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:
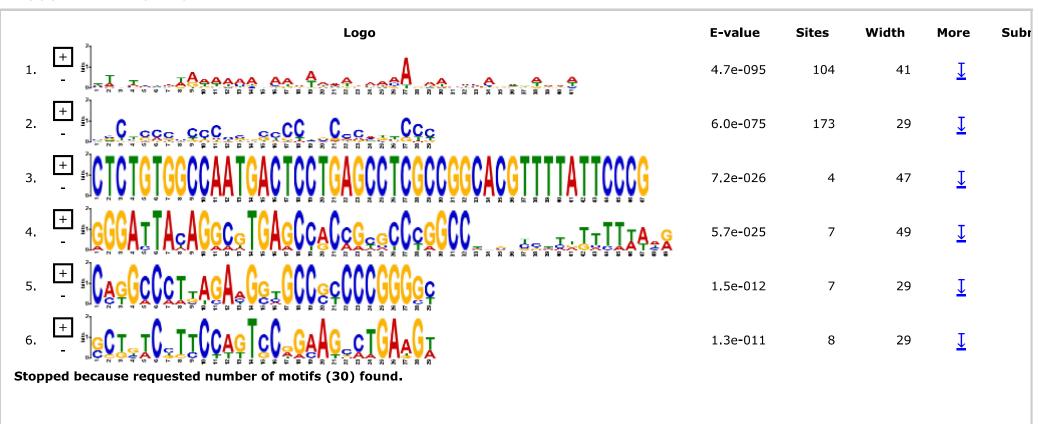Timothy L. Bailey and Charles Elkan, "Fitting a mixture model by expectation maximization to discover motifs in biopolymers", *Proceedings of the Second International Conference on Intelligent Systems for Molecular Biology*, pp. 28-36, AAAI Press, Menlo Park, California, 1994. [full text]

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

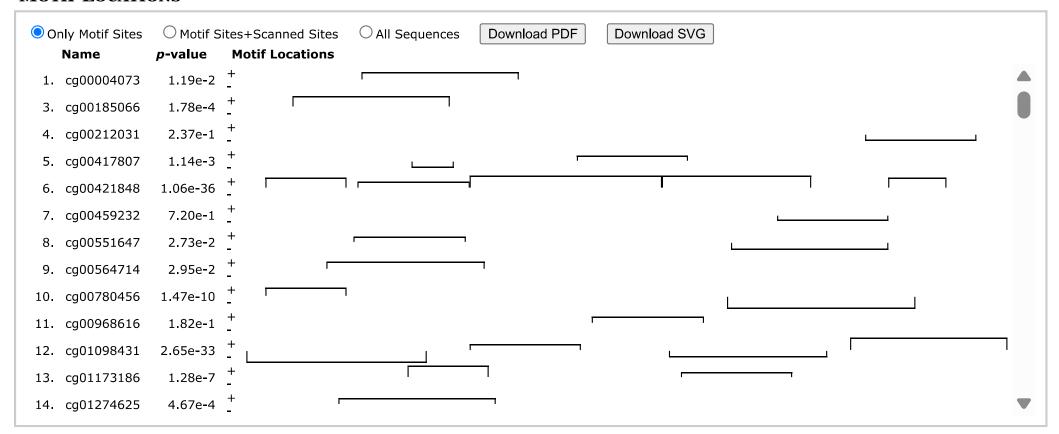MEME results in plain text format.

[close]

DISCOVERED MOTIFS

	Logo	E-value	Sites	Width	More	Subr
1.		4.7e-095	104	41	↓	
2.		6.0e-075	173	29	↓	
3.		7.2e-026	4	47	↓	
4.		5.7e-025	7	49	↓	
5.		1.5e-012	7	29	↓	
6.		1.3e-011	8	29	↓	

Stopped because requested number of motifs (30) found.

		Logo	E-value	Sites	Width	More	Subr
7.	+ −	GGACACCGAGGAACTGCGGTGCGGAAACTAAGATAGTACTGGGAAGACTT	2.1e-011	3	50	↧	
8.	+ −	TTTCCCATcGcAcTGAGcACTgAGATCcTGcTGgaaGCTcTGccGcaGCa	1.3e-010	4	50	↧	
9.	+ −	TGCaGtGAGc.GtGATcGtGCcaCTGCACTCCAGCCTGGGCGaCaGA	4.6e-011	4	47	↧	
10.	+ −	GGGCTGtcTgTGGCCtCAGcGCTcGGCaGGCGCGCACTcA	1.1e-006	4	40	↧	
11.	+ −	CCTGgCGgcTCTgGGgaTGCCCcgCCtGgcCTcCATcCCtG	6.6e-008	6	39	↧	
12.	+ −	tCAtTTgC.CAtTGcAaAAtgae	1.2e-007	21	25	↧	
13.	+ −	CGATgtGCCACcTggTgTTcTTCccAcAggTGgCAAttCggCTGgAGA	8.8e-005	4	49	↧	
14.	+ −	TtTccCCgtGTTGgcCAcTGAtctgATCtCttGgcTC	9.9e-003	7	41	↧	
15.	+ −	CAgCgGTTCGGcGGCcTgGAGcgCcCCccCgGGAtCT	1.7e-002	6	39	↧	
16.	+ −	gtGGGCgGGGc	6.0e-001	42	11	↧	
17.	+ −	aCACAgCTGcaTGGaGggGgGCCCAGcT	2.0e-002	8	29	↧	
18.	+ −	CcCaCTGcCgCgGcAGCgcTCCcAgCgCTgGTGGCTcAgccCTgT	1.1e-005	7	49	↧	

Stopped because requested number of motifs (30) found.

		Logo	E-value	Sites	Width	More	Subm
19.	+ −		6.3e+001	8	41	↓	
20.	+ −		1.8e+002	8	21	↓	
21.	+ −		8.5e+001	18	21	↓	
22.	+ −		4.1e+002	4	41	↓	
23.	+ −		9.1e+002	4	49	↓	
24.	+ −		5.1e+003	2	50	↓	
25.	+ −		2.4e+002	7	50	↓	
26.	+ −		1.7e+004	4	27	↓	
27.	+ −		3.4e+004	14	15	↓	
28.	+ −		3.4e+004	5	47	↓	
29.	+ −		7.0e+004	4	26	↓	
30.	+ −		5.1e+004	11	21	↓	

Stopped because requested number of motifs (30) found.

Motif Locations

Motif Locations

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

Name	*p*-value	Motif Locations
1. cg00004073	1.19e-2	
3. cg00185066	1.78e-4	
4. cg00212031	2.37e-1	
5. cg00417807	1.14e-3	
6. cg00421848	1.06e-36	
7. cg00459232	7.20e-1	
8. cg00551647	2.73e-2	
9. cg00564714	2.95e-2	
10. cg00780456	1.47e-10	
11. cg00968616	1.82e-1	
12. cg01098431	2.65e-33	
13. cg01173186	1.28e-7	
14. cg01274625	4.67e-4	

Inputs & Settings

Sequences

Role	Source	Alphabet	Sequence Count	Total Size
Primary Sequences	dmp_cpg_sequences.fasta	DNA	384	77184

Background Model

Source: built from the (primary) sequences

Order: 0

Name	Freq.	Bg.				Bg.	Freq.	Name
Adenine	0.221	0.221	A	~	T	0.221	0.221	Thymine
Cytosine	0.279	0.279	C	~	G	0.279	0.279	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	384

Show Advanced Settings

Command line

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