1 The *Enteric* server

This tool produces a graphical, hypertext view of alignments of the *E. coli* genome with related bacteria, covering 20 Kb around a user-specified position. For each of the six other bacteria, a locally developed DNA sequence alignment program called *blastz* was used to pre-compute all pairwise alignments with the *E. coli* sequence.

The alignment information is returned in the form of a PDF document. The output is displayed as a set of "PIPs" (Percent Identity Plots), in which:

- **positions in the *E. coli* sequence are numbered along the horizontal axis,**
- **matches are represented as horizontal lines, and**
- **the percent identity of each match (between 50% and 100%) is given by the vertical coordinate.**

Additional information is embedded in each PIP and can be retrieved by clicking on, or pointing at, the relevant alignment segment:

- gene names, which contain hyperlinks to entries in the WIT database (Selkov *et al.*, 1998);
- the name of the contig aligning with that *E. coli* region;
- information about discontinuities in gene or contig order, coded by colored vertical stripes at the ends of some alignments.

Red – In the other species, the immediate neighbor of this aligning sequence has a homolog elsewhere in *E. coli*. When pointed at, it reveals the address of the distant homolog.

Blue – In the other species, the immediate neighbor of this aligning sequence has no detectable homolog in *E. coli*. When pointed at, it reveals the length of the unmatched sequence.

Yellow – This *E. coli* sequence was not found in the other species.

Gray – This region was apparently not sequenced in the other species.