



# STREME

Sensitive, Thorough, Rapid, Enriched Motif Elicitation

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

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

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

Timothy L. Bailey, "STREME: accurate and versatile sequence motif discovery", *Bioinformatics*, Mar. 24, 2021. [\[full text\]](#)

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## DISCOVERED MOTIFS

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Motif	Logo	RC Logo	P-value	E-value	Sites	More	Submit/Download	Pc
1- CCACCCCCACCTCC			3.0e-002	1.5e-001	64 (6.7%)	<a href="#">↓</a>	<a href="#">...&gt;</a>	-50
2-ACTTTG			4.4e-002	2.2e-001	213 (22.2%)	<a href="#">↓</a>	<a href="#">...&gt;</a>	-50
<p><b>Stopped because 3 consecutive motifs exceeded the p-value threshold (0.05).</b>  <b>STREME ran for 20.21 seconds.</b></p>								

Motif	Logo	RC Logo	P-value	E-value	Sites	More	Submit/Download	Pc
3-TAATCCCAGCA			1.1e-001	5.3e-001	50 (5.2%)	<a href="#">↓</a>	<a href="#">...&gt;</a>	-50
4-AAATGCAAAA			2.5e-001	1.2e+000	27 (2.8%)	<a href="#">↓</a>	<a href="#">...&gt;</a>	-50
5-GATGTCAG			3.4e-001	1.7e+000	73 (7.6%)	<a href="#">↓</a>	<a href="#">...&gt;</a>	-50
Stopped because 3 consecutive motifs exceeded the p-value threshold (0.05). STREME ran for 20.21 seconds.								

INPUTS & SETTINGS

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Sequences

Role	Source	Alphabet	Sequence Count	Total Size
Positive (primary) Sequences	./seqs-centered	DNA	958	95800
Negative (control) Sequences	2-Order Shuffled Positive Sequences	DNA	958	95800

Background Model

**Source:** built from the negative (control) sequences

**Order:** 2 (only order-0 shown)

Name	Freq.	Bg.				Bg.	Freq.	Name
Adenine	0.258	0.258	A	~	T	0.258	0.258	Thymine
Cytosine	0.242	0.242	C	~	G	0.242	0.242	Guanine

## Other Settings

<b>Strand Handling</b>	Both the given and reverse complement strands are processed.
<b>Objective Function</b>	Differential Enrichment
<b>Statistical Test</b>	Fisher Exact Test
<b>Minimum Motif Width</b>	6
<b>Maximum Motif Width</b>	15
<b>Sequence Shuffling</b>	Negative sequences are positives shuffled preserving 3-mer frequencies.
<b>Test Set</b>	10% of the input sequences were randomly assigned to the test set.
<b>Word Evaluation</b>	Up to 25 words of each width from 6 to 15 were evaluated to find seeds.
<b>Seed Refinement</b>	Up to 4 seeds of each width from 6 to 15 were further refined.
<b>Refinement Iterations</b>	Up to 20 iterations were allowed when refining a seed.
<b>Random Number Seed</b>	0
<b>Total Length</b>	The total length of each sequence set was limited to 4.00e+6.
<b>Maximum Motif p-value</b>	Stop when the p-value is greater than 0.05 for 3 consecutive motifs.
<b>Maximum Motifs to Find</b>	No maximum number of motifs.
<b>Maximum Run Time</b>	5737 seconds.

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## STREME version

5.5.1 (Release date: Sun Jan 29 10:33:12 2023 -0800)

## Reference

Timothy L. Bailey, "STREME: accurate and versatile sequence motif discovery", *Bioinformatics*, Mar. 24, 2021. [\[full text\]](#)

## Command line

```
streme --verbosity 1 --oc streme_out -dna --p ./seqs-centered --minw 6 --maxw 15 --time 5737 --order 2 --thresh 0.05 --totallength 4000000
```



