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]

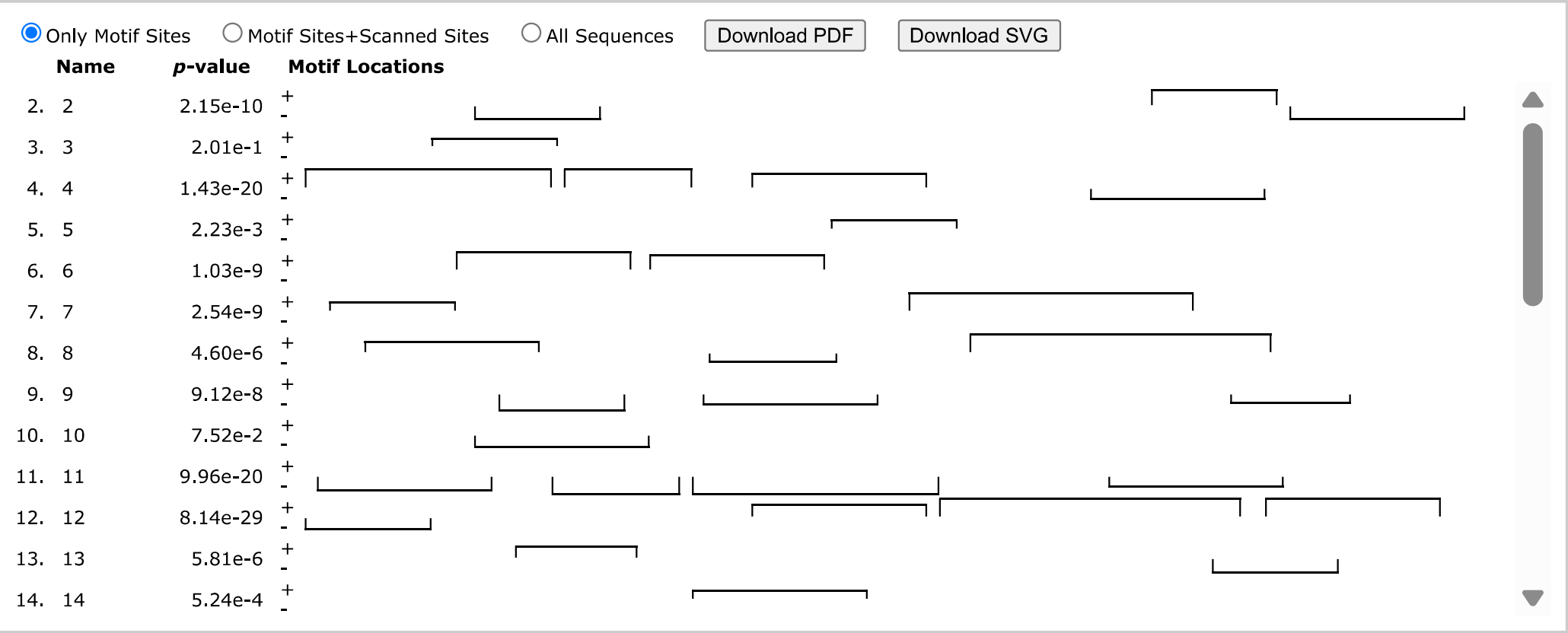**DISCOVERED MOTIFS** | **MOTIF LOCATIONS** | **INPUTS & SETTINGS** | **PROGRAM INFORMATION** | **RESULTS IN TEXT FORMAT** | **RESULTS IN XML FORMAT**

DISCOVERED MOTIFS

	Logo	E-value	Sites	Width	More	Subr
1.		5.0e-083	63	29	↓	
2.		1.3e-042	134	21	↓	
3.		1.2e-036	11	50	↓	
4.		7.6e-033	7	50	↓	
5.		2.0e-024	6	41	↓	
6.		6.2e-021	7	43	↓	

Stopped because requested number of motifs (30) found.

	Logo	E-value	Sites	Width	More	Subr
7.		2.2e-022	7	50	↧	
8.		1.3e-019	7	41	↧	
9.		2.6e-018	5	41	↧	
10.		6.8e-018	30	29	↧	
11.		1.7e-016	7	41	↧	
12.		4.5e-012	56	29	↧	
13.		7.9e-009	7	41	↧	
14.		7.3e-007	9	29	↧	
15.		1.1e-006	7	46	↧	
16.		2.1e-005	8	29	↧	
17.		1.9e-004	14	21	↧	
18.		4.4e-001	4	50	↧	

Stopped because requested number of motifs (30) found.

	Logo	E-value	Sites	Width	More	Subr
19.		2.4e-002	56	20	↧	
20.		4.3e-004	6	50	↧	
21.		1.0e-001	15	28	↧	
22.		1.9e-001	9	41	↧	
23.		2.1e-002	8	29	↧	
24.		2.9e+000	10	21	↧	
25.		3.9e+000	10	29	↧	
26.		1.3e+001	7	28	↧	
27.		1.8e+001	10	21	↧	
28.		4.7e+001	4	50	↧	
29.		1.1e+001	7	41	↧	
30.		2.4e+002	4	47	↧	

Stopped because requested number of motifs (30) found.

Motif Locations

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

	Name	*p*-value	Motif Locations
2.	2	2.15e-10	
3.	3	2.01e-1	
4.	4	1.43e-20	
5.	5	2.23e-3	
6.	6	1.03e-9	
7.	7	2.54e-9	
8.	8	4.60e-6	
9.	9	9.12e-8	
10.	10	7.52e-2	
11.	11	9.96e-20	
12.	12	8.14e-29	
13.	13	5.81e-6	
14.	14	5.24e-4	

Inputs & Settings

Sequences

Role	Source	Alphabet	Sequence Count	Total Size
Primary Sequences	SS_dmp_cpg_sequences.fasta	DNA	329	66129

Background Model

Source: built from the (primary) sequences

Order: 0

Name	Freq.	Bg.				Bg.	Freq.	Name
Adenine	0.242	0.242	A	~	T	0.242	0.242	Thymine
Cytosine	0.258	0.258	C	~	G	0.258	0.258	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	30
Motif E-value Threshold	no limit
Minimum Motif Width	6
Maximum Motif Width	50
Minimum Sites per Motif	2
Maximum Sites per Motif	329

[Show Advanced Settings](#)

MEME version
5.5.8 (Release date: Thu May 15 15:01:46 2025 -0700)

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 SS_dmp_cpg_sequences.fasta -dna -oc . -nostatus -time 14400 -mod zoops -nmotifs 30 -minw 6 -maxw 50 -objfun classic -revcomp -markov_order 0
```