

Genome Report Instructions

This assignment comprises the written portion of your grade for the class Molecular Microbiology. The report describes the genome of the bacterium you sequence in the class, including background information, methods, and key findings. Each group should submit one report, and both members of the group will receive the same grade for the report.

Peer Review

The report will be subjected to peer review. The instructor will assign other members of the class to anonymously provide feedback on your draft report. You will then revise your report based on that feedback to submit the final version.

Timeline

All deadlines are at 23:59 on the given date. Submit drafts, reviews, and final reports as Brightspace assignments found under “Genome Report”.

| Week | Date | Action |
|------|---------------------|------------------------------------------|
| 11 | Monday, March 11 | Submit draft Genome Report |
| 11 | Wednesday, March 13 | Receive anonymous peer review assignment |
| 11 | Monday, March 18 | Submit peer review |
| 12 | Tuesday, March 19 | Receive peer review |
| 12 | Friday, March 22 | Submit final Genome Report |

Report Format

Title

The title should include the name of the organism you have sequenced, the environment it was isolated from, and the genome quality that you obtained.

Abstract (max. 100 words)

The abstract should summarise the report, including background about the organism, key statistics about the genome (length, number of genes, GC content), and interesting findings.

Introduction (max. 200 words)

Give the background about the species of microorganism you have sequenced, including why it is interesting.

Organism Information (max. 300 words)

Describe where and how the organism was isolated, including methods used for its isolation and cultivation. Give relevant physiological data you have for this strain (aerobic/anaerobic, known electron donors/acceptors or carbon sources, any data on pH/temperature/salinity range, etc.) - “relevant” means anything that will be useful in describing your genome later on in the “Insights from the Genome” section. So for example, if you wish to talk about antibiotic resistance genes then talk about results of antibiotic resistance tests here. The organisms central metabolism (how does the organism make ATP?) will be relevant no matter what your chosen focus.

Genome Sequencing Information

Genome project history (max. 50 words) Describe when and where this genome project took place and provide the GenBank accession number for the finalised genome.

Growth conditions and genomic DNA preparation (max. 200 words) Describe how the culture was grown and DNA was extracted for genome sequencing. Cite standard protocols included with the kits, but give details where we deviated from the protocol or where we chose one of several options from the standard protocol.

Genome sequencing and assembly (max. 200 words) Describe how the genome was sequenced, and the bioinformatics involved in trimming, assembly, and contamination checking and removal. Name all software used and be sure to include the correct software version number and citation.

Genome annotation (max. 100 words) Describe the bioinformatic tools used for annotation and pathway analysis. Name all software used and be sure to include the correct software version number and citation.

Genome properties (max. 100 words plus table)

Provide a table with the following data:

- Genome size (in base pairs)
- Genome coverage (total sequencing effort divided by total genome size)
- GC content (percentage)
- Number of contigs
- Completeness (percentage)
- Contamination (percentage)
- Number of protein-coding genes
- Number of RNA genes
- Number of genes assigned a function by KEGG

Comment on these results. Are your basic genome statistics similar to statistics for related genomes? Is your genome high enough quality to make valid taxonomic or metabolic inferences?

Insights from the genome

Taxonomic insights from the genome (max. 200 words plus figure) Show a **figure** with a phylogenetic tree reconstructed from concatenated protein sequences and report results from tools used to determine taxonomy from full genome sequences. Comment on whether this matches your expectation from organism information.

Metabolic insights from the genome (max. 500 words plus figure, no figure necessary for reports written by one person) Show a **figure** outlining a conceptual metabolic model for your organism (one-person reports do not need to include this figure). Include key pathways that reveal how the organism produces ATP and any other traits that you believe are interesting - think about what is unique or interesting for your organism and what is known about its phenotype from previous work (API tests etc.). Relate your findings back to the organism's habitat - where was it isolated and how can the predicted traits be reconciled with this habitat? Some ideas to get you started:

- Central carbon metabolism - glycolysis, TCA cycle, and other key pathways
- Fermentation pathways
- Electron transport pathway, including ATP synthase
- Nitrate/nitrite reduction
- Transporters / Secreted compounds
- Motility and chemotaxis (flagella? pili?)
- Secondary metabolite production
- Salinity adaptation
- Antibiotic resistance/production
- Phage defense mechanisms/prophages

Discuss your organism's gene content relative to what is known about its physiology from work with the culture, and try to make predictions about additional physiological traits that have not yet been tested.

Conclusions (max. 100 words)

Summarise the degree to which the genome sequencing was successful and reiterate key findings about the organism's taxonomy and potential metabolism.

References

Be sure to cite your work throughout the report using the Vancouver citation style (see <https://libguides.murdoch.edu.au/Vancouver> for guidance). Citing the web-based or command-line-based bioinformatics tools used is particularly important - the tool will typically tell you what paper to cite, either in its manual, on its website, or in the software itself.