

Template file

Metadata: Project Title,
Sequence authors,
Publication status
Suffix of file: **.sbt**

Create Submission Template

<http://www.ncbi.nlm.nih.gov/WebSub/template.cgi>

Nucleotide sequence data

in Fasta format
Suffix of file: **.fsa**

Export from
Geneious and run
Benjamin's Script

Feature Table

Suffix of file: **.tbl**

Export flat file from
Geneious and run
convertToFeatureTable.py
script

tbl2asn

Generate in
Terminal(Mac) or
Windows Command
Line(CMD)

**File in
.sqn format**

Load onto Sequin

Submit to Genbank !

