

Your report will be formatted like a research article with the sections described below. You will be able to base your report on any aspect of the provided sequence and metadata. Your report will be evaluated for logical flow of ideas and language (style and grammar), not comprehensiveness.

*The parent article relevant to your study is [Sun et al 2022](#). Note that the Results & Discussion are combined in this study, which is a standard alternative to separating these two sections. Also look up other examples of your own for further comparison. **Do not simply paraphrase the Sun et al study.** There are many stories to tell from a metagenomic analysis, tell your own story.*

Abstract (4 marks) [up to 200 words]

Summarise study including introductory sentence(s) to frame the study, goal of study, approach used, main findings and conclusion.

- Intro sentence, goal, approach and main findings and insightful conclusion are present and appropriate (1.5 marks)
- Abstract matches results and discussion (1 mark)
- Abstract is punchy, succinct, and encourages reader to continue (1.5 marks).

Introduction (5 marks)

Introduce the topic area using recent relevant published literature, and why it is important. Frame the goal of your study and the main findings in the last paragraph. No subheading.

- Sufficient *exploration* of the literature (eg, description of known taxa that degrade plastics, gut microbiome, culture independent methods). At least four references should be included in text (2 marks)
- Sufficient *summary* of the literature including contextual placement of this study in the broader picture (2 marks)
- Summary of goal of the study and the main findings in last paragraph (1 mark)

Materials and Methods (4 marks)

Briefly describe the methods used in your study (may be a subset of all methods that you have learnt). Use subheadings.

- Gene centric analyses (FastQC, Read-mapping eg remove host reads from metagenome, taxonomic profile *etc*) (1.5 marks)
- Genome centric (Functional profile, recover bins, estimate bin quality, taxonomic assignment to bins *etc*). (1.5 marks).
- Clarity and conciseness (1 mark)

Results (6 marks)

Present and discuss your data analysis with minimal reference to published literature. Use subheadings.

- At least four of the different types of data analyses you performed in your bioinformatic practicals should be presented, *e.g.* PCA plot, diversity boxplots, community abundance, log-fold change plots, BLAST search, gene presence/absence tables or heatmaps (2 marks)
- Figures and Tables should be neat, with descriptive captions, and referenced in the text (1 mark)
- Flow of results should tell a story to maintain the readers interest and to improve their retention of information (2 marks)
- Student shows understanding of the statistical interpretation of the data (1 mark)

Discussion (7 marks)

Discuss your results in the context of relevant published literature. Subheadings optional.

- Each of the main results included are mentioned, and no new results are introduced (1 mark)
- Student interprets results and shows insight into their biological meaning (2 marks)
- Results are placed in the context of the literature, with relevant citations (1 mark)
- At least two of these should be present (2 marks)
 - o Student makes a genuine effort to interpret the taxonomic/functional data.
 - o Student shows understanding of the limitations of the data and the experiment
 - o Student discusses future experiments or possible improvements to the method
- Discussion is grammatically sound, well written and has a logical flow (1 mark)

References (2 marks)

Use a consistent citation and reference format e.g. PNAS, Environmental Microbiology

- Consistent referencing system used (1 mark)
- References support statements and are contextually relevant (1 mark)

Overall (2 marks)

- narrative flow, *e.g.* logical segways between sections (1 mark)
- scientific language, *e.g.* species names in italics, no contractions such as don't (1 mark)

Display items (up to six Figures / Tables)

Figures are labeled at the bottom and tables are labeled at the top. See example article.

Supplementary materials

*Many research papers include supplementary materials usually due to limitations in the number of display items that can be included in the main text. However, **please do not include any supplementary materials in your microbiome report!***