



MEME

Multiple Em for Motif Elicitation

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

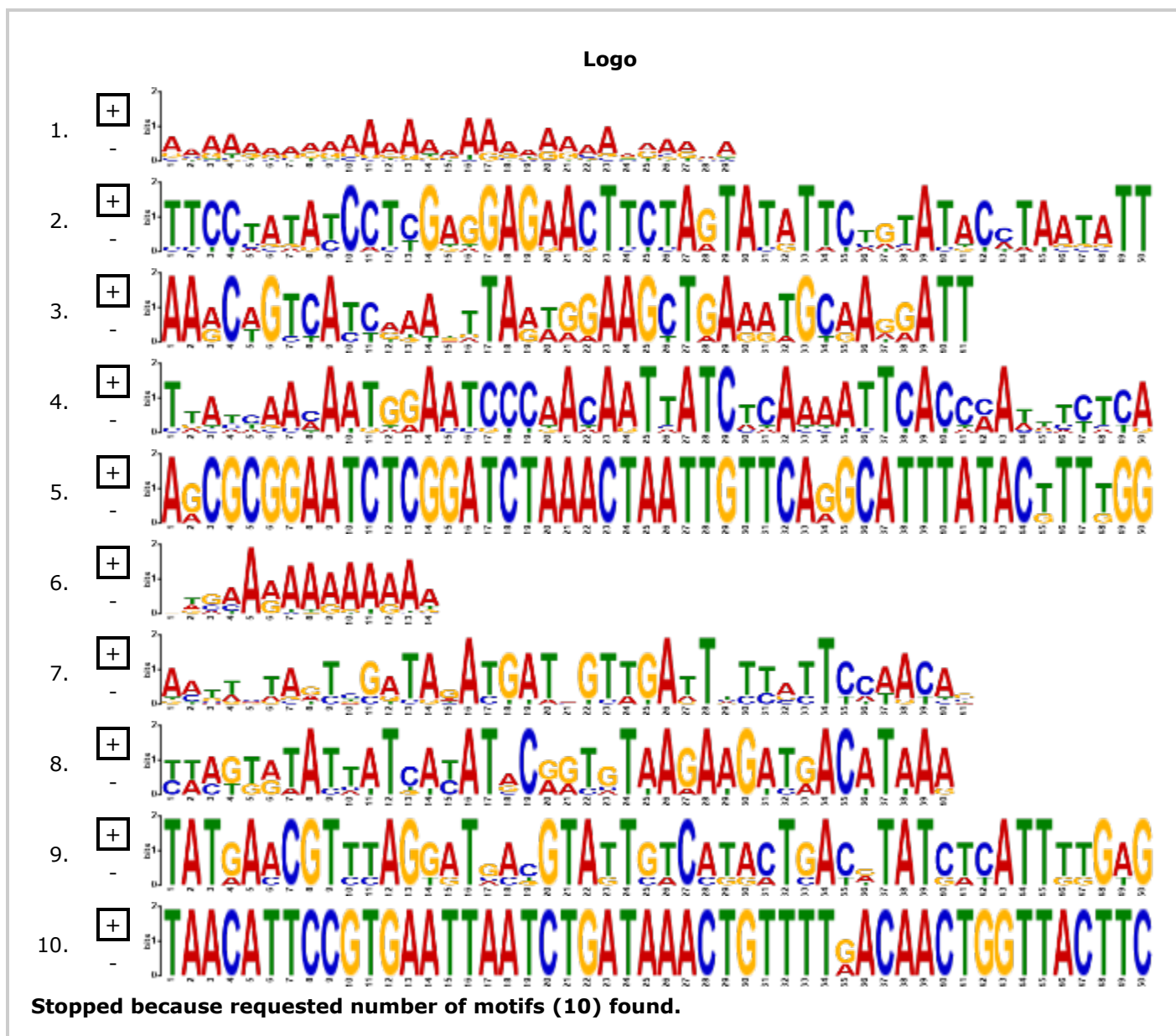
To get a copy of the MEME software please access <https://meme-suite.org>.

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. [\[full text\]](#)

[DISCOVERED MOTIFS](#) | [MOTIF LOCATIONS](#) | [INPUTS & SETTINGS](#) | [PROGRAM INFORMATION](#) | [RESULTS IN TEXT FORMAT](#) | [RESULTS IN XML FORMAT](#)

DISCOVERED MOTIFS



MOTIF LOCATIONS

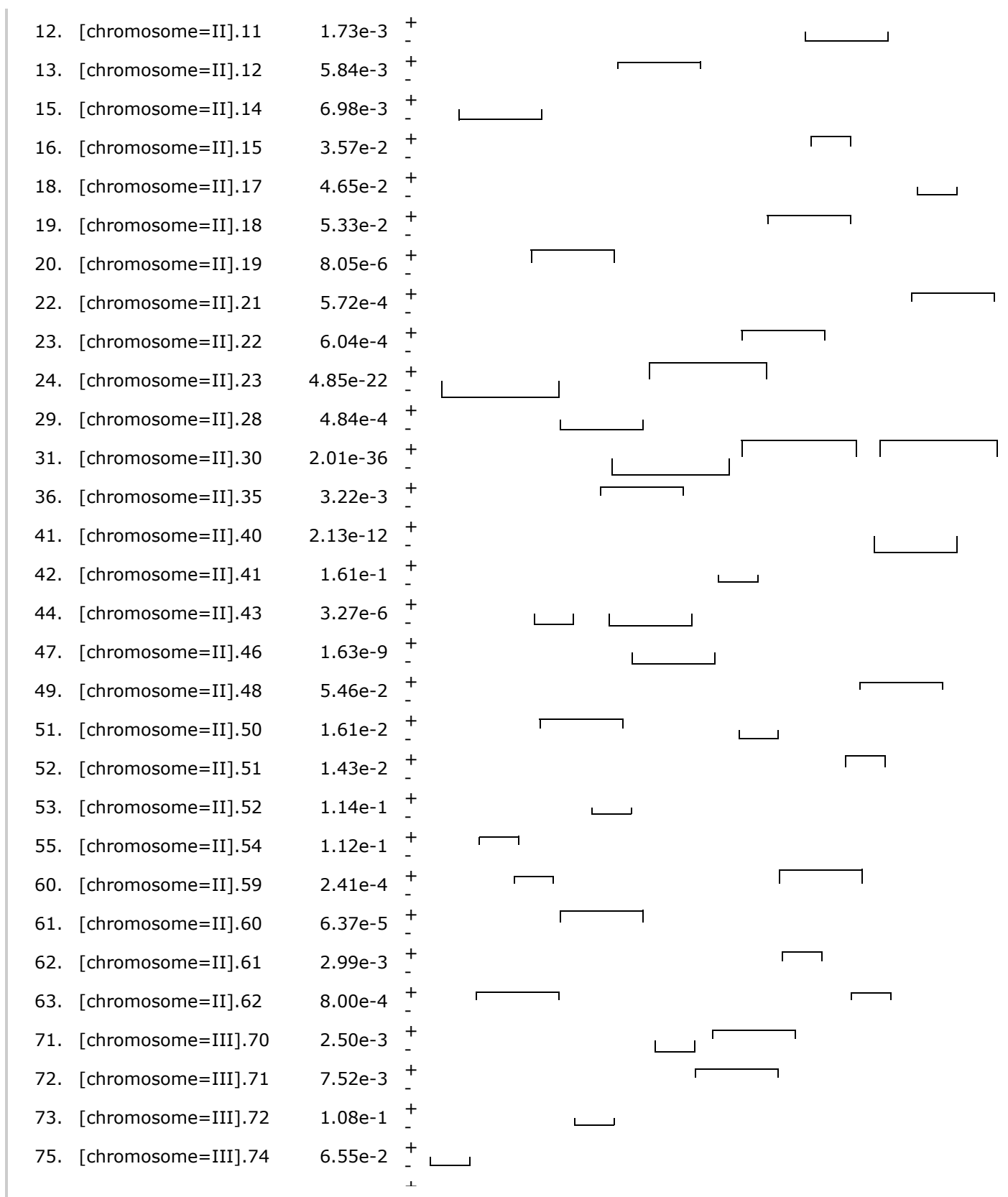
☒ Only Motif Sites ☐ Motif Sites+Scanned Sites ☐ All Sequences

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Motif **Locations** **p-value** **Motif Locations**

4.	[chromosome=I].3	7.73e-4	+	
5.	[chromosome=I].4	2.08e-8	+	
6.	[chromosome=I].5	8.13e-2	+	
7.	[chromosome=I].6	5.14e-2	+	
8.	[chromosome=I].7	4.10e-3	+	
9.	[chromosome=I].8	2.56e-1	+	
11.	[chromosome=II].10	1.27e-3	+	



INPUTS & SETTINGS

Sequences

Background Model

Order: 0

Other Settings

[Show Advanced Settings](#)

5.5.2 (Release date: Sun Jan 29 10:33:12 2023 -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. [\[full text\]](#)

```
meme Boundaries_Q_PeakSeqs.fasta -dna -oc . -nostatus -time 14400 -mod zoops -nmotifs 10 -minw 6
-maxw 50 -objfun classic -revcomp -markov order 0
```