# Online Supporting Material for Chapter 4

# Bacterial genome sequencing and *in* s*ilico* prediction of

# Microbial interactions among partners of the tripartite model system

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# Tables

**Table 4.1 - Genome statistics** for genomes used in Chapter 4, as derived from CheckM1. Excel .xlsx file is contains three spreadsheets. The first shows genome characteristics of *Marinobacter* sp. FDB33 and *Alteromonas* sp. FDB36, sequenced as part of this thesis. The second and third spreadsheets contain a wider set of genomes that were used in the analysis, for the *Marinobacter* and *Alteromonas* genera, respectively.

**Table 4.2 – MAPLE module completion ratio (MCR).** Complete list of KEGG module completion ratio’s, represented as the percentage of a module component filled with KEGG Orhology (KO) assigned genes was calculated for FDB33 and FDB36 using KAAS2 and MAPLE3.

**Table 4.3 – Genome specific KO assigned genes comparing FDB33 and FDB36**. KEGG Ortrhology was assigned using KAAS2 and compared in R. For each genome (FDB33 and FDB36) unique KO identifiers are listed, together with the gene name, functional annotation and respective locus tags.

**Table 4.4 – CAZY and cellular localisation for FDB33 and FDB36.** List of CAZymes for genomes FDB33 and FDB36, with cellular localisation as predicted by SOSUI4, PSORTb5, and SignalP6.

# Data files

Genome assemblies in fasta format for genomes FDB33 and FDB36

* Marinobacter\_sp\_FDB36.fna
* Alteromonas\_sp\_FDB33.fna

Genome annotation files in fasta format for FDB33 and FDB36

* Marinobacter\_sp\_FDB36.faa
* Alteromonas\_sp\_FDB33.faa

# References

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