

## Elenco pubblicazioni e tesi di dottorato presentate

Selezione di 12 pubblicazioni, per ogni articolo l' impact factor del giornale di pubblicazione e il numero di citazioni sono riportati tra parentesi:

1. **Basile A**, Heinken A, Hertel J, Smarr L, Li W, Treu L, Valle G, Campanaro S & Thiele I (2023) Longitudinal flux balance analyses of a patient with episodic colonic inflammation reveals microbiome metabolic dynamics. *Gut Microbes* 15: 2226921 (citations: 1; IF: 9.4)
2. **Basile A\***, Zampieri G, Kovalovszki A, Karkaria B, Treu L, Patil KR & Campanaro S (2023) Modelling of microbial interactions in anaerobic digestion: from black to glass box. *Curr Opin Microbiol* 75: 102363 (citations: 0 ; IF: 5.4)
3. De Bernardini N, **Basile A**, Zampieri G, Kovalovszki A, De Diego Diaz B, Offer E, Wongfaed N, Angelidaki I, Kougias PG, Campanaro S, et al (2022) Integrating metagenomic binning with flux balance analysis to unravel syntrophies in anaerobic CO<sub>2</sub> methanation. *Microbiome* 10: 117 (citations: 18; IF: 16.8)
4. Rossi A, Morlino MS, Gaspari M, **Basile A**, Kougias P, Treu L & Campanaro S (2022) Analysis of the anaerobic digestion metagenome under environmental stresses stimulating prophage induction. *Microbiome* 10: 125 (citations: 4; IF: 16.8)
5. Palù M, **Basile A\***, Zampieri G, Treu L, Rossi A, Morlino MS & Campanaro S (2022) KEMET – A python tool for KEGG Module evaluation and microbial genome annotation expansion. *Comput Struct Biotechnol J* 20: 1481–1486 (citations: 8; IF: 6)
6. Heinken A, **Basile A** & Thiele I (2021) Advances in constraint-based modelling of microbial communities. *Curr Opin Syst Biol* 27: 100346 (citations: 19; IF: 3.7)
7. **Basile A**, De Pascale F, Bianca F, Rossi A, Frizzarin M, De Bernardini N, Bosaro M, Baldissari A, Antoniali P, Lopreiato R, et al (2021) Large-scale sequencing and comparative analysis of oenological *Saccharomyces cerevisiae* strains supported by nanopore refinement of key genomes. *Food Microbiol* 97: 103753 (citations: 8; IF: 5)
8. **Basile A**, Campanaro S, Kovalovszki A, Zampieri G, Rossi A, Angelidaki I, Valle G & Treu L (2020) Revealing metabolic mechanisms of interaction in the anaerobic digestion microbiome by flux balance analysis. *Metab Eng* 62: 138–149 (citations: 32; IF: 15.6)
9. Yan M, Treu L, Zhu X, Tian H, **Basile A**, Fotidis IA, Campanaro S & Angelidaki I (2020) Insights into ammonia adaptation and methanogenic precursor oxidation by genome-centric analysis. *Environ Sci Technol* (citations: 45; IF: 8)
10. Shi Z, Campanaro S, Usman M, Treu L, **Basile A**, Angelidaki I, Zhang S & Luo G (2021) Genome-Centric Metatranscriptomics Analysis Reveals the Role of Hydrochar in Anaerobic Digestion of Waste Activated Sludge. *Environ Sci Technol* 55: 8351–8361 (citations: 57; IF: 11.4)
11. Campanaro S, Treu L, Rodriguez-R LM, Kovalovszki A, Ziels RM, Maus I, Zhu X, Kougias PG, **Basile A**, Luo G, et al (2020) New insights from the biogas microbiome by comprehensive genome-resolved metagenomics of nearly 1600 species originating from multiple anaerobic digesters. *Biotechnol Biofuels* 13: 25 (citations: 113; IF: 6)
12. Fontana A, Falasconi I, Molinari P, Treu L, **Basile A**, Vezzi A, Campanaro S & Morelli L (2019) Genomic Comparison of *Lactobacillus helveticus* Strains Highlights Probiotic Potential. *Front Microbiol* 10 (citations: 39; IF: 4.23)

Tesi di dottorato:

*English title: Combining omics approaches with flux balance analysis for unraveling population dynamics in anaerobic microbiomes*

*Titolo italiano: Combinazione di approcci omici con analisi di equilibri di flusso per esplorare le dinamiche di popolazione in microbiomi anaerobici*

### **Peer reviewed publications (published):**

1. **2022.** The biofouling process: The science behind a valuable phenomenon for aquaculture. *Review in Aquaculture* **2022**;1–15. <https://doi.org/10.1111/raq.12770>. **FI:10.6; Q1**
2. **2022.** Mature biofloc harbor similar bacterial communities regardless of the vegetal floating substrates (oat, amaranth, or wheat) used as promoters. *Aquaculture International* (2022) <https://doi.org/10.1007/s10499-022-00970-z>. **FI:2.9; Q2**
3. **2022.** Detection of human pathogenic bacteria in sea lions rectal DNA samples from Gulf of California, Mexico. *Scientific Reports* **12**, 14859 (2022) <https://doi.org/10.1038/s41598-022-18903-4>. **FI:4.6; Q1**
4. **2022.** Multi-locus evaluation of gastrointestinal bacterial communities from *Zalophus californianus* pups in the Gulf of California, Mexico. *PeerJ* **10**:e13235 <https://doi.org/10.7717/peerj.13235>. **FI:3.06; Q1**
5. **2022.** The role of diversity in mediating microbiota structural and functional responses in two abalone species under stressed withering syndrome conditions. *Microbial Ecology* **2022**:1-11 <https://doi.org/10.1007/s00248-022-01970-5>. **FI:4.19; Q1**
6. **2021.** Environmental conditions drive zooplankton community structure in the deep-water region of the southern Gulf of Mexico: a molecular approach. *Molecular Ecology* **31**:546-561 <https://doi.org/10.1111/mec.16251>. **FI:6.62; Q1**
7. **2021.** Longitudinal variations in the gastrointestinal microbiome of the white shrimp, *Litopenaeus vannamei*. *PeerJ* **9**:e11827 <https://doi.org/10.7717/peerj.11827>. **FI:3.06; Q1**
8. **2021.** Therapeutic modulation of fish gut microbiota, a feasible strategy for aquaculture? *Aquaculture*, **544**:737050 <https://doi.org/10.1016/j.aquaculture.2021.737050>. **FI:5.13; Q1**
9. **2020.** Gut microbiota shifts in the giant tiger shrimp, *Penaeus monodon*, during postlarvae, juvenile and adult stages. *Aquaculture International*, **28**:1421–1433 <https://doi.org/10.1007/s10499-020-00532-1>. **FI:2.95; Q2**
10. **2018.** Structure, dynamics and predicted functional ecology of the gut microbiota of the blue (*Haliotis fulgens*) and yellow (*H. corrugata*) abalone from Baja California Sur, Mexico, **2018**. *PeerJ*, **6**:e5830 <https://doi.org/10.7717/peerj.5830>. **FI:3.06; Q1**
11. **2018.** Monomorphic pathogens: the case of *Candidatus Xenohalictis californiensis* from abalone in California, USA and Baja California, Mexico. *Journal of Invertebrate Pathology*, **154**:19-23. <https://doi.org/10.1016/j.jip.2018.03.012>. **FI:2.97; Q1**
12. **2017.** Multigenetic characterization of “*Candidatus Xenohalictis californiensis*.” *International journal of systematic and evolutionary microbiology*, **67**:42–49. <https://doi.org/10.1099/ijsem.0.001563>. **FI:2.68; Q2**

### **PhD Thesis:**

Genetic characterization of “*Candidatus Xenohalictis californiensis*” associated with blue (*Haliotis fulgens*) and yellow abalone (*Haliotis corrugata*) on the Pacific coast of Baja California.

# Arianna Basile- *Curriculum Vitae*

## Personal Data

## Education & Relevant Positions

I have contributed to developing novel bioinformatics approaches for analysis of transcriptome data and reconstruction of microbial genomes from metagenomic data. I use bioinformatics to build metabolic models of microbial species in projects aimed to process optimization and to develop new tools for **integrating metagenomics with flux balance analyses**. I am currently studying the **molecular and metabolic mechanisms involved in shaping environmental and human-related microbiomes to unravel population dynamics**.

### Positions:

- *Jan 2022 - ongoing*: **Research associate** at MRC Toxicology Unit, University of Cambridge under the supervision of professor Kiran Raosaheb Patil: My main area of expertise is a computational approach called Flux Balance Analysis, used in particular to analyse the complex metabolism of bacteria and the network of interactions participated by microbial species. In order to quantitatively study microbiomes.
- *Oct 2021 to Jan 2022*: **Research assistant** at University of Padua, Department of biology under the supervision of Prof. Stefano Campanaro topic: “Analisi molecolare e bioinformatica a partire da campioni di DNA e RNA di ceppi di *Saccharomyces cerevisiae* di interesse enologico”: During these two months of collaboration, I developed and applied a pipeline for transcriptomics data analysis. The aim of the experiment was the analysis of differences between two *Saccharomyces cerevisiae* strains (i.e. CE2P and D20) and their differential use of sulphate.

### Education:

- *Oct 2018 to Sep 2021*: **PhD** in Bioscience cum laude – Bioinformatics, genetics and genomics curriculum, Department of Biology, University of Padua. Thesis: “*Combining omics approaches with flux balance analysis for unraveling population dynamics in anaerobic microbiomes*.”
- *Oct 2020 to Mar 2021* **PhD** external period at National University of Ireland in Galway. Title project: “*Integrated Analyses of Longitudinal Metabolome Data in long-term time course of a cohort of patients affected by Crohn's Disease*.”
- *Oct 2016 to July 2018*: **M.Sc. Diploma** in Bioinformatics, final mark 110/110 cum laude.
- *Oct 2014 to July 2016*: **B.Sc. Diploma** in Biology, University of Tor Vergata, final mark 110/110 cum laude.

## Project Writing, Management

List of relevant **funded** projects at national and international level:

- ✓ EMBO short-term fellowship n. 8720, title: “*Integrated Analyses of Longitudinal Metabolome Data in long-term time course of a cohort of patients affected by Crohn's Disease*.” Total budget: €9,000

## Supervising, Teaching & Reviewing

### Teaching activity

- ✓ I participated in the teaching of Part III Systems Biology, course of Systems biology (ID 24 INT, theme “Metabolic modelling”) at University of Cambridge (AA 2021/2022, AA 2022/2023)
- ✓ I organized and tutored the laboratory course at Part III Systems Biology at University of Cambridge (AA 2022/2023) under the supervision of Prof. Kiran Raosaheb Patil. For this aim I realized the github repository: <https://github.com/arianccbasile/Systems-Biology-practical2022>
- ✓ I supervised the laboratory course (Didattica di supporto) of Bioinformatics (AA 2018/2019, AA 2019/2020, AA 2020/2021) and Informatics (AA 2018/2020, AA 2020/2021) courses in the Bachelor Degree of Molecular Biology, Department of Biology, University of Padua
- ✓ I supervised the laboratory course (Didattica di supporto) of Metagenomics (AA 2020/2021) courses in the Master Degree of Molecular Biology, Department of Biology, University of Padua. The supervision culminated in the development of the software NEMETEX: <https://github.com/palakela/NEMETEX>,

## Student supervision

I have been co-supervisor of 2 Master students at University of Padua, Biology Department and at MRC Toxicology Unit, University of Cambridge in a collaborative framework with Imperial college in London.

## Article, Grant Reviewing and Editorials

I serve as a **scientific reviewer** for a number of journals including: Frontiers in Microbiology, Bioresource Technology, Applied Energy, Applied Microbiology and Biotechnology.

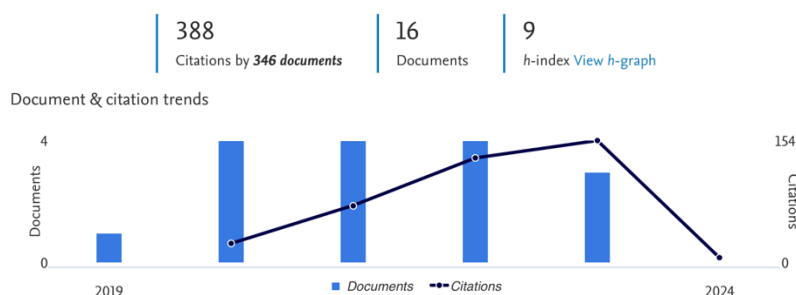
I am member of the Science Media Centre (SMC) expert database with the aim of ensuring that news journalists have access to good evidence-based science, when science hits the headlines. My views are included in Daily Mail and New Atlas articles.

## Dissemination & Scientific Publications

During my career I have personally attended to **more than 10 international congress and conferences in person or online**. Relevant **oral contribution** that I presented at national and international conferences:

1. QuantBio symposium 2023, 30/11/2023-01/12/2023. Arianna Basile, Extensive depiction of microbial metabolism improves modelling of gut communities
2. 6<sup>th</sup> conference on innovation in nutrition and food science (INFS2022) 06/10/2022-08/10/2022. Arianna Basile, Comparative genomics for probiotics and yeast strain selection
3. 7th Conference on Constraint-Based Reconstruction and Analysis (COBRA 2021). 1/03/2021-2/03/2021, Online. Arianna Basile, Modeling the Syntrophy between Methanothermobacter sp. DTU051 and Clostridiales sp. DTU010 in biofilm samples Using a Combination of Physicochemical Evidence
4. HELLENIC BIOINFORMATICS 12. 11-13 October 2019, Heraklion (GR). Arianna Basile, Flux balance analysis unveiled the dynamicity of microbial interactions in anaerobic digestion system during the shift between different experimental conditions

Bibliometric statistics from Scopus, one of the most relevant bibliographic source:



Top selection of 12 relevant ISI publications (\*corresponding author; +co-first author), the IF is reported according to the year of publication for each manuscript, in parenthesis number of citations and IF reported according to the year of publication for each manuscript:

1. **Basile A**, Heinken A, Hertel J, Smarr L, Li W, Treu L, Valle G, Campanaro S & Thiele I (2023) Longitudinal flux balance analyses of a patient with episodic colonic inflammation reveals microbiome metabolic dynamics. Gut Microbes 15: 2226921 (citations: 1; IF: 9.4)
2. **Basile A\***, Zampieri G, Kovalovszki A, Karkaria B, Treu L, Patil KR & Campanaro S (2023) Modelling of microbial interactions in anaerobic digestion: from black to glass box. Curr Opin Microbiol 75: 102363 (citations: 0 ; IF: 5.4)
3. De Bernardini N, **Basile A**, Zampieri G, Kovalovszki A, De Diego Diaz B, Offer E, Wongfaed N, Angelidaki I, Kougias PG, Campanaro S, et al (2022) Integrating metagenomic binning with flux balance analysis to unravel syntrophies in anaerobic CO<sub>2</sub> methanation. Microbiome 10: 117 (citations: 18; IF: 16.8)

4. Rossi A, Morlino MS, Gaspari M, **Basile A**, Kougias P, Treu L & Campanaro S (2022) Analysis of the anaerobic digestion metagenome under environmental stresses stimulating prophage induction. *Microbiome* 10: 125 (citations: 4; IF: 16.8)
5. Palù M, **Basile A**<sup>+</sup>, Zampieri G, Treu L, Rossi A, Morlino MS & Campanaro S (2022) KEMET – A python tool for KEGG Module evaluation and microbial genome annotation expansion. *Comput Struct Biotechnol J* 20: 1481–1486 (citations: 8; IF: 6)
6. Heinken A, **Basile A** & Thiele I (2021) Advances in constraint-based modelling of microbial communities. *Curr Opin Syst Biol* 27: 100346 (citations: 19; IF: 3.7)
7. **Basile A**, De Pascale F, Bianca F, Rossi A, Frizzarin M, De Bernardini N, Bosaro M, Baldisseri A, Antoniali P, Lopreiato R, et al (2021) Large-scale sequencing and comparative analysis of oenological *Saccharomyces cerevisiae* strains supported by nanopore refinement of key genomes. *Food Microbiol* 97: 103753 (citations: 8; IF: 5)
8. **Basile A**, Campanaro S, Kovalovszki A, Zampieri G, Rossi A, Angelidaki I, Valle G & Treu L (2020) Revealing metabolic mechanisms of interaction in the anaerobic digestion microbiome by flux balance analysis. *Metab Eng* 62: 138–149 (citations: 32; IF: 15.6)
9. Yan M, Treu L, Zhu X, Tian H, **Basile A**, Fotidis IA, Campanaro S & Angelidaki I (2020) Insights into ammonia adaptation and methanogenic precursor oxidation by genome-centric analysis. *Environ Sci Technol* (citations: 45; IF: 8)
10. Shi Z, Campanaro S, Usman M, Treu L, **Basile A**, Angelidaki I, Zhang S & Luo G (2021) Genome-Centric Metatranscriptomics Analysis Reveals the Role of Hydrochar in Anaerobic Digestion of Waste Activated Sludge. *Environ Sci Technol* 55: 8351–8361 (citations: 57; IF: 11.4)
11. Campanaro S, Treu L, Rodriguez-R LM, Kovalovszki A, Ziels RM, Maus I, Zhu X, Kougias PG, **Basile A**, Luo G, et al (2020) New insights from the biogas microbiome by comprehensive genome-resolved metagenomics of nearly 1600 species originating from multiple anaerobic digesters. *Biotechnol Biofuels* 13: 25 (citations: 113; IF: 6)
12. Fontana A, Falasconi I, Molinari P, Treu L, **Basile A**, Vezzi A, Campanaro S & Morelli L (2019) Genomic Comparison of *Lactobacillus helveticus* Strains Highlights Probiotic Potential. *Front Microbiol* 10 (citations: 39; IF: 4.23)

Full list of the **16 ISI Web of Science publications** (\*corresponding author; <sup>+</sup>co-first author), in parenthesis number of citations and IF reported according to the year of publication for each manuscript:

1. **Basile A**, Heinken A, Hertel J, Smarr L, Li W, Treu L, Valle G, Campanaro S & Thiele I (2023) Longitudinal flux balance analyses of a patient with episodic colonic inflammation reveals microbiome metabolic dynamics. *Gut Microbes* 15: 2226921 (citations: 1; IF: 9.4)
2. **Basile A**<sup>\*</sup>, Zampieri G, Kovalovszki A, Karkaria B, Treu L, Patil KR & Campanaro S (2023) Modelling of microbial interactions in anaerobic digestion: from black to glass box. *Curr Opin Microbiol* 75: 102363 (citations: 0 ; IF: 5.4)
3. Cesur MF, **Basile A**, Patil KR & Çakır T (2023) A new metabolic model of *Drosophila melanogaster* and the integrative analysis of Parkinson's disease. *Life Sci Alliance* 6 (citations: 0; IF: 6.8)
4. Rossi A, Morlino MS, Gaspari M, **Basile A**, Kougias P, Treu L & Campanaro S (2022) Analysis of the anaerobic digestion metagenome under environmental stresses stimulating prophage induction. *Microbiome* 10: 125 (citations: 4; IF: 16.8)
5. De Bernardini N, **Basile A**, Zampieri G, Kovalovszki A, De Diego Diaz B, Offer E, Wongfaed N, Angelidaki I, Kougias PG, Campanaro S, et al (2022) Integrating metagenomic binning with flux balance analysis to unravel syntrophies in anaerobic CO<sub>2</sub> methanation. *Microbiome* 10: 117 (citations: 18; IF: 16.8)
6. Centurion VB, Campanaro S, **Basile A**, Treu L & Oliveira VM (2022) Microbiome structure in biofilms from a volcanic island in Maritime Antarctica investigated by genome-centric metagenomics and metatranscriptomics. *Microbiol Res* 265: 127197 (citations: 1; IF: 6.7)
7. Palù M, **Basile A**<sup>+</sup>, Zampieri G, Treu L, Rossi A, Morlino MS & Campanaro S (2022) KEMET – A python tool for KEGG Module evaluation and microbial genome annotation expansion. *Comput Struct Biotechnol J* 20: 1481–1486 (citations: 8; IF: 6)



8. Heinken A, **Basile A**, Hertel J, Thinnies C & Thiele I (2021) Genome-Scale Metabolic Modeling of the Human Microbiome in the Era of Personalized Medicine. *Annu Rev Microbiol* 75: 199–222 (citations: 23; IF: 16.23)
9. Heinken A, **Basile A** & Thiele I (2021) Advances in constraint-based modelling of microbial communities. *Curr Opin Syst Biol* 27: 100346 (citations: 19; IF: 3.7)
10. **Basile A**, De Pascale F, Bianca F, Rossi A, Frizzarin M, De Bernardini N, Bosaro M, Baldisseri A, Antoniali P, Lopreiato R, et al (2021) Large-scale sequencing and comparative analysis of oenological *Saccharomyces cerevisiae* strains supported by nanopore refinement of key genomes. *Food Microbiol* 97: 103753 (citations: 8; IF: 5)
11. Shi Z, Campanaro S, Usman M, Treu L, **Basile A**, Angelidaki I, Zhang S & Luo G (2021) Genome-Centric Metatranscriptomics Analysis Reveals the Role of Hydrochar in Anaerobic Digestion of Waste Activated Sludge. *Environ Sci Technol* 55: 8351–8361 (citations: 57; IF: 11.4)
12. Campanaro S, Treu L, Rodriguez-R LM, Kovalovszki A, Ziels RM, Maus I, Zhu X, Kougias PG, **Basile A**, Luo G, et al (2020) New insights from the biogas microbiome by comprehensive genome-resolved metagenomics of nearly 1600 species originating from multiple anaerobic digesters. *Biotechnol Biofuels* 13: 25 (citations: 113; IF: 6)
13. **Basile A**, Campanaro S, Kovalovszki A, Zampieri G, Rossi A, Angelidaki I, Valle G & Treu L (2020) Revealing metabolic mechanisms of interaction in the anaerobic digestion microbiome by flux balance analysis. *Metab Eng* 62: 138–149 (citations: 32; IF: 15.6)
14. Gatto V, Binati RL, Lemos Junior WJF, **Basile A**, Treu L, de Almeida OGG, Innocente G, Campanaro S & Torriani S (2020) New insights into the variability of lactic acid production in *Lachancea thermotolerans* at the phenotypic and genomic level. *Microbiol Res* 238: 126525 (citations: 20; IF: 7.5)
15. Yan M, Treu L, Zhu X, Tian H, **Basile A**, Fotidis IA, Campanaro S & Angelidaki I (2020) Insights into ammonia adaptation and methanogenic precursor oxidation by genome-centric analysis. *Environ Sci Technol* (citations: 45; IF: 8)
16. Fontana A, Falasconi I, Molinari P, Treu L, **Basile A**, Vezzi A, Campanaro S & Morelli L (2019) Genomic Comparison of *Lactobacillus helveticus* Strains Highlights Probiotic Potential. *Front Microbiol* 10 (citations: 39; IF: 4.23)

**Academic formation:**

- PhD in Marine Ecology at Center for Scientific Research and Higher Education of Ensenada (CICESE, Mexico). (2012-2017)

Thesis: Genetic characterization of “*Candidatus Xenohaliotis californiensis*” associated with blue (*Haliotis fulgens*) and yellow abalone (*Haliotis corrugata*) on the Pacific coast of Baja California.

Advisor: Dr. Axayácatl Rocha Olivares ([arocho@cicese.mx](mailto:arocho@cicese.mx))

- Master degree in Eco-Biology at University of Rome La Sapienza (Rome, Italy). (2009-2011)

Thesis: Effects of the *Posidonia oceanica* fragmentation (L.) Delile 1813, in the center part of Italy.

Advisor: Dr. Loreto Rossi ([loreto.rossi@uniroma1.it](mailto:loreto.rossi@uniroma1.it))

- Under graduate degree in Biology at University of Rome La Sapienza (Rome, Italy). (2003-2009)

Thesis: Locomotion and morphological plasticity in genus *Podarcis* Wagler, 1830; Reptilia, Lacertidae.

Advisor: Dr. Riccardo Castiglia ([riccardo.castiglia@uniroma1.it](mailto:riccardo.castiglia@uniroma1.it))

**Previous research experience:**

- Postdoctoral researcher at University of Padua (Italy) (2022-2023)
- Department of Comparative Biomedicine and Food Science
  - Investigation: Adaptation strategies to climate change in bivalve mollusks.
  - Advisor: Dr. Massimo Milan ([massimo.milan@unipd.it](mailto:massimo.milan@unipd.it)) and Dr. Luca Peruzza ([luca.peruzza@unipd.it](mailto:luca.peruzza@unipd.it))

- Postdoctoral researcher at Center for Scientific Research and Higher Education of Ensenada (CICESE, Mexico) (2021-2022)
- Department of Biomedical Innovation
  - Investigation: Genotypic characterization of SARS-CoV-2 in reinfecting patients from Ensenada (Baja California, Mexico).
  - Advisor: PhD Alexei Licea Navarro ([alicea@cicese.mx](mailto:alicea@cicese.mx))

- Postdoctoral researcher at Center for Scientific Research and Higher Education of Ensenada (CICESE, Mexico) (2019-2020)
- Department of Marine Biotechnology
  - Investigation: Molecular taxonomic identification and genetic connectivity of zooplankton in the Gulf of Mexico.
  - Advisor: PhD Clara Galindo Sanchez ([cgalindo@cicese.mx](mailto:cgalindo@cicese.mx)) and PhD Maria Clara Arteaga ([arteaga@cicese.mx](mailto:arteaga@cicese.mx))

- Postdoctoral researcher at Center for Scientific Research and Higher Education of Ensenada (CICESE, Mexico) (2018-2019)
- Department of Biomedical Innovation
  - Investigation: Metagenomics analysis of bacterial communities associated with marine sponges of Cabo Pulmo National Park (BCS), to identify genes involved in the synthesis of polyketides and peptides with antimicrobial activity

- Advisor: PhD. Asuncion Lago-Lestón ([asun.lago@gmail.com](mailto:asun.lago@gmail.com))
- Postdoctoral researcher at Center for Scientific Research and Higher Education of Ensenada (CICESE, Mexico) (2017-2018)
  - Department of Molecular Ecology
  - Investigation: Use of morphological and molecular tools for the characterization of deep sea meiofauna of Gulf of Mexico.
  - Advisor: PhD. Axayácatl Rocha Olivares ([arocho@cicese.mx](mailto:arocho@cicese.mx))

**Peer reviewed publications (published & in press):**

1. The use of microbiome profiles and machine-learning analysis to assess the collection areas of Manila clam. *Plos biology* (in review).
2. Garlic (*Allium sativum*) as a dietary ingredient can cause dysbiosis in the microbiota of the California yellowtail (*Seriola dorsalis*) at high concentrations. *Aquaculture International* (2023). <https://doi.org/10.1007/s10499-023-01301-6> **FI:2.96; Q2**
3. Microbiota plasticity in tilapia gut revealed by meta-analysis evaluating the effect of probiotics, prebiotics, and biofloc. *PeerJ* **11**:e16213 <https://doi.org/10.7717/peerj.16213> **FI:3.06; Q1**
4. Effects of six diets on the growth and survival rates of red abalone (*Haliotis rufescens*) and its hybrid (*H. rufescens* ♀ x *H. fulgens* ♂). *Scientia Marina* **87**, 1:e055 <https://doi.org/10.3989/scimar.05300.055> **FI:1.4; Q2**
5. The biofouling process: The science behind a valuable phenomenon for aquaculture. *Review in Aquaculture* **2022**;1–15. <https://doi.org/10.1111/raq.12770> **FI:10.6; Q1**
6. Mature biofloc harbor similar bacterial communities regardless of the vegetal floating substrates (oat, amaranth, or wheat) used as promoters. *Aquaculture International* (2022) <https://doi.org/10.1007/s10499-022-00970-z> **FI:2.9; Q2**
7. Detection of human pathogenic bacteria in sea lions rectal DNA samples from Gulf of California, Mexico. *Scientific Reports* **12**, 14859 (2022) <https://doi.org/10.1038/s41598-022-18903-4> **FI:4.6; Q1**
8. Multi-locus evaluation of gastrointestinal bacterial communities from *Zalophus californianus* pups in the Gulf of California, Mexico. *PeerJ* **10**:e13235 <https://doi.org/10.7717/peerj.13235> **FI:3.06; Q1**
9. Hydrocarbon exposure effect on energetic metabolism and immune response in *Crassostrea virginica*. *Marine Pollution Bulletin* **180**(2022):113738. <https://doi.org/10.1016/j.marpolbul.2022.113738> **FI:7.00; Q1**
10. The role of diversity in mediating microbiota structural and functional responses in two abalone species under stressed withering syndrome conditions. *Microbial Ecology* **2022**:1-11 <https://doi.org/10.1007/s00248-022-01970-5> **FI:4.19; Q1**



11. Environmental conditions drive zooplankton community structure in the deep-water region of the southern Gulf of Mexico: a molecular approach. *Molecular Ecology* **31**:546-561 <https://doi.org/10.1111/mec.16251> **FI:6.62; Q1**
12. Longitudinal variations in the gastrointestinal microbiome of the white shrimp, *Litopenaeus vannamei*. *PeerJ* **9**:e11827 <https://doi.org/10.7717/peerj.11827> **FI:3.06; Q1**
13. Exploring the garlic (*Allium sativum*) properties for fish aquaculture. *Fish Physiology and Biochemistry*, **47**:1179–1198 <https://doi.org/10.1007/s10695-021-00952-7> **FI:3.01; Q2**
14. Therapeutic modulation of fish gut microbiota, a feasible strategy for aquaculture? *Aquaculture*, **544**:737050 <https://doi.org/10.1016/j.aquaculture.2021.737050> **FI:5.13; Q1**
15. Growth performance and transcriptomic response of warm-acclimated hybrid abalone *Haliotis rufescens* (♀) x *H. corrugata* (♂). *Marine Biotechnology*, **23**:62-76. <https://doi.org/10.1007/s10126-020-10002-7> **FI:3.72; Q2**
16. Water microbiota is not affected by stocking density of the yellowtail kingfish (*Seriola lalandi*) in a recirculation aquaculture system. *Aquaculture Research*, **52**:410–414. <https://doi.org/10.1111/are.14883> **FI:2.18; Q2**
17. Gut microbiota shifts in the giant tiger shrimp, *Penaeus monodon*, during postlarvae, juvenile and adult stages. *Aquaculture International*, **28**:1421–1433 <https://doi.org/10.1007/s10499-020-00532-1> **FI:2.95; Q2**
18. Structure, dynamics and predicted functional ecology of the gut microbiota of the blue (*Haliotis fulgens*) and yellow (*H. corrugata*) abalone from Baja California Sur, Mexico, **2018**. *PeerJ*, **6**:e5830 <https://doi.org/10.7717/peerj.5830> **FI:3.06; Q1**
19. Monomorphic pathogens: the case of *Candidatus Xenohaliotis californiensis* from abalone in California, USA and Baja California, Mexico. *Journal of Invertebrate Pathology*, **154**:19-23. <https://doi.org/10.1016/j.jip.2018.03.012> **FI:2.97; Q1**
20. Multigenetic characterization of “*Candidatus Xenohaliotis californiensis*”. *International journal of systematic and evolutionary microbiology*, **67**:42–49. <https://doi.org/10.1099/ijsem.0.001563> **FI:2.68; Q2**

### **Books Collaboration:**

- Herzka, Sharon Z. (Ed.) (2021). Comunidades marinas. En S. Z. Herzka, R. A. Zaragoza Álvarez, E. M. Peters y G. Hernández Cárdenas. (Coord. Gral.). *Atlas de línea base ambiental del golfo de México (tomo III, segunda parte)*, México: Consorcio de Investigación del Golfo de México; pp:8 at <https://atlascigom.cicese.mx/es/dataset/libro-atlas-tomo-3-subtomo-2>.

**Distinctions:**

- Member of National Research System of Mexico (Sistema Nacional de Investigadores-CONACYT), Level: 1, 2023-present.
- Member of National Research System of Mexico (Sistema Nacional de Investigadores-CONACYT), Level: *Candidate*, 2018-2021.
- Doctorate thesis defense: *Unanimously approved*, 2017.
- Master thesis defense: Approved with *Ad Honorem*, 2011.

**Human resources trained**

➤ ***Member of thesis committee:***

- Student: Jesus Salvador Oliver Guidaro Flores
- Level: PhD; 2023 – present.
- Institution: Center for Research in Food and Development, A.C. (Hermosillo, Sonora).
- Thesis title: Effect of diseases by infection of *Staphylococcus haemolyticus*, *Nocardia* sp. and *Providencia* sp. in the composition of intestinal microeukaryoma of tilapia (*Oreochromis niloticus*)
  
- Student: David Rajme Manzur
- Level: PhD; 2021 – *present*.
- Institution: Center for Research in Food and Development, A.C. (Hermosillo, Sonora).
- Thesis title: Transcriptomic analysis of granulomatous diseases in Tilapia: a model to study host-pathogen interactions in fish.
  
- Student: Rocío Aracely Valenzuela Gutiérrez
- Level: PhD; 2019 –2023.
- Institution: Center for Research in Food and Development, A.C. (Hermosillo, Sonora).
- Thesis title: Composition and functionality of the intestinal microbiota of mackerel (*Seriola lalandi*) fed with added garlic diets.

➤ ***Director of academic courses:***

- Transcriptome and differential expression (Postgraduate number: 293/23) (March/May, 2023)
- Basic Bioinformatics at CICESE (Postgraduate number: 002241) (January/Abril, 2021)
- Basic Bioinformatics at CICESE (Postgraduate number: 002241) (January/Abril, 2020)
- Basic Bioinformatics at CICESE (Postgraduate number: 002241) (January/Abril, 2019)

**Congresses, Workshops, Symposia:**

- Webinar in the Coastal Oceanography Seminar series, September 29th 2022. Oral presentation titled: Microbiota influences on mollusks health: the case of abalone Withering Syndrome
- Summer School Congress - Topics of Microbiota in Animal Production, January 10-17 (Santiago de Chile, Chile, 2022). Oral presentation titled: Microbiota influence on mollusks health: The case of abalone Withering Syndrome.

- Workshop Genome Assembly, January 11-14, 2021, (Mansfield, Connecticut, United States - *remote access*).
- Western Society of Naturalist 100<sup>th</sup> Meeting, November 01, 2019 (Ensenada, Baja California, Mexico). Poster presentation titled: *Growth and transcriptomic profile of warm-acclimated hybrid abalone (Haliotis rufescens x Haliotis corrugata)*.
- 6<sup>th</sup> Bioinformatics Workshop. Mining Microbial and Viral Genomes and Metagenomes for Biotechnological Applications using IMG Workshop, September 30-October 1, 2019 (Ensenada, Baja California, Mexico).
- Environmental Metatranscriptomics Workshop, September 8-9, 2018 (Ensenada, Baja California, Mexico).
- 3<sup>th</sup> Workshop of Meiofauna from the deep see of Gulf of Mexico, November 24-26, 2018. (Ensenada, Baja California, Mexico).
- 2<sup>nd</sup> Benthic Invertebrate Taxonomy, Metagenomics, and Bioinformatics (BITMaB-2) Workshop, January 15-19, 2018 (Corpus Christi, Texas, United States).
- 3<sup>th</sup> Workshop of genomic sequence analysis and metagenomics, September 23-26, 2014 (Ensenada, Baja California, Mexico).
- 49<sup>th</sup> Western Society of Malacologists, 82<sup>th</sup> American Malacological Society Annual Meetings, June 12-16 (Ensenada, Baja California, Mexico, 2014). Oral presentation titled: *Molecular description of the intestinal bacterial flora in wild Mexican population of Haliotis corrugata and Haliotis fulgens*.

### **Work Abilities and Skills**

#### **➤ *Bioinformatics Skills:***

- Operating systems: Linux/Ubuntu and Windows.
- Next-generation sequencing Technologies: Illumina MiSeq and HiSeq, Ion Torrent and 454 Pyrosequencing.
- Bioinformatics analysis: Quality control, structural microbiome characterization, *de-novo* and reference assembly, sequences alignment, differential expression, ontology analysis, metabolic pathways and protein network analysis.
- Bioinformatics Platforms: Qiime1 and Qiime2, RStudio, Galaxy, MG-RAST and IMG.
- Software for DNA and RNA-Seq analysis: Fastqc, Multiqc, Trimmomatic, Trinity, SPAdes, Mira, MegaHits, Quast, Transrate, Blast, Mafft, Kraken, Pplacer, SortMeRNA, PiCRUST.
- Software for Phylogenetic analysis: MrBayes, BEAST, RAxML, Fasttree, Paup, MEGAX.
- Software for Protein analysis: Busco, David and STRING.
- Software for Population genetics analysis: Primer6, STATISTICA, MEGAX, Geneious, CodonCode, ARLEQUIN, GenePop.

#### **➤ *Practical laboratory and organizational skills:***

- DNA/RNA isolation and quantification (Bioanalyzer™, Qubit®, and nanodrop).
- DNA cloning and cDNA synthesis.
- Primer design, Polymerase Chain Reaction (PCR) and quantitative-PCR (qPCR and RT-qPCR).

## Curriculum Vitae

- Transcriptome and Metagenome library construction.
- Microbiological tests for water, sediment, and tissues for aquaculture
- Experimental design, troubleshooting and protocol adaptation and optimization.
- Interdisciplinary team-based research.
- Publication of complex research in formal and informal settings.

### ➤ *Language experience:*

- Italian: Native speaker.
- Spanish: Advanced speaking, writing and oral expression.
- English: Advanced speaking, writing and oral expression.

### **Journal reviewer:**

- *Fishes* (<https://www.mdpi.com/journal/fishes>) reviewer since 2022.
- *iMeta* (<https://onlinelibrary.wiley.com/journal/2770596x>) reviewer since 2022.
- *Frontiers in Marine Science* (<https://www.frontiersin.org/journals/marine-science>) reviewer since 2022.
- *Molecular Ecology* (Wiley Online Library at <https://onlinelibrary.wiley.com/journal/1365294x>) reviewer since 2022.
- *Ecological Genetics and Genomics* (Elsevier publisher at <https://www.journals.elsevier.com/ecological-genetics-and-genomics>) reviewer since 2021.
- *Aquaculture Reports* (Elsevier publisher at <https://www.journals.elsevier.com/aquaculture-reports;>) reviewer since 2020.
- *Animal Gene* (Elsevier publisher at <https://www.journals.elsevier.com/animal-gene>) candidate reviewer.

### **Additional work experiences:**

- Histopathological analysis for the detection of *Candidatus Xenohaliotis californiensis*. Supervised by PhD. James Douglas Moore at Bodega Marine Laboratory, University of California at Davis (UC MEXUS-CICESE fellowship winner). (January/Abril, 2015)
- Photography volunteer in the research project “*Sea lions as sentinels of global change on vulnerable ecosystems in the coast and islands in the west of the Baja California Peninsula*”, supervised by PhD. Yolanda Schramm at UABC (Ensenada, Baja California, Mexico) (2009-2010)
- Volunteer in the research project “*Genetic characterization of Elephant Sea, Sea lions and seals in the Pacific islands of Baja California*”. Supervised by PhD Gisela Heckel at CICESE (Ensenada, Baja California, Mexico) (2009-2010)

Roma 18/12/23