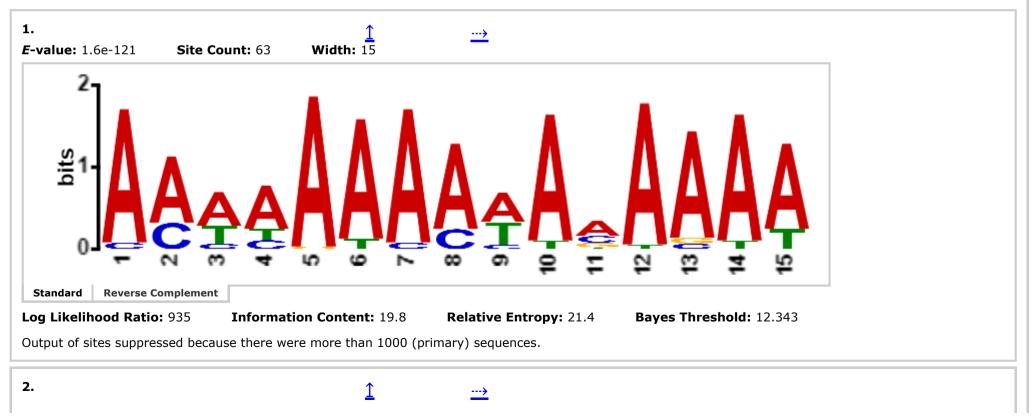# MEME
Multiple Em for Motif Elicitation

For further information on how to interpret these results please access https://meme-suite.org/meme/doc/meme.html.
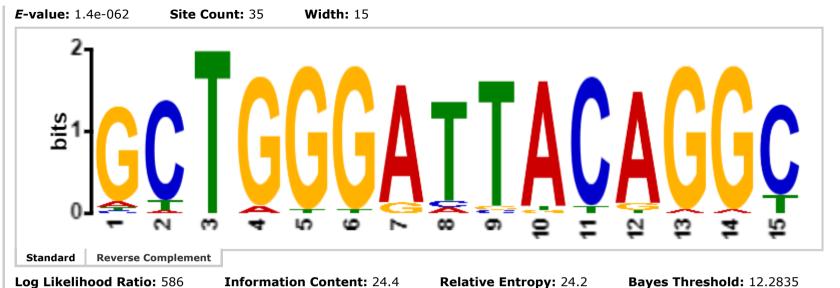To get a copy of the MEME software please access https://meme-suite.org.

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

1.

E-value: 1.6e-121   **Site Count:** 63   **Width:** 15

Standard | Reverse Complement

Log Likelihood Ratio: 935   **Information Content:** 19.8   **Relative Entropy:** 21.4   **Bayes Threshold:** 12.343

Output of sites suppressed because there were more than 1000 (primary) sequences.

2.

E-value: 1.4e-062   **Site Count:** 35   **Width:** 15

Standard | Reverse Complement

Log Likelihood Ratio: 586   **Information Content:** 24.4   **Relative Entropy:** 24.2   **Bayes Threshold:** 12.2835

Output of sites suppressed because there were more than 1000 (primary) sequences.

3.

E-value: 6.4e-068   **Site Count:** 79   **Width:** 15

Standard | Reverse Complement

Log Likelihood Ratio: 967   **Information Content:** 18.1   **Relative Entropy:** 17.7   **Bayes Threshold:** 11.219

Output of sites suppressed because there were more than 1000 (primary) sequences.

Motif Locations

Output of sites suppressed because there were more than 1000 (primary) sequences.

Inputs & Settings

Sequences

Role	Source	Alphabet	Sequence Count	Total Size
Primary Sequences	./seqs-centered	DNA	1148	114800

Background Model

Source: the file './background'

Order: 2 (only order-0 shown)

Name	Freq.	Bg.				Bg.	Freq.	Name
Adenine	0.219	0.228	A	~	T	0.228	0.219	Thymine
Cytosine	0.281	0.272	C	~	G	0.272	0.281	Guanine

Other Settings

Motif Site Distribution	ZOOPS: Zero or one site per sequence
Objective Function	E-value of product of p-values
Starting Point Function	E-value of product of p-values
Site Strand Handling	Sites may be on either strand
Maximum Number of Motifs	3
Motif E-value Threshold	no limit
Minimum Motif Width	6
Maximum Motif Width	15
Minimum Sites per Motif	2
Maximum Sites per Motif	1148

Show Advanced Settings

MEME version
5.5.1 (Release date: Sun Jan 29 10:33:12 2023 -0800)

Reference
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]

Command line
```
meme ./seqs-centered -oc meme_out -mod zoops -nmotifs 3 -minw 6 -maxw 15 -bfile ./background -dna -searchsize 100000 -time 2919 -revcomp -nostatus
```