```
bglA13   TGCCCCAAGAAACTGAAATAAATAATTATTTATAAACTATAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA------------------- 940
bglA16   TGCCCCAAGAAACTAAAATAAATAATTTTTTATAAACTATAAAAAACAAAAATAATAACAAATAATTCATTAAATGAATTAAAAAATTAA 965
bglA51   TGCCCCAAGAAATTAAAAATAAATAATTTTTTATGAACTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA--------------------- 955
bglM2    TGCCCCAAGAAATTAAAAATAAATAATTTTTTATAAACTATAAAAAATTACAATAATAACAAATAATTCATTAAATGAATTAAAAAAAAAA 990
lic6     TGCCCCAAGAAATTAAAAATAAATAATTTTTATGAATTACAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA------------------- 961
```

FIG. S1. Alignment of the ends of the coding regions and adjacent 3' untranslated regions of four cDNAs coding β-1,3–1,4-glucanase from *Neocallimastix patriciarum* J11. Stop codons are presented in bold and underlined. Premature stop codons are shown in bold. The sequences that were predicted to be able to form self-pairing regions are shown in italics and are underlined. The *lic6* gene of *Neocallimastix patriciarum* was accessed from Genbank (accession no. EU314934).