3 The *Maj* viewer

This tool uses a Java applet to provide an interactive graphical display for the alignment data, combining some of the features from the other tools. It has two distinct viewing modes that correspond roughly to the *Enteric* and *Menteric* tools, respectively, and buttons that allow the user to switch back and forth.

- ***The "wide" view*** displays *Enteric*-like PIPs aligning a 20 Kb region from *E. coli* with each of the other bacteria, and uses the same color coding scheme. The gene arrows are links to the WIT database, and information about the location of the mouse pointer (*e.g.*, coordinates and contig name) appears in a box near the top of the window.

- ***The "close-up" view*** adds *Menteric*'s nucleotide-level multiple alignment in a scrollable panel. The PIPs now display pairwise projections of the 1 Kb multiple alignment, and the colored underlays reflect *Menteric*'s GenBank annotations.

In addition, *Maj* allows the user to zoom in on areas of interest to examine the PIPs more closely, and to “mark” a particular local alignment to obtain more information.

Maj entry form