**akn tblastn Notes**

Identifying akn genes in the ATCC 31615 draft genome

EMBOSS v6.5.7

BLAST v2.2.31

Change FASTA headers to NCBI style:

module load emboss

seqret ATCC\_31615.scaffolds.fasta ATCC\_31615.scaffolds.ncbi.fasta -osf ncbi

Make the draft genome a BLAST-able database:

makeblastdb -in ATCC\_31615.scaffolds.ncbi.fasta -parse\_seqids -dbtype nucl

Search for each gene:

tblastn -query ../akn\_genes/aknB\_pep.fasta -db ../draft\_genome/ATCC\_31615.scaffolds.ncbi.fasta -out aknB\_results.txt

See first hit and identify the scaffold:

gnk|unk|**scaffold8.1**

Find the scaffold in the draft genome (ATCC\_31615.rast.merged.gbk) in Artemis:

command + G

“Goto Feature With This Qualifier Value:” **scaffold8.1**

Identify the start of the scaffold:

5835139

Identify the start and end of the BLAST hit:

Sbjct **81599 ... 80331**

Add the start of the scaffold and the start of the BLAST hit (the same for the end):

5835139 + 81599 = **5916738**

5835139 + 80331 = **5915470**

Search for those bases in Artemis:

“Select” 🡪 “Base Range ... “ **5916738..5915470**

Change the color of the annotation:

“Edit” 🡪 “Qualifier of Selected Feature(s)” 🡪 “Change ...”

Select “colour” from the dropdown menu 🡪 “Insert qualifier:”

Set the color using a color code (e.g. red = 255 0 0) 🡪 “Add”

Edit the name of the annotation:

/product= “**aknB** Polyketide ...”

“Add Qualifier:” **gene 🡪** “**aknB**”

Save akn Cluster region as a separate Genbank file:

Select bases 🡪 “Edit” 🡪 “Subsequence (and Features)”

(A new window pops up with selected region)

“File” 🡪 “Save An Entry As” 🡪 “GENBANK Format”

Save BLAST results in a zipped filed:

zip -r tblastn\_results.zip tblastn\_results/