

|     | Logo | E-value   | Sites | Width |
|-----|------|-----------|-------|-------|
| 1.  |      | 1.6e-4598 | 845   | 21    |
| 2.  |      | 6.2e-3670 | 845   | 21    |
| 3.  |      | 9.8e-2269 | 845   | 21    |
| 4.  |      | 1.6e-2002 | 845   | 15    |
| 5.  |      | 9.6e-1694 | 845   | 11    |
| 6.  |      | 1.4e-1396 | 845   | 11    |
| 7.  |      | 7.7e-1381 | 845   | 15    |
| 8.  |      | 9.3e-1192 | 845   | 11    |
| 9.  |      | 4.7e-1090 | 845   | 11    |
| 10. |      | 2.9e-983  | 845   | 11    |
| 11. |      | 3.9e-772  | 845   | 11    |
| 12. |      | 1.8e-615  | 845   | 11    |
| 13. |      | 3.6e-481  | 845   | 21    |

## MOTIF LOCATIONS

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

| Name | <i>p</i> -value | Motif Location |
|------|-----------------|----------------|
|------|-----------------|----------------|

## INPUTS & SETTINGS

## Sequences

| Role              | Source     | Alphabet | Sequence Count | Total Size |
|-------------------|------------|----------|----------------|------------|
| Primary Sequences | 3AC-d10.fa | DNA      | 169            | 1786364    |

## Background Model

**Source:** the file 'AR-background.hmm'

**Order:** 6 (only order-0 shown)

| Name     | Freq. | Bg.   |   |   |   | Bg.   | Freq. | Name    |
|----------|-------|-------|---|---|---|-------|-------|---------|
| Adenine  | 0.263 | 0.293 | A | ~ | T | 0.293 | 0.263 | Thymine |
| Cytosine | 0.237 | 0.207 | C | ~ | G | 0.207 | 0.237 | Guanine |

## Other Settings

|                                 |                                       |
|---------------------------------|---------------------------------------|
| <b>Motif Site Distribution</b>  | ANR: Any number of sites per sequence |
| <b>Objective Function</b>       | E-value of product of p-values        |
| <b>Starting Point Function</b>  | E-value of product of p-values        |
| <b>Site Strand Handling</b>     | Sites may be on either strand         |
| <b>Maximum Number of Motifs</b> | 1000                                  |
| <b>Motif E-value Threshold</b>  | 0.05                                  |
| <b>Minimum Motif Width</b>      | 4                                     |
| <b>Maximum Motif Width</b>      | 60                                    |
| <b>Minimum Sites per Motif</b>  | 2                                     |
| <b>Maximum Sites per Motif</b>  | 845                                   |

[Show Advanced Settings](#)

#### 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.

#### Command line

```
meme -dna -revcomp -mod anr -minw 4 -maxw 60 -minsites 2 -nmotifs 1000 -evt 0.05 -bfile AR-background.hmm -oc 3AC-d10  
3AC-d10.fa -mpi
```

