***Streptomyces* Assembly Completeness**

BUSCO v1.22

BLAST+ v2.2.31

HMMER v3.1b2

EMBOSS v6.5.7

PYTHON 3.4.0

AUGUSTUS 3.2.2

**Loading**

Load programs

module load biokit

module load python-env/3.4.0

PATH=$PATH:$HOME/appl\_taito/augustus-3.2.2/bin/

export AUGUSTUS\_CONFIG\_PATH=$HOME/appl\_taito/augustus-3.2.2/config/

**NOTE!** This command must be run every time logging into Taito

**RUNNING**

Run on final scaffolds

python3 $USERAPPL/BUSCO\_v1.22/BUSCO\_v1.22.py -o ATCC\_31615 \

-in scaffolds.fa -l $USERAPPL/BUSCO\_v1.22/bacteria -m genome -c 8