

A/T rich blocks in genes repressed by H-NS

ssrA (S. typhimurium)

```
481 aaccagcaag tacaggcctt caccgtcccg tagctcatag tctgtgctac ggggcttcgc
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1261 tttgatggg
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traJ

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micF

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2311081 ttcactcgca actagaataa ctcccgtat catcattaac ttattttatt accgtcattc
2311141 atttctgaat gtctgtttac cctatttca accggatgcc tcgcattcgg ttttttttac
2311201 ctttctttac aacttttca ttattctgtg ctaccacaga aaaactataa cgcttgtaa
2311261 ctatttcaca aataattaac atccgcataa tttccagcaa tctttgttta tttgaatta
2311321 tttttgttgg gctttttgta ggttatttgt acagcaaaat ggcgcttgta catctatttc
2311381 cccaatgca ggatgataaa tatcacggga gaatagagaa tcatcaatca ggtaagagtc
2311441 tggaaattca cactgtacc tttatactgc cctatcactt cgcgaagttt taacaggtca
2311501 taaacacgaa tgcgtcagaa agagacaacg gccacgacc gcttttctact cctaccgggg
2311561 agcattacc gcttctttt actggtgatc attgtgttac tggtgacgat ggggtgtaatg

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The sequences highlight blocks of A/T sequences containing at least 6 consecutive A-T basepairs and a TpA step. Where these blocks are flanked by CpG, as in the template motif, this is indicated in red. In the *ssrA* and *spvR* sequences two blocks that do not fully meet these criteria but in other respects closely resemble the template motif are highlighted in red. The translation start site (cat or atg) is, where relevant, indicated in italics as is the transcription start site (g) in *micF*. The *ssrA*, *traJ*, *traH*, *spvR* and *flgA/B* sequences are preferentially bound by H-NS *in vitro* (21). Except for *ssrA* the nucleotide numbers are taken from the *E. coli* K12 genomic sequence (NC\_000913).