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]

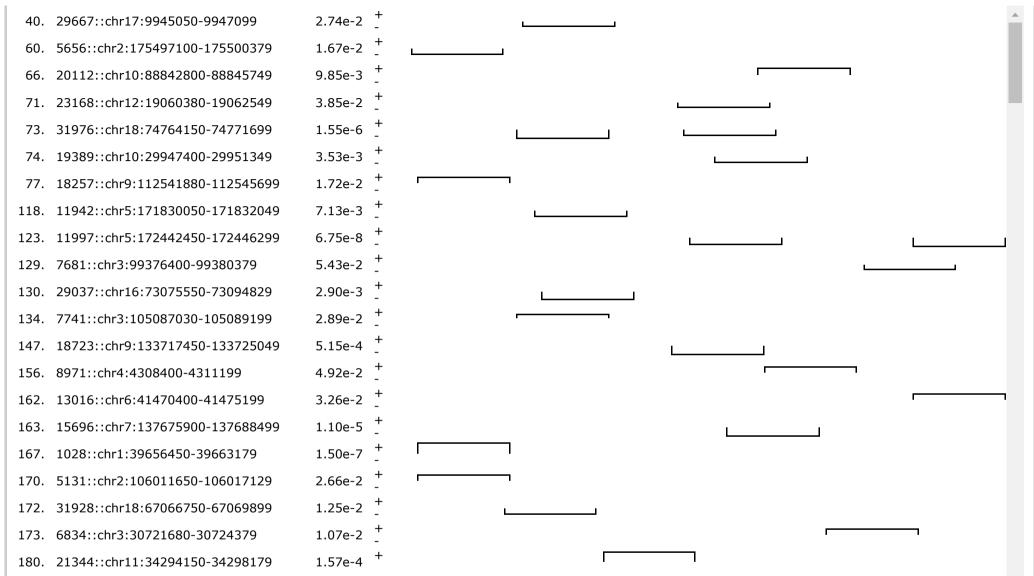**DISCOVERED MOTIFS** | **MOTIF LOCATIONS** | **INPUTS & SETTINGS** | **PROGRAM INFORMATION** | **RESULTS IN TEXT FORMAT** | **RESULTS IN XML FORMAT**

DISCOVERED MOTIFS

	Logo	E-value	Sites	Width	More	Submit/Download
1.		1.3e-068	96	15	↓	⋯→
2.		2.2e-014	92	15	↓	⋯→
3.		3.1e-028	20	15	↓	⋯→

Stopped because requested number of motifs (3) found.

MOTIF LOCATIONS

◉ Only Motif Sites   ◯ Motif Sites+Scanned Sites   ◯ All Sequences   [Download PDF]   [Download SVG]

Name	*p*-value	Motif Locations
6. 3707::chr2:1654950-1661929	1.66e-2	
33. 34715::chr21:36256180-36261749	3.41e-3	

40.	29667::chr17:9945050-9947099	2.74e-2
60.	5656::chr2:175497100-175500379	1.67e-2
66.	20112::chr10:88842800-88845749	9.85e-3
71.	23168::chr12:19060380-19062549	3.85e-2
73.	31976::chr18:74764150-74771699	1.55e-6
74.	19389::chr10:29947400-29951349	3.53e-3
77.	18257::chr9:112541880-112545699	1.72e-2
118.	11942::chr5:171830050-171832049	7.13e-3
123.	11997::chr5:172442450-172446299	6.75e-8
129.	7681::chr3:99376400-99380379	5.43e-2
130.	29037::chr16:73075550-73094829	2.90e-3
134.	7741::chr3:105087030-105089199	2.89e-2
147.	18723::chr9:133717450-133725049	5.15e-4
156.	8971::chr4:4308400-4311199	4.92e-2
162.	13016::chr6:41470400-41475199	3.26e-2
163.	15696::chr7:137675900-137688499	1.10e-5
167.	1028::chr1:39656450-39663179	1.50e-7
170.	5131::chr2:106011650-106017129	2.66e-2
172.	31928::chr18:67066750-67069899	1.25e-2
173.	6834::chr3:30721680-30724379	1.07e-2
180.	21344::chr11:34294150-34298179	1.57e-4

INPUTS & SETTINGS

Sequences

Role	Source	Alphabet	Sequence Count	Total Size
Primary Sequences	./seqs-centered	DNA	958	95800

Background Model

Source: the file './background'

Order: 2 (only order-0 shown)

Name	Freq.	Bg.				Bg.	Freq.	Name
Adenine	0.258	0.267	A	~	T	0.267	0.258	Thymine
Cytosine	0.242	0.233	C	~	G	0.233	0.242	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	958

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
```