Fig. 3.10. Alignment between 3’UTRs of TBFV. The following features were superimposed on the alignment:

1. The boundaries of structural domains I, II and III according to the GA-model of gradual folding (Proutski et al., 1997b) are depicted by green right-directed arrows.

2. The boundaries of loops or SLs are specified by black lines with oval lines on the top and bottom. Numbers of loops correspond to those depicted in Fig. 3.13 (Gritsun et al., 1997).

3. The boundaries of the dumbbell-like structure DB1 are outlined by brackets.

4. Long repeated sequences (specified as LRS in Fig. 3.11) are shown in red right-directed arrows.

5. Circularization sequences are highlighted in brown emboldened underlined letters. The 11-nucleotide CYCL is specified in the brown open box.

6. The boundaries of the pseudoknots P1 and P2 (brown background) are depicted by brown lines with double-oval lines on top and bottom. Other elements of the secondary structures predicted by the pseudoknot model are specified as C1, B3 and B2 as on Fig. 3.9 and their boundaries are shown by brown brackets (Olsthoorn and Bol, 2001).

7. Navy blue lines with left-directed arrows show the boundaries of the engineered deletions that are specified as follows:
   - **Non-viable TBEV** – deletion after stop codon that was lethal for a virus (Mandl et al., 1998)
   - **Non-viable LGTV- deletion after stop codon that was lethal LGTV** (Pletnev, 2001)
   - **Turbid plaques** - deletions after the stop codon that produced virus with turbid plaques for (1) TBEV strain Neu (Mandl et al., 1998), (2) TBEV strain Vs (Gritsun, unpublished) and (3) LGTV (Pletnev, 2001).
   - **Maximum spontaneous deletion** – the longest deletion that spontaneously appeared in TBEV during passage in the laboratory (Mandl et al., 1998)
   - **The deepest deletion for the WT plaques** – the longest deletion after the stop codon that produces virus with wild-type plaques (Mandl et al., 1998).