

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:

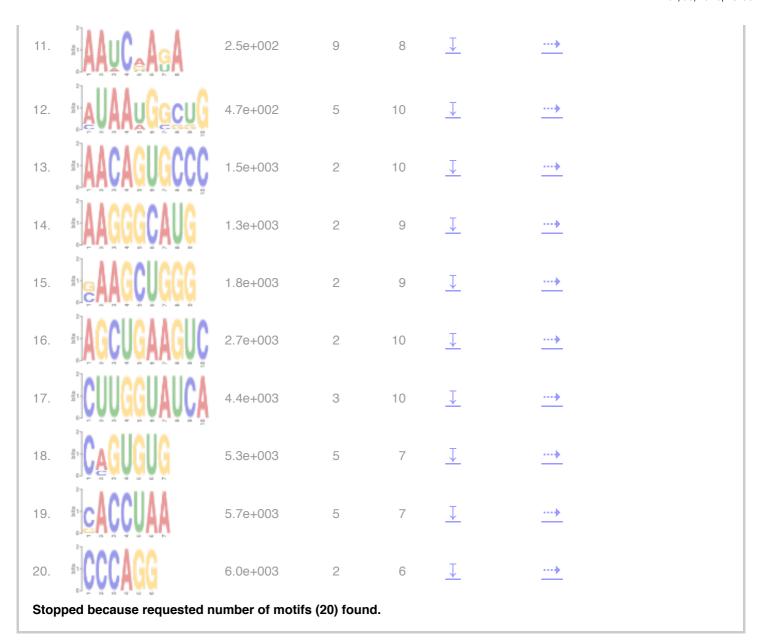
Timothy L. Bailey and Charles Elkan, "Fitting a mixture model by expectation maximization to discover motifs in biopolymers", *Proceedings of the Second International Conference on Intelligent Systems for Molecular Biology*, pp. 28-36, AAAI Press, Menlo Park, California, 1994. [pdf]

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

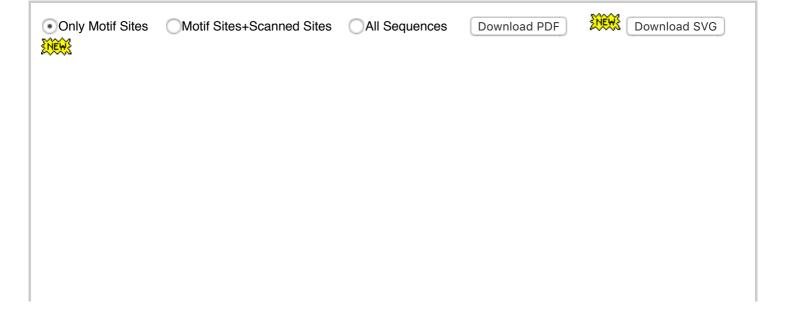
| RESULTS IN XML FORMAT | RESULTS IN XML FORMAT | RESULTS IN TEXT FORMATION | RESULTS IN TEXT

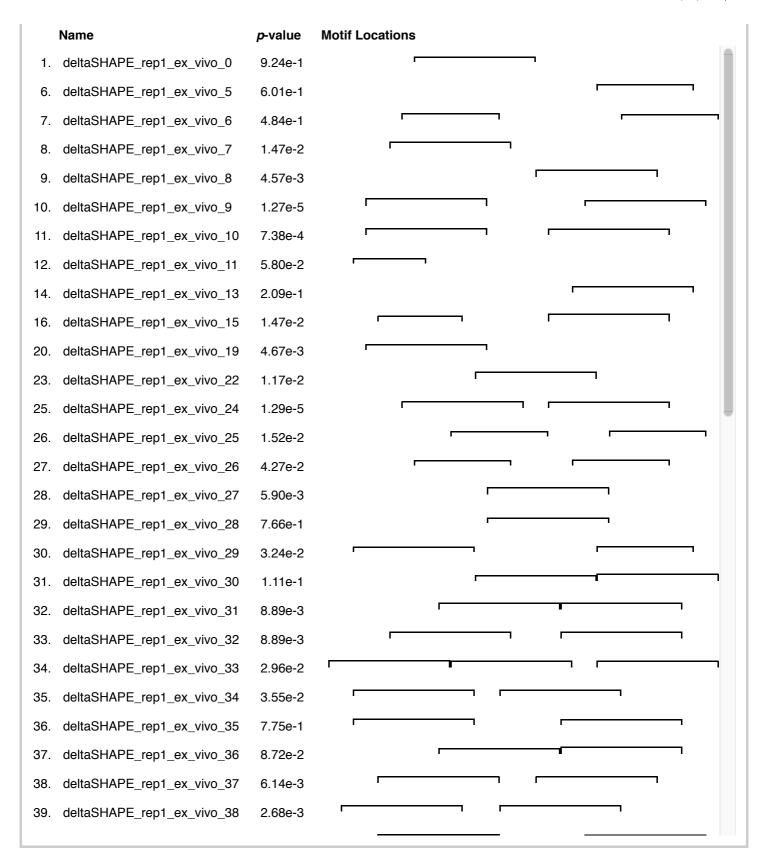
DISCOVERED MOTIFS

D 150	OVERED MOTIFS					
	Logo	E-value	Sites	Width	More	Submit/Download
1.	ij <mark>ĕĬĊŃŸ^ĸĬĬĬĊĨ</mark>	3.6e-090	53	10	<u> </u>	<u></u>
2.	ij <mark>ŎĊĊŎŎ</mark> ĈŎĸŎ	2.1e-050	35	10	<u> </u>	<u>+</u>
3.	ŢĠŎŢŢŎŎĠŊĠ	6.8e-006	13	10	<u> </u>	··· ·
4.	ij <mark>čďĕÝČ[*]ňčď</mark> ě	3.7e-006	15	10	<u> </u>	··· ·
5.	ij <mark>Ÿ^ĕĊĊĬĊ</mark> ĕĬĊĊ	2.8e-004	7	10	<u> </u>	<u></u>
6.		5.8e-002	11	8	<u> </u>	<u></u>
7.	ij <mark>ŶĔĊĊ</mark> ŢĔĬſĠĔ	3.3e-002	14	10	<u> </u>	<u></u>
8.	ŢĠĸĸĸĸĸĸĸĸĸĸĸĸĸĸĸĸĸĸĸĸĸĸĸĸĸĸĸĸĸĸĸĸĸĸĸĸ	8.0e+000	8	10	<u> </u>	<u>···</u>
9.		1.3e+002	6	10	<u> </u>	<u>···</u>
10.	aj <mark>œaccacca</mark>	1.8e+002	2	10	<u> </u>	<u>···</u>



MOTIF LOCATIONS





INPUTS & SETTINGS

Sequences

Role	Source	Alphabet	Sequence Count	Size
Primary Sequences	MEME_deltaSHAPE_rep_1_ex_vivo_30_mers/seqs-centered	RNA	162	5184

Background Model

Source: the file 'MEME_deltaSHAPE_rep_1_ex_vivo_30_mers/background'

Order: 1 (only order-0 shown)

	Name	Freq.	Bg.
A	Adenine	0.246	0.246
C	Cytosine	0.189	0.189
G	Guanine	0.176	0.176
U	Uracil	0.389	0.389

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
This alphabet only has one strand

Maximum Number of Motifs20Motif E-value Thresholdno limitMinimum Motif Width4Maximum Motif Width10Minimum Sites per Motif2Maximum Sites per Motif810

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_1_ex_vivo_30_mers/seqs-centered -oc MEME_deltaSHAPE_rep_1_ex_vivo_30_mers/meme_out - mod anr -nmotifs 20 -minw 4 -maxw 10 -bfile MEME_deltaSHAPE_rep_1_ex_vivo_30_mers/background -rna -p 8 -nostatus