How to use the Artemis on Roseobase.org
Feng Sun, May 6, 2005

1. Go to Artemis page: http://www.roseobase.org/artemis/

2. Download the data you want to view by right click the link and save the target as a file.

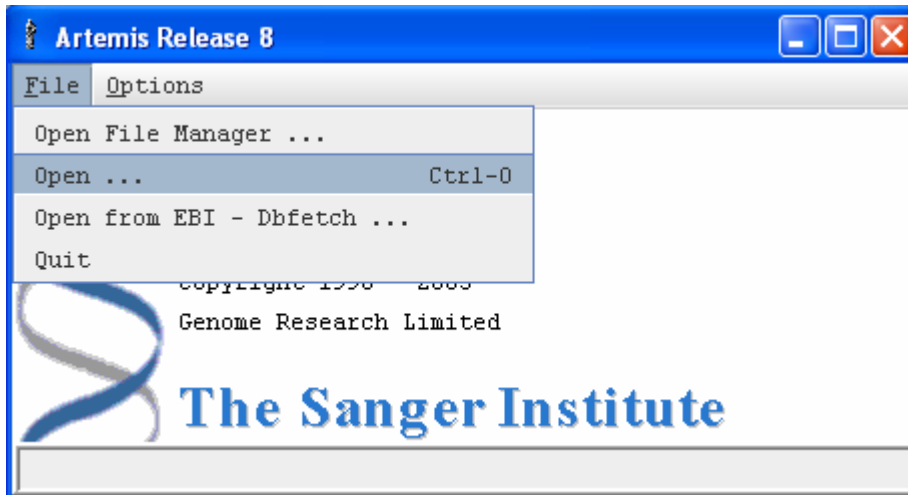3. Click "LAUNCH ARTEMIS" to launch it.

    Depending on your network speed, it takes a few second to a few minutes to download the program.
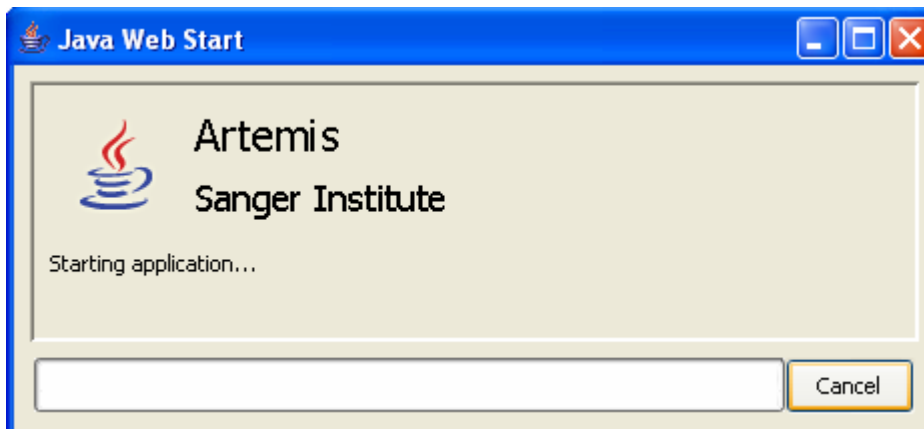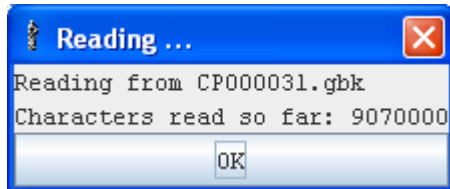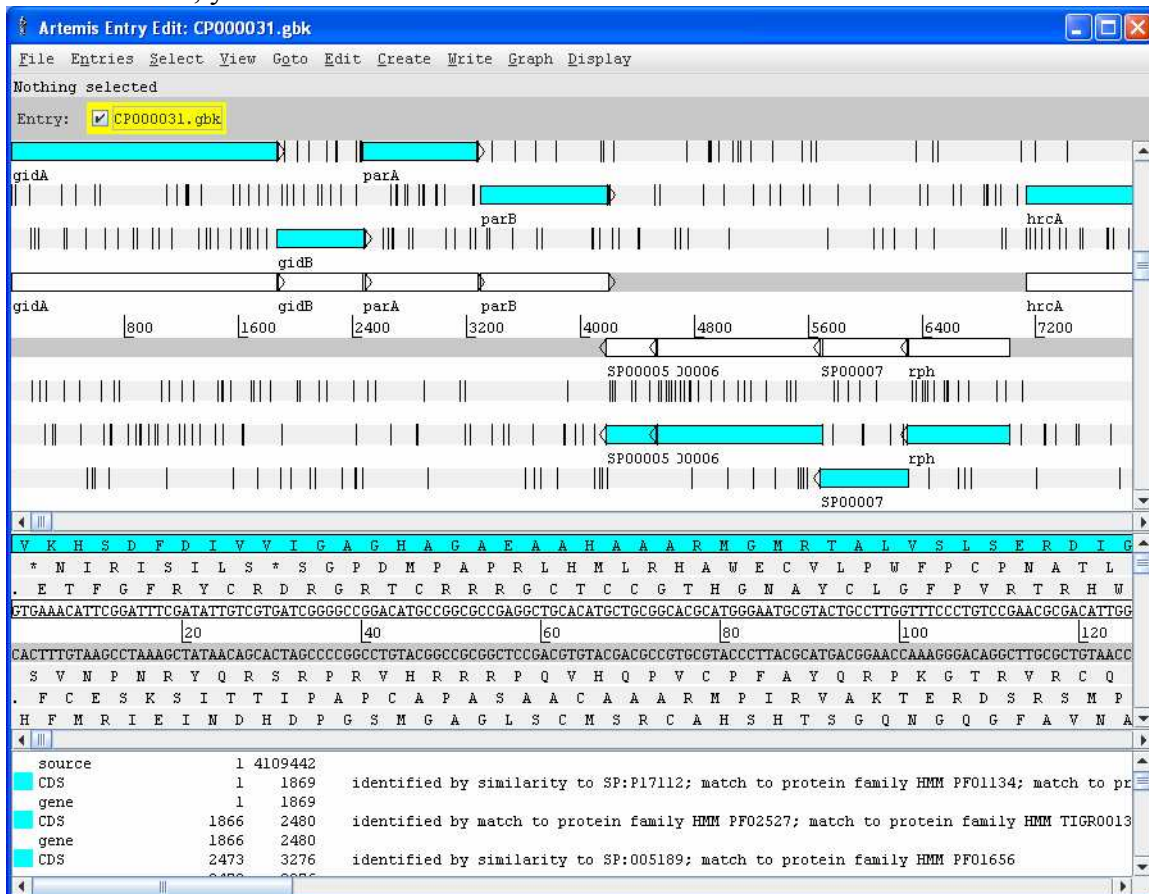

Click Yes when you see next page:

The program will be launched. Then click "File -> Open", find the file you just downloaded and click open.

The next window shows the data loading process:

After it's done, you'll see the next window.

At the bottom, the panel shows annotation information. However, the default is not convenient because it tell us neither the protein products nor the gene name. So first we need to turn those two on. Right click the panel and then click "Show Gene Names". Repeat and click "Show Products".
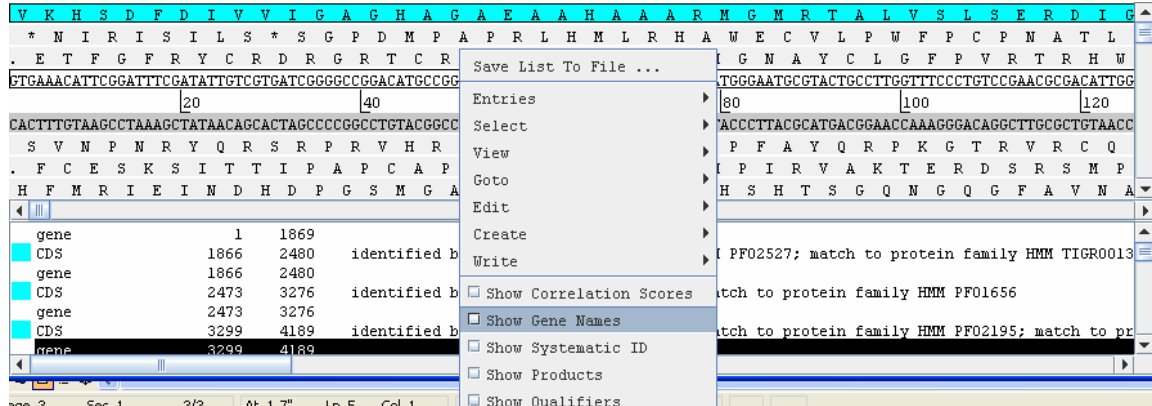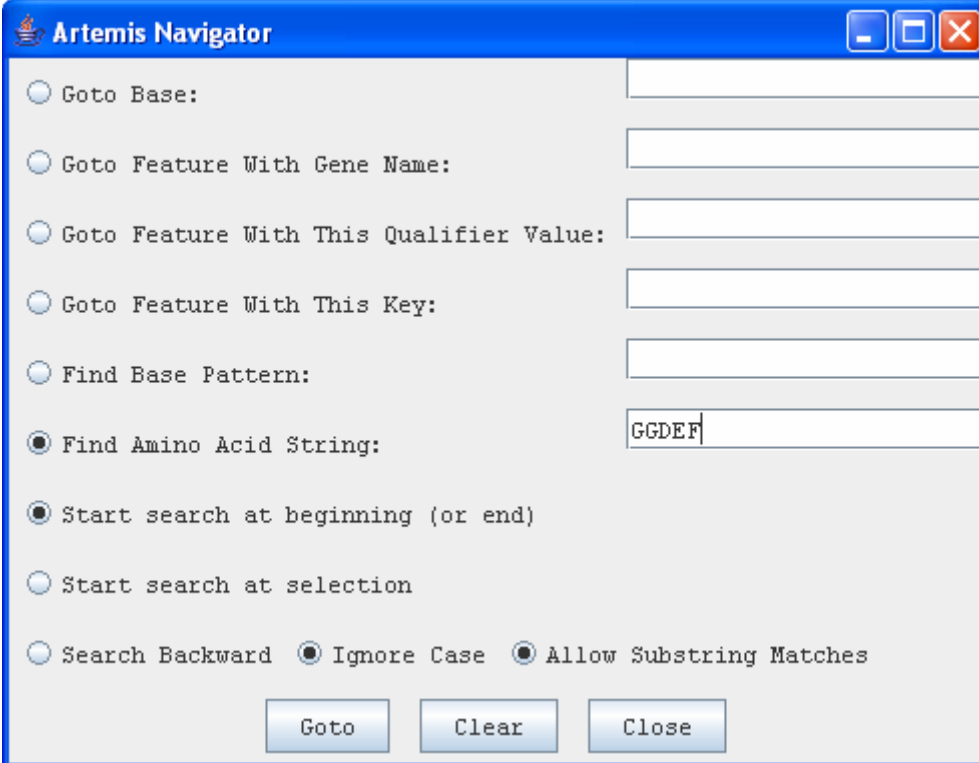

Now it looks like:
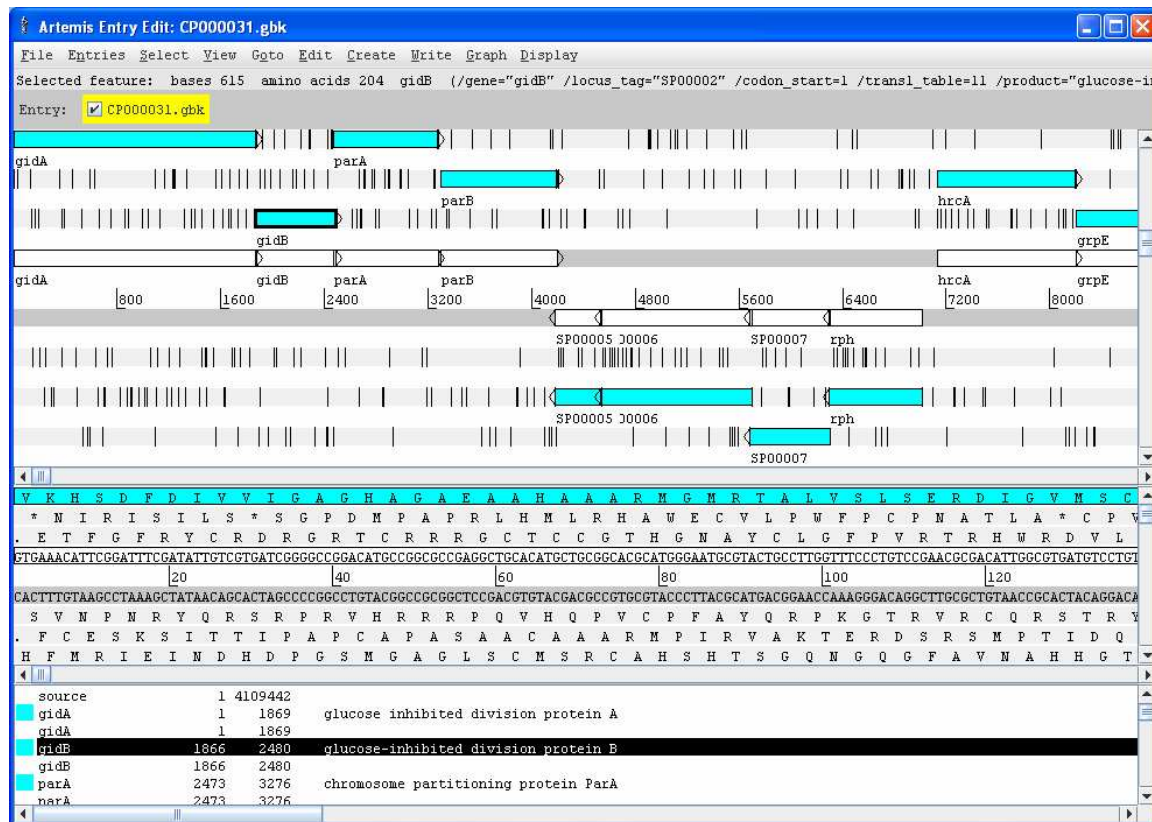
4. In this part, we show how to find a short sequence in the genome. For example, we want to locate "GGDEF".

   In the previous window, click menu "Goto -> Navigator". In the window opened, check "Find Amino Acid String:" and then type GGDEF in the field after it. Then click "Goto".

The program will jump to the first "GGDEF" it finds:

Please be aware that Artemis will search in all six frames. So it will find more instances than just do a scan of the coding sequences in the genome.