

[illegible]

Sequence logo for the 12 bp motif. The y-axis is 'Information content' (0 to 2) and the x-axis is 'Position' (1 to 12). The sequence AGGGAAG is highlighted in green, AGG in orange, and AAG in blue. The sequence logo shows the information content of each base at each position, with the highest information content at positions 4, 5, 6, 7, and 8.

Sequence logo for the CAGCCTG motif. The y-axis represents 'Information content' (0 to 2) and the x-axis represents 'Position' (1 to 9). The motif is CAGCCTG, with positions 1-2 and 8-9 showing low information content.

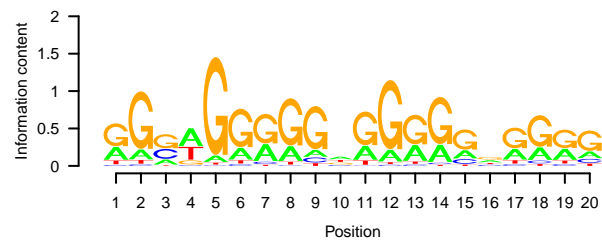
Sequence logo for the TGA(T)CA motif. The y-axis represents 'Information content' (0 to 2) and the x-axis represents 'Position' (1 to 7). The sequence is T (red, pos 1), G (orange, pos 2), A (green, pos 3), T (blue, pos 4), C (red, pos 5), A (blue, pos 6), and A (green, pos 7).

Sequence logo for the 16 bp motif. The y-axis represents 'Information content' (0 to 2) and the x-axis represents 'Position' (1 to 16). The logo shows the relative frequency of nucleotides at each position. Key features include a high 'C' at position 5, a high 'T' at position 9, and a high 'G' at position 13.

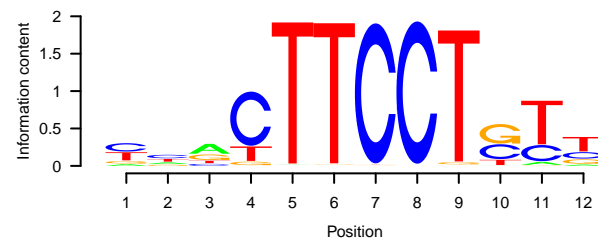
Sequence logo for the 7bp motif AGATAAG. The y-axis represents 'Information content' (0 to 2) and the x-axis represents 'Position' (1 to 7). The sequence is A (green), G (orange), A (green), T (red), A (green), A (green), G (orange).

Sequence logo for the 12 bp motif. The y-axis is 'Information content' (0 to 2) and the x-axis is 'Position' (1 to 12). The sequence is approximately GCGCCGCCCCCGCC. Positions 3-6 and 8-10 show high information content (mostly C). Positions 1-2 and 7-12 show lower information content with more varied bases.

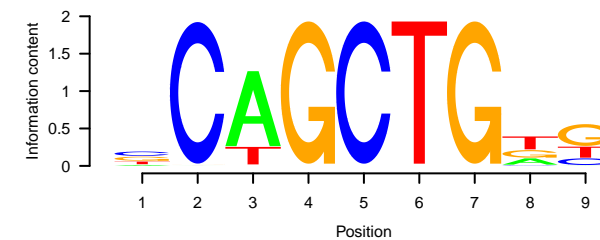
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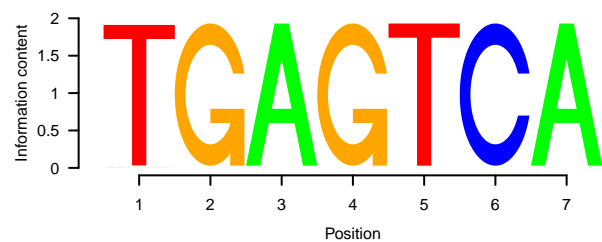
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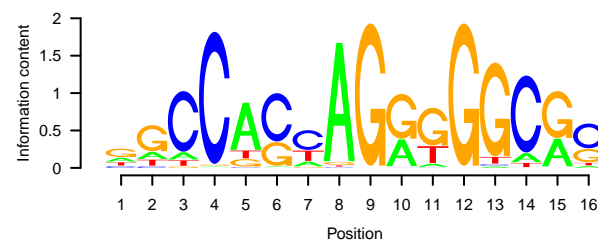
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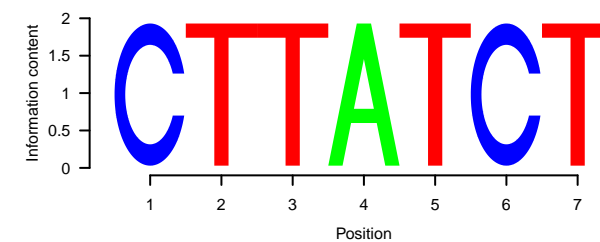
Sites= 467 / Total inputs= 4000



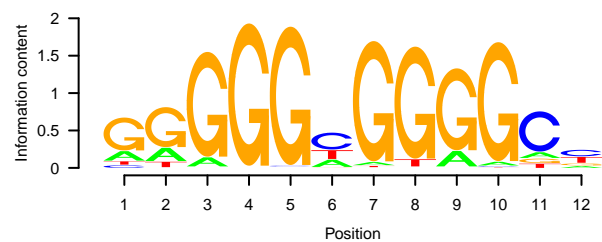
Sites= 218 / Total inputs= 4000



Sites= 393 / Total inputs= 4000



Sites= 403 / Total inputs= 4000



Sites= 239 / Total inputs= 4000

