentari della Campania (P.O.R. Campania FSE 2007-2013)

#### Reviewer for scientific journals

- MDPI *Gene*
- MDPI *Foods*
- MDPI *Biology*