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-570 CTCATCAAG AACTATTAA AAAATTGGA CAATTATTAA TTAAATTGA AAAAAATTT TAKTTTCAA ATCTTTTAAA
-490 GATTTTAGAG GTTATTAAA AAAAAAAAA AAAAAAAAA TCCAAAAAA AATCCATAA AGTCCAAAT CAAATATTT
-410 AAATTTAAT TATTTTAAA TTTAAAACTA ATCAAAAAT AAAAAAATA ATAAAAATA TAATTAACA AATAAAAATA
-330 TTAAAAATA ATATTATAA AGAACAAATA AATTATTGAT TGTTGTTTTT AAAATAATA TAATTCAAA AAAAAAAAA
-250 AAAAAAATT AAATTTAAA AATATTTAT AATATTTATA ATATTAATAA TATATGTTAT AATTAIGAAA ATTAATTAATA
-170 ATGGATAAC TAAAAATGA ATTTTTTTTT TTTTTTTTT TTTTATTAT TTTTTTAAAT AATGTAGTT ACAATGTAT
-90 ATCTAACC CTATTGTTG AAAAAAAAA CAGTGCBAAC TCACCCACTC ACBAATTTTT AAACAAAT AAAAAAATT
-10 TGGTGGTTC TGIGAAAAA TAGCTCCATA CAAAAACAA ATTTTATCAA ACACCACCA ATATTATTAT TTTATTTAA
+70 TTAAATTAAT TTTTTTTTT TATTAAATAT ATATTTTTTT TTTTTTTTT TTTTTTTATA TTTTGGTTT TTTCAATAT
+150 TATTATATA TTTTTTTTT CACTAATAA TTAATATTT TTTGATTTT TTTTATATT ATTCATTA AAAAAAAAA
+230 TAAAAAAAA AACAAAATA AAAAAAAT AAAATAATA AACAAATTA AAAAAATGG AAAAAAAG AAGT

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Figure 8. EMSA probes in the *gp-2* promoter sequence.

The sequence of the *gp2* promoter is represented here. Like most *Dicystotellium* promoters, it shows an 88% AT bias. Three sets of repeat elements known as the TA-, TAG- and C-boxes are underlined. The position of the start site of transcription is indicated by an arrow. Translation of the *gp-2* mRNA is initiated from the ATG (*italicized*). Sequences within the boxed regions were used to design oligonucleotides for EMSA. The names of these oligonucleotide probes are shown above the boxes.