

## Frequently Asked Questions and Troubleshooting

**Q:** *I've loaded my gene but cannot drag it into the workspace. How do I properly place my gene into my workspace?*

**A:** There are two workspaces shown, one is above the genomic axis and one is below. This is due to the directionality of DNA (5' to 3' and 3' to 5'). If you right click on the sequence in the lower right "Consensus Sequence" panel you can select "Show" and then "Display Complement". If you are working on the forward strand (i.e. 5' to 3') then you should be working in the workspace above the axis. If you are working on the reverse stand (i.e. 3' to 5') then you should be working on the workspace (rev).

**Q:** *How do I properly set my SubView range?*

**A:** You have to left click and drag the mouse to select a genomic axis area; you should see a section of the genomic axis with a red bar on it. Then you can either press ctrl+K (command+K for macs) or select Data Manipulation → Set SubView Range.

**Q:** *I cannot located the species in the Open Species... dialog. Why?*

**A:** You must be entering the full Latin taxonomic name (e.g. Homo sapiens). Also, verify that you have a valid internet connection and that the URL <http://eutils.ncbi.nlm.nih.gov/entrez/eutils/efetch.fcgi> is reachable.

**Q:** *I cannot find the gene in the paper?*

**A:** Have you tried synonyms of the gene you are looking for? Genes often have many different names as they are discovered in different species, by different researchers, etc... Use NCBI to find the gene's synonyms and try searching for them. Also make sure your species is loaded using the *Open Species...* dialog!

**Q:** *Why isn't my CRM attaching to the gene?*

**A:** Make sure that you've left click dragged the gene into your workspace area (the area just above and below the genomic axis).

**Q:** I've saved my workspace but when I try to open it CYRENE fails or freezes. How can I save my work and continue working later?

**A:** This functionality was not testing thoroughly and is currently being investigated. We believe it should work if the axis is already loaded. Regardless, your annotations should be properly saved within the workspace file (you can check this by opening it in a text editor... search for "TFBS" or "CRM\_SPAN").