

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. [\[pdf\]](#)

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DISCOVERED MOTIFS



MOTIF LOCATIONS



INPUTS & SETTINGS

Sequences

Role	Source	Alphabet	Sequence Count	Total Size
Primary Sequences	upstream25.txt	DNA	36	900

Background Model

Source:

built from the (primary) sequences

Order:

0

Name	Freq.	Bg.				Bg.	Freq.	Name
Adenine	0.203	0.203	A	~	T	0.203	0.203	Thymine
Cytosine	0.297	0.297	C	~	G	0.297	0.297	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

1

Motif E-value Threshold

no limit

Minimum Motif Width

20

Maximum Motif Width

20

Minimum Sites per Motif

2

Maximum Sites per Motif

36

[Show Advanced Settings](#)

MEME version  
5.3.3 (Release date: Sun Feb 7 15:39:52 2021 -0800)

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 upstream25.txt -dna -oc . -nostatus -time 14400 -mod zoops -nmotifs 1 -minw 20 -maxw 20 -objfun classic -revcomp -markov\_order 0