

For further information on how to interpret these results please access <a href="http://meme-suite.org/">http://meme-suite.org/</a>. To get a copy of the MEME software please access <a href="http://meme-suite.org">http://meme-suite.org</a>.

## If you use MEME in your research, please cite the following paper:

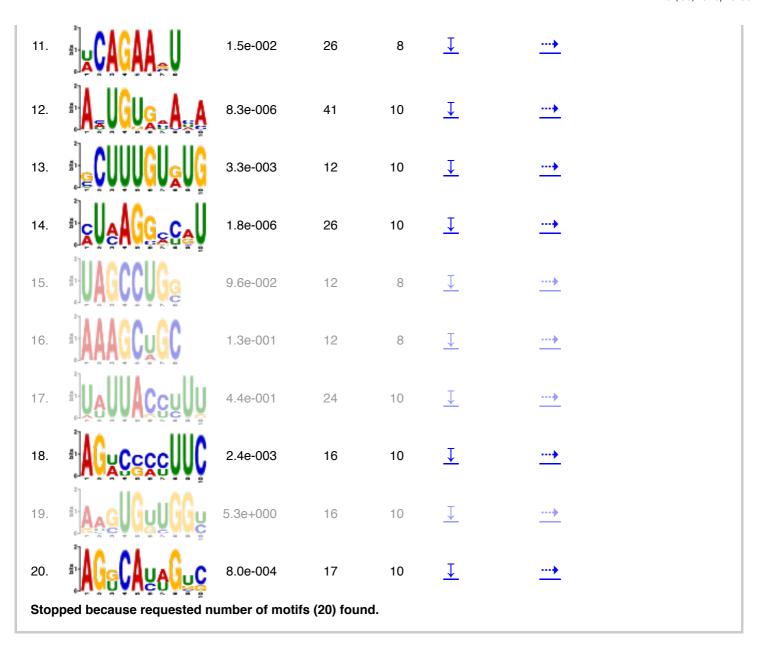
Timothy L. Bailey and Charles Elkan, "Fitting a mixture model by expectation maximization to discover motifs in biopolymers", *Proceedings of the Second International Conference on Intelligent Systems for Molecular Biology*, pp. 28-36, AAAI Press, Menlo Park, California, 1994. [pdf]

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

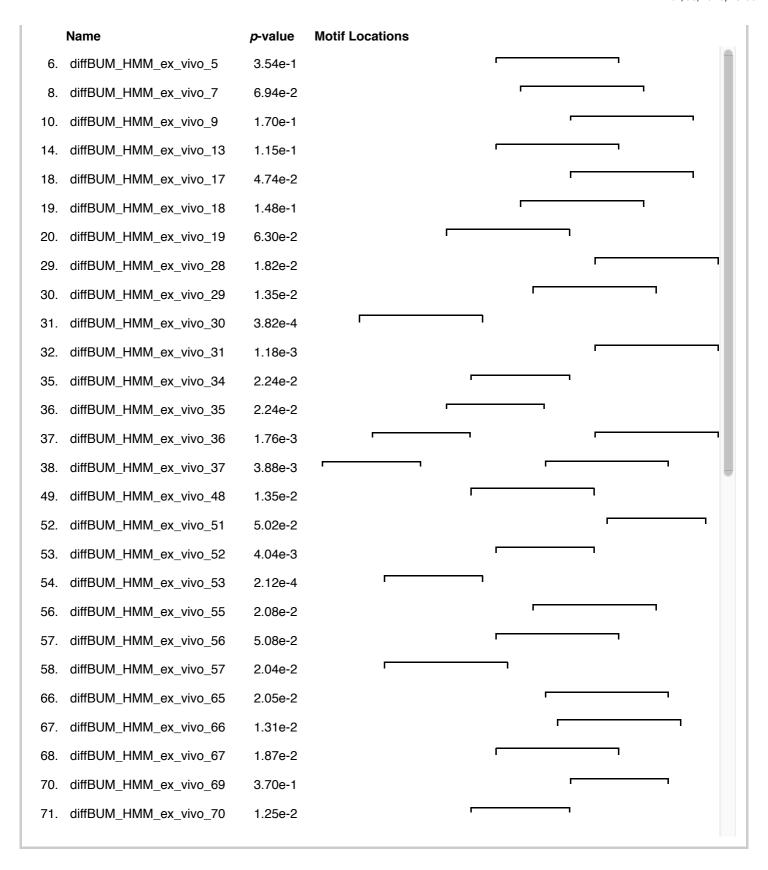
# **DISCOVERED MOTIFS**

Logo	E-value	Sites	Width	More	Submit/Download	
¹ Í <mark>ŲċñŸňȟñĈ</mark> Ĭ	3.2e-058	82	10	<u> </u>	<u></u>	
	1.0e-013	44	10	<u> </u>	<u>···</u>	
	1.8e-009	26	10	<u> </u>	<u>···</u>	
	1.6e-010	31	10	<u> </u>	<u>···→</u>	
5. #JAAGAAUGÇA	1.5e-010	25	10	<u> </u>	··· <b>&gt;</b>	
	5.4e-007	13	10	<u> </u>	<u>···</u>	
7 #1 <b>GgG(</b>	4.3e-004	19	10	<u> </u>	<u>···</u>	
8 #JECCNVENCE	3.8e-004	10	10	<u> </u>	<u>···→</u>	
9. #1 <mark>0000</mark>	5.3e-004	17	10	<u> 1</u>	··· <b>&gt;</b>	
10. # CCNUGCUŲ	1.2e-003	21	8	<u> </u>	<u>···</u>	



# **MOTIF LOCATIONS**

Only Motif Sites Motif Sites+Scanned Sites All Sequences Download PDF Download SVG



# **INPUTS & SETTINGS**

Sequences			
	Alphabet	Sequence	Total

Role	Source		Count	Size
Primary Sequences	MEME_diffBUM_HMM_ex_vivo_30_mers/seqs-centered	RNA	849	27168

### **Background Model**

Source: the file 'MEME\_diffBUM\_HMM\_ex\_vivo\_30\_mers/background'

Order: 1 (only order-0 shown)

	Name	Freq.	Bg.
A	Adenine	0.274	0.274
C	Cytosine	0.2	0.2
G	Guanine	0.196	0.196
U	Uracil	0.33	0.33

# **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 Motif1000

**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\_diffBUM\_HMM\_ex\_vivo\_30\_mers/seqs-centered -oc MEME\_diffBUM\_HMM\_ex\_vivo\_30\_mers/meme\_out -mod anr -nmotifs 20 -minw 4 -maxw 10 -bfile MEME\_diffBUM\_HMM\_ex\_vivo\_30\_mers/background -rna -p 8 -nostatus