

The procedure to annotate genes in CYRENE can be summed up as follows:

- 1) Extract the relevant information from the literature.
- 2) Open CYRENE
- 3) Open the species. File->Open Species...
 - a. If the species isn't cached, type in the taxonomic name into the text box and hit enter.
- 4) Open the gene. File->Open Gene...
 - a. Type in the gene name and hit enter
- 5) After the gene is loaded, left click drag the gene to your workspace.
- 6) Select the region where you would like to search for the CRM with a left click drag motion on genomic axis; load this region by maneuvering to Data Manipulation->Set SubView Range or by pressing Ctrl+k (command+k in mac).
- 7) Right click anywhere in the Consensus Sequence panel on the lower right and select seqFinder.
- 8) Enter in the start and ending sequences that were extracted from the literature.
- 9) Right click in the Consensus Sequence panel and create a new CRM (New->Forward/Reverse CRM).
- 10) Locate (by using the seqFinder or by eye) and create binding sites (New->Forward/Reverse Binding Site)
- 11) Give the binding sites and CRM an appropriate name (derived from the literature) in the lower left hand properties box.
- 12) Attach the genomic entities to each other.
 - a. Left click select the CRM.
 - b. Right click each binding site and select "Attach site to CRM"
 - c. Left click select the gene.
 - d. Right click each binding site and select "Attach CRM to gene"
- 13) Save your workspace when done, File-> Save Workspace...
- 14) You're done! The GBW file is what you will be submitting.