



MEME

Multiple Em for Motif Elicitation

For further information on how to interpret these results please access <http://meme-suite.org/>.

To get a copy of the MEME software please access <http://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. [[pdf](#)]

[DISCOVERED MOTIFS](#) | [MOTIF LOCATIONS](#) | [INPUTS & SETTINGS](#) | [PROGRAM INFORMATION](#) | [RESULTS IN TEXT FORMAT](#)

























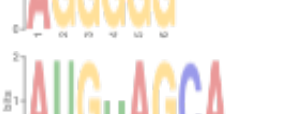







[RESULTS IN XML FORMAT](#)



DISCOVERED MOTIFS

	Logo	E-value	Sites	Width	More	Submit/Download
1.		1.7e-040	32	10	↓	...→
2.		4.2e-015	23	10	↓	...→
3.		7.0e-006	14	10	↓	...→
4.		2.9e-003	6	10	↓	...→
5.		7.9e-006	16	10	↓	...→
6.		2.8e-001	8	8	↓	...→
7.		2.9e-001	8	10	↓	...→
8.		1.8e+001	10	8	↓	...→
9.		9.7e+001	5	10	↓	...→
10.		9.5e+000	6	10	↓	...→

11.		4.3e+001	4	10		
12.		6.7e+001	6	8		
13.		2.4e+002	2	10		
14.		7.0e+002	2	10		
15.		4.8e+002	4	10		
16.		7.2e+002	8	6		
17.		1.1e+003	2	9		
18.		1.2e+003	2	10		
19.		1.5e+003	2	6		
20.		1.8e+003	5	8		

Stopped because requested number of motifs (20) found.

MOTIF LOCATIONS




































☒ Only Motif Sites
 ☐ Motif Sites+Scanned Sites
 ☐ All Sequences

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Name	p-value	Motif Locations
1. deltaSHAPE_rep2_ex_vivo_0	6.59e-1	
3. deltaSHAPE_rep2_ex_vivo_2	2.41e-2	
4. deltaSHAPE_rep2_ex_vivo_3	2.71e-2	
9. deltaSHAPE_rep2_ex_vivo_8	2.52e-3	 
10. deltaSHAPE_rep2_ex_vivo_9	3.75e-3	 
11. deltaSHAPE_rep2_ex_vivo_10	3.94e-1	
12. deltaSHAPE_rep2_ex_vivo_11	3.83e-2	
14. deltaSHAPE_rep2_ex_vivo_13	5.47e-1	
15. deltaSHAPE_rep2_ex_vivo_14	2.38e-1	
16. deltaSHAPE_rep2_ex_vivo_15	4.37e-3	 
18. deltaSHAPE_rep2_ex_vivo_17	1.24e-2	
19. deltaSHAPE_rep2_ex_vivo_18	1.36e-2	
20. deltaSHAPE_rep2_ex_vivo_19	1.84e-2	
21. deltaSHAPE_rep2_ex_vivo_20	1.56e-3	
22. deltaSHAPE_rep2_ex_vivo_21	1.95e-3	
23. deltaSHAPE_rep2_ex_vivo_22	5.16e-2	
24. deltaSHAPE_rep2_ex_vivo_23	2.62e-6	 
25. deltaSHAPE_rep2_ex_vivo_24	3.92e-7	 
29. deltaSHAPE_rep2_ex_vivo_28	2.96e-1	
35. deltaSHAPE_rep2_ex_vivo_34	1.45e-2	
37. deltaSHAPE_rep2_ex_vivo_36	8.58e-1	
38. deltaSHAPE_rep2_ex_vivo_37	2.59e-1	
41. deltaSHAPE_rep2_ex_vivo_40	1.26e-4	 
42. deltaSHAPE_rep2_ex_vivo_41	4.78e-4	 
46. deltaSHAPE_rep2_ex_vivo_45	9.29e-4	
48. deltaSHAPE_rep2_ex_vivo_47	1.76e-2	
49. deltaSHAPE_rep2_ex_vivo_48	1.64e-1	 

INPUTS & SETTINGS

Sequences

Total

Role	Source	Alphabet	Sequence Count	Size
Primary Sequences	MEME_deltaSHAPE_rep_2_ex_vivo_30_mers/seqs-centered	RNA	186	5952

Background Model

Source: the file 'MEME_deltaSHAPE_rep_2_ex_vivo_30_mers/background'

Order: 1 (only order-0 shown)

	Name	Freq.	Bg.
A	Adenine	0.288	0.288
C	Cytosine	0.189	0.189
G	Guanine	0.174	0.174
U	Uracil	0.348	0.348

Other Settings

Motif Site Distribution	ANR: Any number of sites per sequence
Objective Function	E-value of product of p-values
Starting Point Function	E-value of product of p-values
Site Strand Handling	This alphabet only has one strand
Maximum Number of Motifs	20
Motif E-value Threshold	no limit
Minimum Motif Width	4
Maximum Motif Width	10
Minimum Sites per Motif	2
Maximum Sites per Motif	930

[Show Advanced Settings](#)

MEME version

5.1.0 (Release date: Fri Oct 11 15:53:28 2019 -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.

Command line

```
meme MEME_deltaSHAPE_rep_2_ex_vivo_30_mers/seqs-centered -oc MEME_deltaSHAPE_rep_2_ex_vivo_30_mers/meme_out -mod anr -nmotifs 20 -minw 4 -maxw 10 -bfile MEME_deltaSHAPE_rep_2_ex_vivo_30_mers/background -rna -p 8 -nostatus
```

