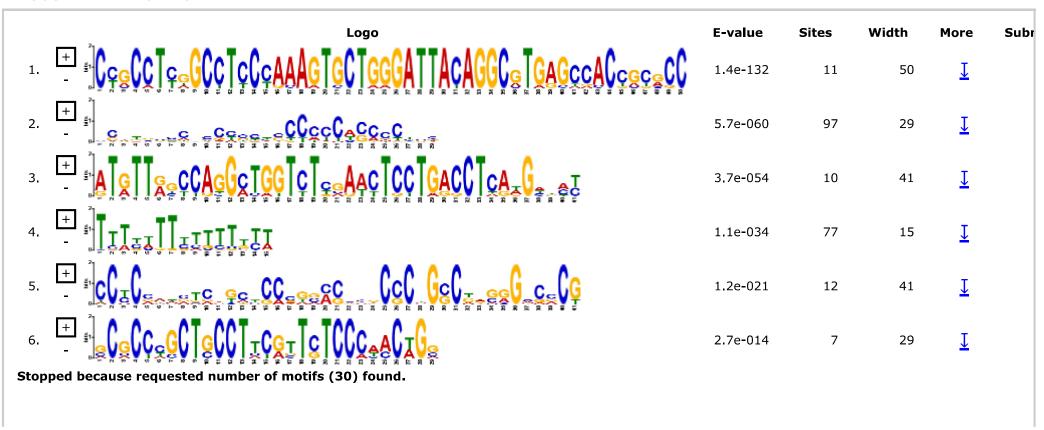# MEME
Multiple Em for Motif Elicitation

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]

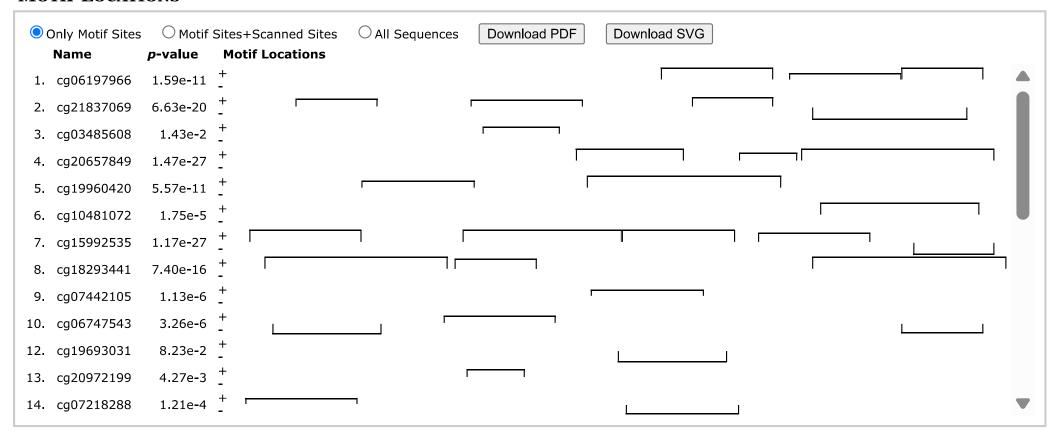**DISCOVERED MOTIFS** | **MOTIF LOCATIONS** | **INPUTS & SETTINGS** | **PROGRAM INFORMATION** | **RESULTS IN TEXT FORMAT** | **RESULTS IN XML FORMAT**

DISCOVERED MOTIFS

	Logo	E-value	Sites	Width	More	Subr
1.		1.4e-132	11	50	⏬	
2.		5.7e-060	97	29	⏬	
3.		3.7e-054	10	41	⏬	
4.		1.1e-034	77	15	⏬	
5.		1.2e-021	12	41	⏬	
6.		2.7e-014	7	29	⏬	

Stopped because requested number of motifs (30) found.

	Logo	E-value	Sites	Width	More	Subr
7.		5.4e-013	5	29	↧	
8.		5.0e-012	4	50	↧	
9.		3.0e-005	22	21	↧	
10.		3.8e-001	4	50	↧	
11.		2.3e+001	5	35	↧	
12.		8.3e+000	5	41	↧	
13.		1.3e-003	14	47	↧	
14.		5.7e-001	24	20	↧	
15.		6.7e-001	6	49	↧	
16.		2.4e+000	6	49	↧	
17.		3.5e+001	9	29	↧	
18.		8.8e+000	7	29	↧	

Stopped because requested number of motifs (30) found.

	Logo	E-value	Sites	Width	More	Subr
19.		1.1e+002	29	15	↓	
20.		3.9e+001	19	21	↓	
21.		2.0e+002	5	40	↓	
22.		3.2e+002	8	28	↓	
23.		3.0e+002	15	29	↓	
24.		3.5e+003	9	28	↓	
25.		2.6e+002	11	21	↓	
26.		7.2e+003	5	41	↓	
27.		2.4e+004	11	15	↓	
28.		1.3e+005	11	50	↓	
29.		6.8e+002	15	21	↓	
30.		1.5e+004	5	21	↓	

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
1.	cg06197966	1.59e-11	
2.	cg21837069	6.63e-20	
3.	cg03485608	1.43e-2	
4.	cg20657849	1.47e-27	
5.	cg19960420	5.57e-11	
6.	cg10481072	1.75e-5	
7.	cg15992535	1.17e-27	
8.	cg18293441	7.40e-16	
9.	cg07442105	1.13e-6	
10.	cg06747543	3.26e-6	
12.	cg19693031	8.23e-2	
13.	cg20972199	4.27e-3	
14.	cg07218288	1.21e-4	

Inputs & Settings

Sequences

Role	Source	Alphabet	Sequence Count	Total Size
Primary Sequences	UC_dmp_cpg_sequences.fasta	DNA	334	67134

Background Model

Source: built from the (primary) sequences

Order: 0

Name	Freq.	Bg.				Bg.	Freq.	Name
Adenine	0.272	0.272	A	~	T	0.272	0.272	Thymine
Cytosine	0.228	0.229	C	~	G	0.229	0.228	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	334

Show Advanced Settings

Command line

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