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

Logo

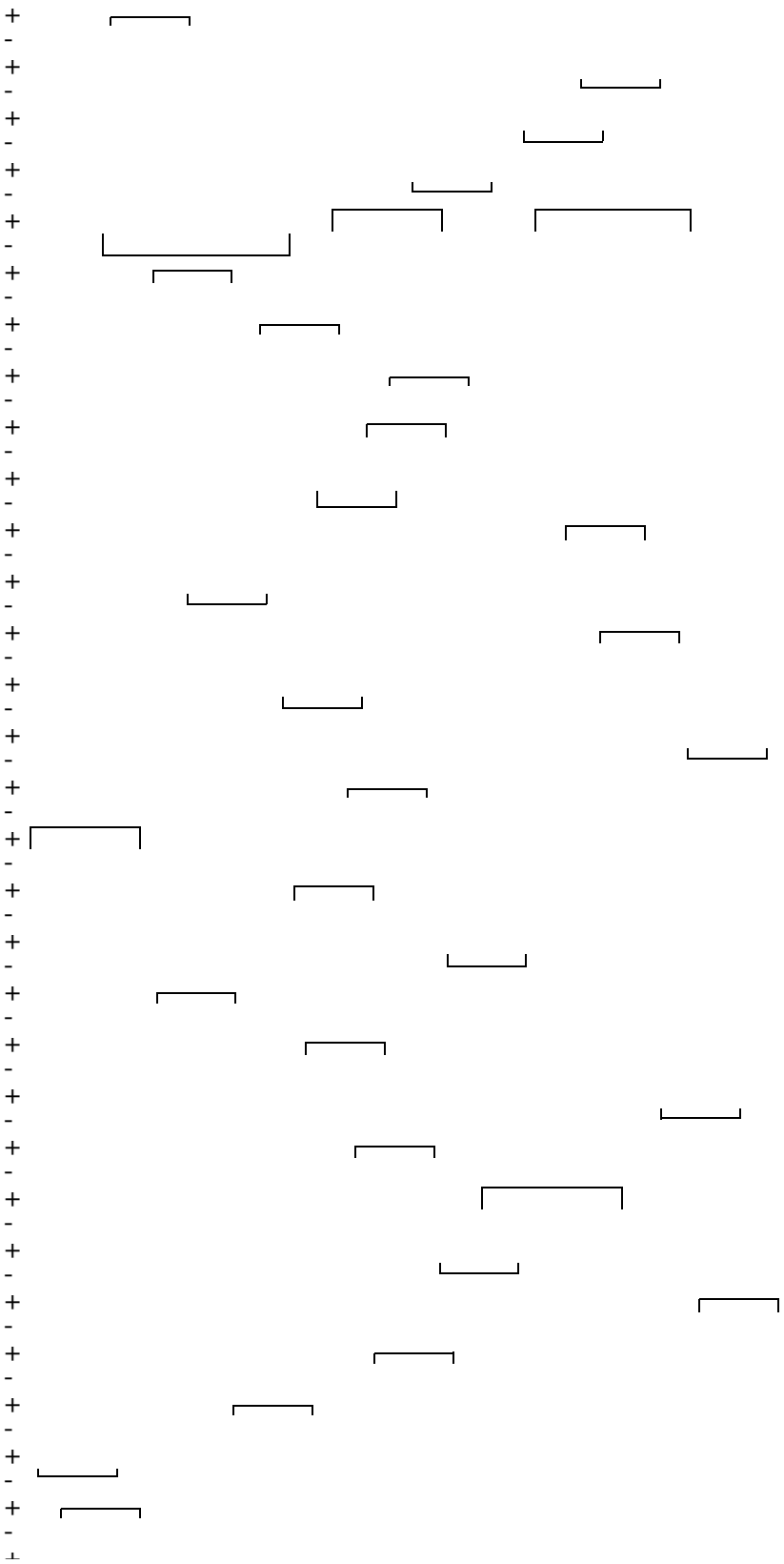
Stopped because requested number of motifs (10) found.

Motif Locations

Only Motif Sites | Motif Sites+Scanned Sites | All Sequences | Download PDF | Download SVG

	Motif Locations	*p*-value	Motif Locations
1.	[chromosome=I].0	4.85e-2	+ -
2.	[chromosome=I].1	7.91e-1	+ -
3.	[chromosome=I].2	6.96e-2	+ -
4.	[chromosome=I].3	4.03e-1	+ -
6.	[chromosome=I].5	3.41e-1	+ -
7.	[chromosome=I].6	6.29e-4	+ -
12.	[chromosome=II].11	4.83e-1	+ -

13.	[chromosome=II].12	5.45e-1	+ -
15.	[chromosome=II].14	5.03e-2	+ -
17.	[chromosome=II].16	9.81e-2	+ -
20.	[chromosome=II].19	6.12e-2	+ -
22.	[chromosome=II].21	4.97e-73	+ -
27.	[chromosome=II].26	2.57e-2	+ -
30.	[chromosome=II].29	1.46e-1	+ -
34.	[chromosome=II].33	5.89e-2	+ -
37.	[chromosome=II].36	2.79e-2	+ -
42.	[chromosome=II].41	1.51e-2	+ -
46.	[chromosome=II].45	1.76e-2	+ -
47.	[chromosome=II].46	2.29e-2	+ -
51.	[chromosome=II].50	1.10e-1	+ -
54.	[chromosome=II].53	1.44e-1	+ -
55.	[chromosome=II].54	6.36e-2	+ -
61.	[chromosome=III].60	3.36e-1	+ -
62.	[chromosome=III].61	2.98e-6	+ -
63.	[chromosome=III].62	5.11e-2	+ -
65.	[chromosome=III].64	2.84e-1	+ -
66.	[chromosome=III].65	6.15e-2	+ -
67.	[chromosome=III].66	2.71e-2	+ -
68.	[chromosome=III].67	1.28e-2	+ -
69.	[chromosome=III].68	5.12e-1	+ -
70.	[chromosome=III].69	4.30e-16	+ -
72.	[chromosome=III].71	2.26e-1	+ -
73.	[chromosome=III].72	2.50e-2	+ -
80.	[chromosome=IV].79	1.48e-1	+ -
81.	[chromosome=IV].80	1.70e-1	+ -
82.	[chromosome=IV].81	1.35e-1	+ -
83.	[chromosome=IV].82	1.05e-1	+ -



Inputs & Settings

Sequences

Role	Source	Alphabet	Sequence Count	Total Size
Primary Sequences	Boundaries_Log_PeakSeqs2.fasta	DNA	757	151400

Background Model

Source: built from the (primary) sequences

Order: 0

Name	Freq.	Bg.				Bg.	Freq.	Name
Adenine	0.301	0.301	A	~	T	0.301	0.301	Thymine
Cytosine	0.199	0.199	C	~	G	0.199	0.199	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	10
Motif E-value Threshold	no limit
Minimum Motif Width	6
Maximum Motif Width	50
Minimum Sites per Motif	2
Maximum Sites per Motif	757

Show Advanced Settings

MEME version
5.5.2 (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 Boundaries_Log_PeakSeqs2.fasta -dna -oc . -nostatus -time 14400 -mod zoops -nmotifs 10
-minw 6 -maxw 50 -objfun classic -revcomp -markov_order 0
```