

## Extended abstract

# Brilliant Marine Research Idea 2024

This extended abstract is part of the full report which should be submitted no later than 28 February 2025 via [filantropie@vliz.be](mailto:filantropie@vliz.be). Data of this specific final report are under embargo and are therefore not yet published online.

## 1. General information

Title of the idea	Revealing the gut microbiome of orcas ( <i>Orcinus orca</i> ) as indicator of pollution impact pollution impact
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## 2. Brilliant Marine Research Idea

### Extended abstract

Orcas (*Orcinus orca*) serve as valuable indicators of ocean health due to their sensitivity to environmental pollution. However, their susceptibility to pollutants poses significant health risks, pushing populations near industrialized regions toward extinction. This grave situation has heightened interest in understanding how pollution impacts the gut microbiome and overall health of orcas. Despite advanced sequencing technologies enabling high-throughput profiling of gut microbial communities in many terrestrial mammals, the orca gut microbiome has remained largely unexplored. This study represents a pioneering effort to explore the gut microbiome of orcas using a comprehensive whole metagenome sequencing approach. The main objectives were to characterize the diversity, composition, and functional gene profiles of the orca gut microbiome, with a particular focus on the diversity and prevalence of microbial genes involved in the degradation of persistent organic pollutants (POPs). Gut content samples were collected from an orca that stranded in De Panne (Belgium) in October 2023. Bacterial DNA was isolated for Nextera XT library preparation. Shotgun sequencing on the Illumina NovaSeq platform yielded 100 million reads. Taxonomic classification using Kraken2 and Bracken revealed that the gut microbiome is dominated by four major bacterial phyla: Bacillota, Bacteroidota, Fusobacteriota, and Pseudomonadota. In addition, functional analysis identified 23 genes involved in degradation steps of pollutants such as DDT and flame retardants. These findings suggest that the orca gut microbiome harbours genes capable of metabolizing environmental pollutants, highlighting the potential of microbiome functional profiling as a tool for assessing pollutant impacts on cetaceans.