## 2 The *Menteric* server

This tool computes and displays on-the-fly nucleotide-level multiple alignments of sequences from several related genomes in a 1 Kb region surrounding a user-specified address. The alignment is rendered as a PostScript or PDF document in which annotations of ORFs, promoters and protein binding sites are color coded.

Features displayed:

- ***Color underlays***. These are used to mark known functional and regulatory regions (*green* = promoters, *red* = protein binding sites, *light chocolate* = ORFs).

  The annotation data were obtained from two sources:

  - the GenBank version M54 of the *E. coli* annotated sequence (Blattner *et al.*, 1997), and
  - the web-based RegulonDB database (Salgado *et al.*, 2000).

- ***Annotation labels.*** Locations of interest in the ***E. coli*** sequence (*e.g.*, transcription start sites, names of binding proteins) appear along the top of the alignment.

- ***Boxes around conserved regions.*** The user can select from five different programs for determining the conserved regions (*infocon*, *agree*, *phylogen*, *kkno*, and *kunk*; Stojanovic *et al.*, 1999), each using different conservation criteria.

  Depending on the method used, a "conserved" block in the alignment is one with high information content (*infocon*), good letter agreement (*agree*), low phylogenetic distance (*phylogen*), or in which any of the alignment rows differs in at most one position from either an a priori specified sequence (*kkno*) or an unknown "center" sequence (*kunk).*

  In the example shown, regions longer than 6 nucleotides in which all columns have a letter agreement better than 80% are reported as conserved.