



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

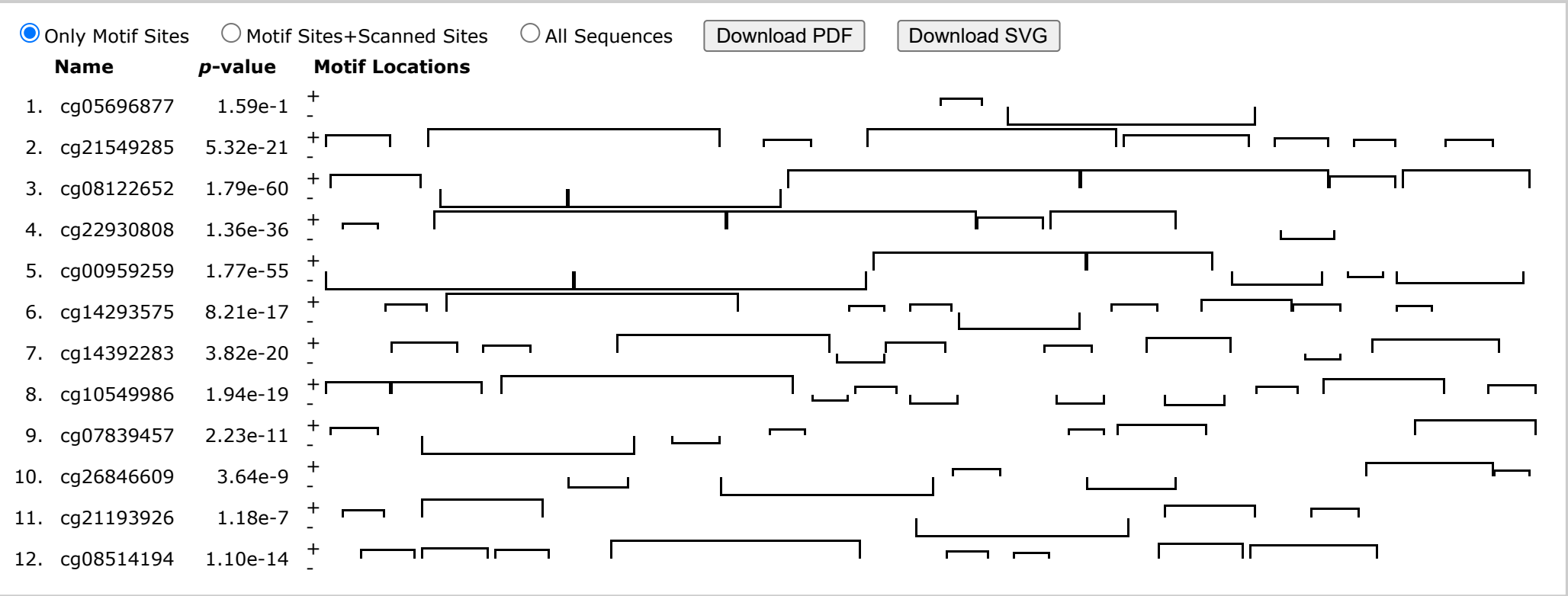
	Logo	E-value	Sites	Width	More	Submit/
1.		1.3e-017	6	48	↓	
2.		1.1e-010	6	41	↓	
3.		2.2e-002	6	35	↓	
4.		5.7e+001	7	15	↓	
5.		1.2e+002	7	21	↓	
6.		3.9e+004	2	21	↓	

Stopped because requested number of motifs (30) found.

	Logo	E-value	Sites	Width	More	Submit/
7.		5.1e+004	3	10	↓	
8.		7.8e+004	2	14	↓	
9.		1.5e+005	4	20	↓	
10.		2.2e+005	2	6	↓	
11.		2.2e+005	2	6	↓	
12.		1.9e+005	2	8	↓	
13.		1.4e+005	2	7	↓	
14.		2.5e+005	2	11	↓	
15.		2.7e+005	2	11	↓	
16.		2.8e+005	2	9	↓	
17.		3.2e+005	2	8	↓	
18.		3.3e+005	2	11	↓	

Stopped because requested number of motifs (30) found.

MOTIF LOCATIONS



INPUTS & SETTINGS

Sequences				
Role	Source	Alphabet	Sequence Count	Total Size
Primary Sequences	SLE_dmp_cpg_sequences.fasta	DNA	12	2412
Background Model				
Source: built from the (primary) sequences				

Order: 0

Name	Freq.	Bg.				Bg.	Freq.	Name
Adenine	0.256	0.256	A	~	T	0.256	0.256	Thymine
Cytosine	0.244	0.244	C	~	G	0.244	0.244	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	12

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



