

For further information on how to interpret these results please access https://meme-suite.org/meme/doc/meme.html.

To get a copy of the MEME software please access https://meme-suite.org.

If you use MEME in your research, please cite the following paper:

Timothy L. Bailey and Charles Elkan, "Fitting a mixture model by expectation maximization to discover motifs in biopolymers", Proceedings of the Second International Conference on Intelligent Systems for Molecular Biology, pp. 28-36, AAAI Press, Menlo Park, California, 1994. [pdf]

DISCOVERED MOTIFS | MOTIF LOCATIONS | INPUTS & SETTINGS | PROGRAM INFORMATION | RESULTS IN TEXT FORMAT | RESULTS IN XML FORMAT | PROGRAM INFORMATION | RESULTS IN TEXT FORMAT | RESULTS IN XML FORMAT

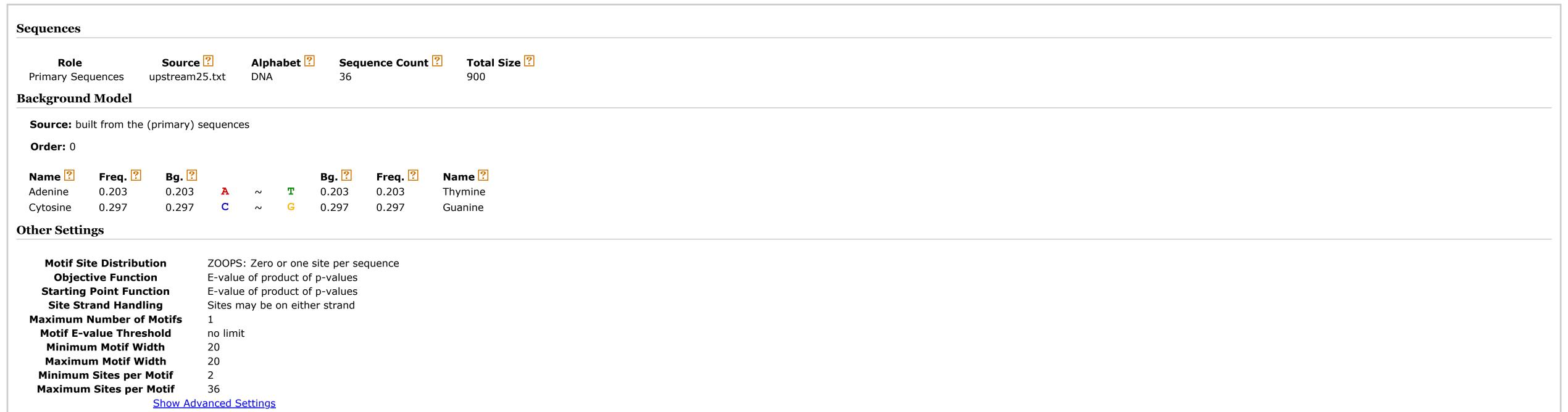
DISCOVERED MOTIFS



MOTIF LOCATIONS



INPUTS & SETTINGS



MEME version

5.3.3 (Release date: Sun Feb 7 15:39:52 2021 -0800)

Timothy L. Bailey and Charles Elkan, "Fitting a mixture model by expectation maximization to discover motifs in biopolymers", Proceedings of the Second International Conference on Intelligent Systems for Molecular Biology, pp. 28-36, AAAI Press, Menlo Park, California, 1994.

meme upstream25.txt -dna -oc . -nostatus -time 14400 -mod zoops -nmotifs 1 -minw 20 -maxw 20 -objfun classic -revcomp -markov_order 0