



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>.

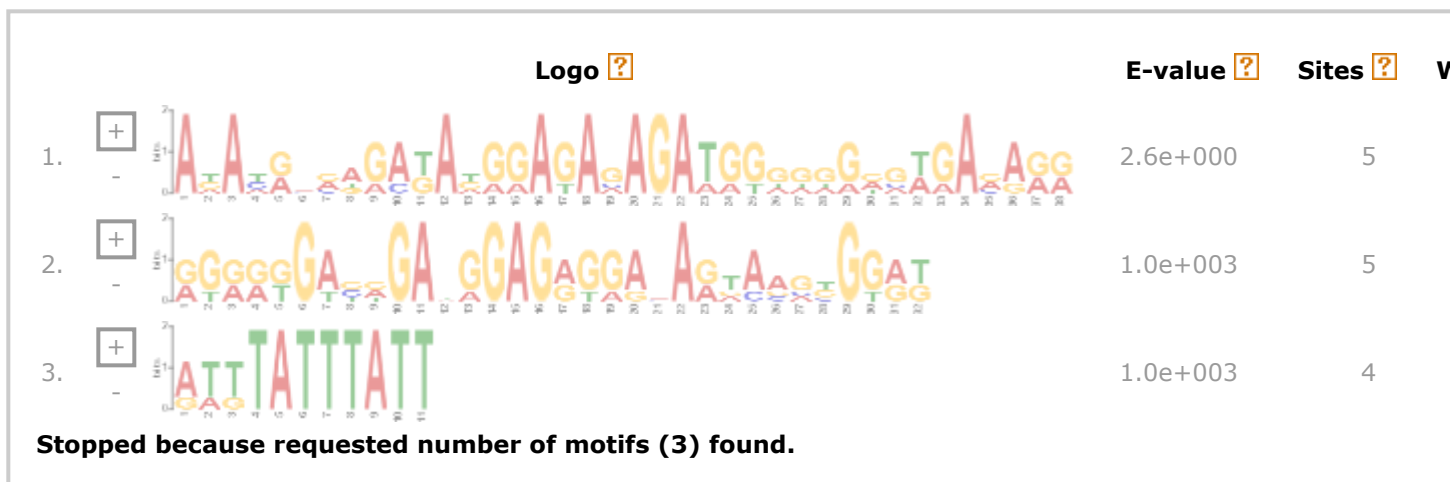
To get a copy of the MEME software please access <https://meme-suite.org>.

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

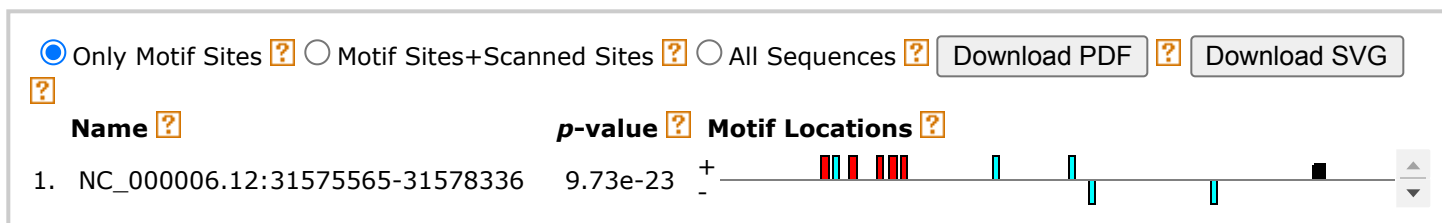
Timothy L. Bailey and Charles Elkan, "Fitting a mixture model by expectation maximization to discover motifs in biopolymers", *Proceedings of the Second International Conference on Intelligent Systems for Molecular Biology*, pp. 28-36, AAAI Press, Menlo Park, California, 1994. [\[full text\]](#)

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DISCOVERED MOTIFS



MOTIF LOCATIONS



INPUTS & SETTINGS

Sequences				
Role	Source ?	Alphabet ?	Sequence Count ?	Total Size ?
Primary Sequences	sequence.fasta_2_1.txt	DNA	1	2772
Background Model				

8/18/24, 9:27 PM

MEME Results

Source: built from the (primary) sequences

Order: 0

Name ?	Freq. ?	Bg. ?				Bg. ?	Freq. ?	Name ?
Adenine	0.236	0.236	A	~	T	0.236	0.236	Thymine
Cytosine	0.264	0.264	C	~	G	0.264	0.264	Guanine

Other Settings

Motif Site Distribution

Objective Function

Starting Point Function

Site Strand Handling

Maximum Number of Motifs

Motif E-value Threshold

Minimum Motif Width

Maximum Motif Width

Minimum Sites per Motif

Maximum Sites per Motif

ANR: Any number of sites per sequence

E-value of product of p-values

E-value of product of p-values

Sites may be on either strand

3

no limit

6

50

2

5

[Show Advanced Settings](#)

MEME version

5.5.6 (Release date: Wed Jun 19 13:59:04 2024 -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. [\[full text\]](#)

Command line

meme sequence.fasta_2_1.txt -dna -oc . -nostatus -time 14400 -mod anr -nmotifs 3 -minw 6 -maxw 50 -objfun classic -revcomp -markov_order 0

