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+ AAGCCCATTA AGGGTGTAAA GCTTAATTCC ACTAATGGCC CATTAAGTAA AAAGCGCTAT  AGTATTAGG
- TTCGGGTAAT TCCCACATTT CGAATTAAGG TGATTACCGG GTAATTCATT TTTCGCGATA  TCATAATCC

+ CCTTGTTCGA GAATCTCCTA ATGCCATGAC TTAGACACAA TCTTTGGACT T GACATCAA TACATCATCT
- GGAACAAGCT CTTAGAGGAT TACGGTACTG AATCTGTGTT AGAAACCTGA A CTGTAGTT ATGTAGTAGA

+ CTGACGATGA CCGATTTCCT TTGGTAAATC TCTGACGATG AC CAATCCA GAAGAGAAAC CTAAGAGTAG
- GACTGCTACT GGCTAAAGGA AACCATTTAG AGACTGCTAC TG GTTAGGT CTTCTCTTTG GATTCTCATC

+ ATAGAATGAT GCAAAAAGA AGTGAAAGGA TAA CCCCAC ATCACATCTC TTTCCATGTG TCACCTTCTG
- TATCTTACTA CGTTTTTTCT TCACTTTCCT ATT GGGGTG TAGTGTAGAG AAAGGTACAC AGTGGAAGAC

+ CATGAATCCA CACATTGCTA TTTT AAGAA GGTGAAAATA TTTTAAAATG TAGACAATAA GCTTCGGTGT
- GTACTTAGGT GTGTAACGAT AAAA TTCTT CCACTTTTAT AAAATTTAC ATCTGTTATT CGAAGCCACA

+ GAACTTCGGA GAAGC CTGT GGTTCTTGTG ATAAAGGGGA TATCGAATTC AAAGTTTGTT GCACTGCTTT
- CTTGAAGCCT CTTCG GACA CCAAGAACAC TATTTCCCCT ATAGCTTAAG TTTCAAACAA CGTGACGAAA

+ CCACCA ACA ATTTAACAAA CATAAAAAAT AAAATAAAAA AGTTTCACTT CTTTTGCAAT TTTGTAG TT
- GGTGGT TGT TAAATTGTTT GTATTTTTTA TTTTATTTTT TCAAAGTGAA GAAAACGTTA AAACATC AA

+ ATTTAATTTG CTTTTTGAAA TCGTCTAAGT AGTGCCAACG TGGATGGCTT GTTCGGAG A GAGCCTTCCA
- TAAATTAAAC GAAAAACTTT AGCAGATTCA TCACGGTTGC ACCTACCGAA CAAGCCTC T CTCGGAAGGT

+ CAAGCAATTG AAACTTGGAA TAACGTTGCA TAAGTAAAAT GTTGCAATC  ATCAATTTTA AAAGCACAAG
- GTTCGTTAAC TTTGAACCTT ATTGCAACGT ATTCATTTTA CAACGTTAG  TAGTTAAAAT TTTCGTGTTC

+ GCACATGACA TTAACACGTT ATTTGAAAGT TTTTTTGATG  AGAATATCC AACTACTTTA CCGTCCTCAC
- CGTGTACTGT AATTGTGCAA TAAACTTTCA AAAAAACTAC  TCTTATAGG TTGATGAAAT GGCAGGAGTG

+ TCTCTTAACC TTTGAAACTC TAGGCTTTAT G TTCCAAAA TTCAACGTAA CATATATTCT CATACTTAAT
- AGAGAATTGG AAACTTTGAG ATCCGAAATA C AAGGTTTT AAGTTGCATT GTATATAAGA GTATGAATTA

+ TTTTCAGGTT TTCTTAAACC AA ACATTAT GTAAAAGTCA ACTTACCTAT ATTAACATGC AAAGTCAACA
- AAAAGTCCAA AAGAATTTGG TT TGTAATA CATTTTCAGT TGAATGGATA TAATTGTACG TTTCAGTTGT

+ TCTCTTTTTT TGT TTAAGC AAAGTCAACA ACTTAACCCA CAAACAAAAA GCAAAACATG CAAAATTATT
- AGAGAAAAAA ACA AATTCG TTTCAGTTGT TGAATTGGGT GTTTGTTTTT CGTTTGTAC GTTTTAATAA

+ AATG TGCTT CACTCTGACT CTCACCACCA TAAGGTAAAC ATAAAATACT CTCACCGCCG AAGTT ACCC
- TTAC ACGAA GTGAGACTGA GAGTGGTGGT ATTCCATTTG TATTTTATGA GAGTGGCGGC TTCAA TGGG

+ CCACAAGGTT TCTATTTTAA TCTCTTAGTT CCATTACTTT ATCTACATTA ACATAC AAA AGAACATTCT
- GGTGTTCCAA AGATAAAATT AGAGAATCAA GGTAATGAAA TAGATGTAAT TGTATG TTT TCTTGTAAGA

+ ATCACTCCAA AATATACGCA TAAAGATATT ATTATTTGAA CTAACAG AA TCTAAGTTAG ATAGATAGAT
- TAGTGAGGTT TTATATGCGT ATTTCTATAA TAATAAACTT GATTGTC TT AGATTCAATC TATCTATCTA

+ TATATTAAAT ACCATACATA CTATCACGTG GATCGTTT C TAGAATATAC AGTAAAAAAA AAACGTTAGG
- ATATAATTTA TGGTATGTAT GATAGTGCAC CTAGCAAA G ATCTTATATG TCATTTTTTT TTTGCAATCC

+ CGATATGTAG TCTAAGCAAG GTTTATAAC  CTTTTGTATA TTTCAAAGGA CGTGGCATAT TAGGTACATG
- GCTATACATC AGATTCGTTC CAAATATTG  GAAAACATAT AAAGTTTCCT GCACCGTATA ATCCATGTAC

+ CCAAGTGGAA TTGACCTTGG  CTCTCTTCT ACATTGATAA AGTTCTTCGC ATAATTCACA TCCCTATATA
- GGTTCACCTT AACTGGAACC  GAGAGAAGA TGTAACTATT TCAAGAAGCG TATTAAGTGT AGGGATATAT
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+ AACAAATGAA C GGAGAAGG TATGAGTACA TCCACACATT GACATTTCTA AAATCCAACT CCTCTTTTTG
- TTGTTTACTT G CCTCTTCC ATACTCATGT AGGTGTGTAA CTGTAAAGAT TTTAGGTTGA GGAGAAAAAC


+ AA AATTAAG AAACTCCACT TGGCTCTTCG ATTTTTTCTA TCTAAATAAC AGAACCAAAT CAT TATCGA
- TT TTAATTC TTTGAGGTGA ACCGAGAAGC TAAAAAAGAT AGATTTATTG TCTTGGTTTA GTA ATAGCT


+ AATTTAAAGT TGTGCGAAAC AAAACAAA
- TTAAATTTCA ACACGCTTTG TTTTGTTT
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 Motifs found

 A-box
 AACA_motif
 ABRE (positions: 1145, 1240, 1237)
 ACE
 ARE
 AT-rich sequence
 ATCT-motif
 Box 4
 Box I
 Box W1
 CAAT-box
 CCGTCC-box
 ERE
 G-box
 GAG-motif
 GCN4_motif
 GT1-motif
 HSE
 I-box
 LAMP-element
 MBS
 MBSI
 MRE
 Skn-motif
 TATA-box
 TC-rich repeats
 TGACG-motif
 Unnamed_1
 Unnamed_3
 Unnamed_4
 W box
 box II
 chs-CMA1a