

Anaerobic acetate production from H₂ and CO₂ by acetogenic bacteria

Example case: *Moorella thermoacetica*

```
# the setup
gapseq=-/path/to/gapseq/./gapseq
model="Moorella_thermoacetica_ATCC39073"

# Reconstruction
$gapseq find -p all -b 200 -m Bacteria $model.fna.gz
$gapseq find-transport -b 200 $model.fna.gz

$gapseq draft -r $model-all-Reactions.tbl \
-t $model-Transporter.tbl \
-p $model-all-Pathways.tbl \
-c $model.fna.gz \
-u 200 -l 100

$gapseq fill -m $model-draft.RDS \
-n ../dat/media/MM_anaerobic_CO2_H2.csv \
-c $model-rxnWeights.RDS \
-g $model-rxnXgenes.RDS \
-b 100 -e highH2
```

Example case: *Blautia hydrogenotrophica* DSM 10507

```
# the setup
model="Blautia_hydrogenotrophica_DSM_10507"

# Reconstruction
$gapseq find -p all -b 200 -m Bacteria $model.fna.gz
$gapseq find-transport -b 200 $model.fna.gz

$gapseq draft -r $model-all-Reactions.tbl \
-t $model-Transporter.tbl \
-p $model-all-Pathways.tbl \
-c $model.fna.gz \
-u 200 -l 100

$gapseq fill -m $model-draft.RDS \
-n ../dat/media/MM_anaerobic_CO2_H2.csv \
-c $model-rxnWeights.RDS \
-g $model-rxnXgenes.RDS \
-b 100 -e highH2
```

Syntrophic acetate oxidizing (SAO) bacteria

Example case: *[Clostridium] ultunense* DSM 10521

```
# the setup
model="Clostridium_ultunense_DSM_10521"

# Reconstruction
$gapseq find -p all -b 200 -m Bacteria $model.fna.gz
$gapseq find-transport -b 200 $model.fna.gz

$gapseq draft -r $model-all-Reactions.tbl \
-t $model-Transporter.tbl \
-p $model-all-Pathways.tbl \
-c $model.fna.gz \
-u 200 -l 100

$gapseq fill -m $model-draft.RDS \
-n ../dat/media/MM_anaerobic_Acetate.csv \
-c $model-rxnWeights.RDS \
-g $model-rxnXgenes.RDS \
-b 100
```

Example case: *Syntrophaceticus schinkii*

```
# the setup
model="Syntrophaceticus_schinkii"

# Reconstruction
$gapseq find -p all -b 200 -m Bacteria $model.fna.gz
$gapseq find-transport -b 200 $model.fna.gz

$gapseq draft -r $model-all-Reactions.tbl \
-t $model-Transporter.tbl \
-p $model-all-Pathways.tbl \
-c $model.fna.gz \
-u 200 -l 100

$gapseq fill -m $model-draft.RDS \
-n ../dat/media/MM_anaerobic_Acetate.csv \
-c $model-rxnWeights.RDS \
-g $model-rxnXgenes.RDS \
-b 100
```