



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](#)]



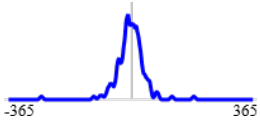
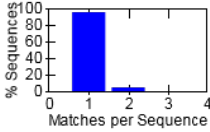


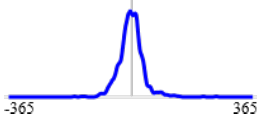
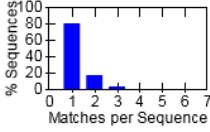


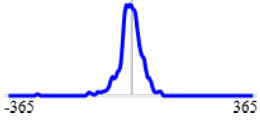
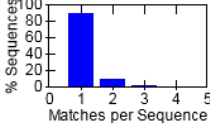


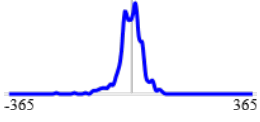
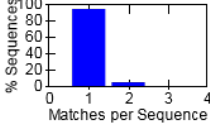

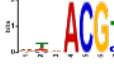
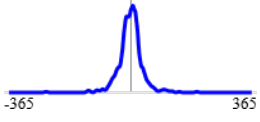
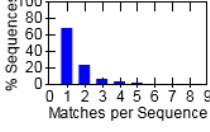


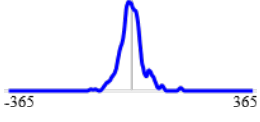
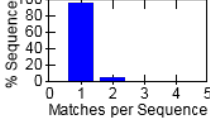


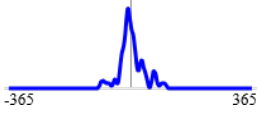
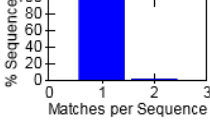


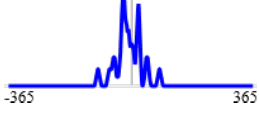
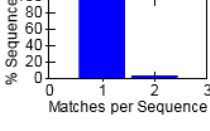
[DISCOVERED MOTIFS](#) |
 [INPUTS & SETTINGS](#) |
 [PROGRAM INFORMATION](#) |
 [MOTIFS IN MEME TEXT FORMAT](#) |
 [MATCHING SEQUENCES](#) |
 [RESULTS IN XML FORMAT](#)

DISCOVERED MOTIFS



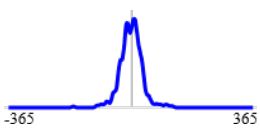
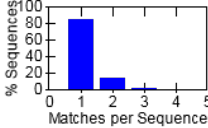


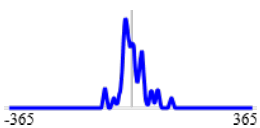
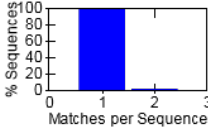


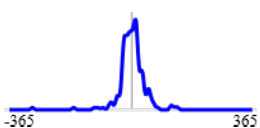
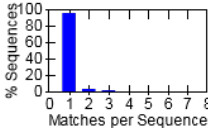


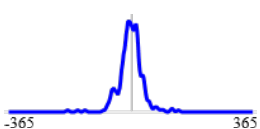
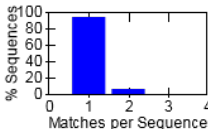


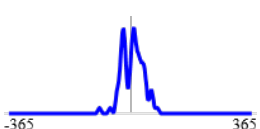
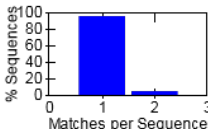


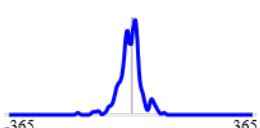
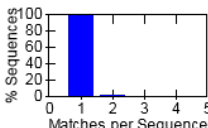


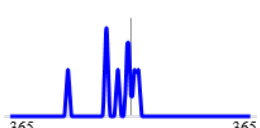
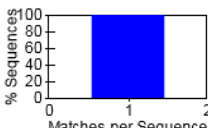


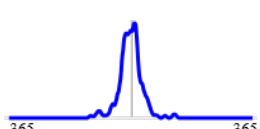
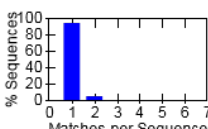
[Next Top](#)

Motif	Logo	RC Logo	P-value	E-value	Sites	More	Submit/Download	Positional Distribution	Matches per Sequence
1-WATTAATW			8.9e-023	2.0e-021	1746 (35.4%)	↓	→		
2-ATTTATAA			1.0e-014	2.4e-013	1483 (30.0%)	↓	→		
3-TTAAATAW			1.4e-009	3.1e-008	1387 (28.1%)	↓	→		
4-MTAATAT			2.8e-008	6.3e-007	674 (13.6%)	↓	→		
5-ATTAAT			5.9e-008	1.4e-006	1660 (33.6%)	↓	→		
6-TATCCA			4.7e-005	1.1e-003	353 (7.1%)	↓	→		

Stopped because 3 consecutive motifs exceeded the p-value threshold (0.05).
 STREME ran for 1667.29 seconds.

Motif	Logo	RC Logo	P-value	E-value	Sites	More	Submit/Download	Positional Distribution	Matches per Sequence
7-ATTTAA			9.9e-005	2.3e-003	211 (4.3%)	↓	→		
8-AWAACGW			3.0e-004	7.0e-003	1021 (20.7%)	↓	→		
9-AGTCAA			8.7e-004	2.0e-002	466 (9.4%)	↓	→		
10-TAACAAA			1.4e-003	3.3e-002	568 (11.5%)	↓	→		
11-MCACGTDAY			4.1e-003	9.5e-002	716 (14.5%)	↓	→		
12-CATTTAV			9.7e-003	2.2e-001	406 (8.2%)	↓	→		
13-ATTATAAT			1.2e-002	2.8e-001	87 (1.8%)	↓	→		
14-TCTAGA			1.3e-002	3.1e-001	31 (0.6%)	↓	→		

Stopped because 3 consecutive motifs exceeded the p-value threshold (0.05).
STREME ran for 1667.29 seconds.

Motif	Logo	RC Logo	P-value	E-value	Sites	More	Submit/Download	Positional Distribution	Matches per Sequence
15-ATATAC			1.5e-002	3.4e-001	584 (11.8%)	↓	→		
16-TATTAAAA			2.3e-002	5.3e-001	52 (1.1%)	↓	→		
17-NHTCTAGADN			2.6e-002	5.9e-001	257 (5.2%)	↓	→		
18-YACGWAW			3.0e-002	6.9e-001	356 (7.2%)	↓	→		
19-RRACCATTA			4.6e-002	1.1e+000	99 (2.0%)	↓	→		
20-AGTCCTHW			4.9e-002	1.1e+000	275 (5.6%)	↓	→		
21- AAARACTTTRTTKTAAA			1.3e-001	3.0e+000	9 (0.2%)	↓	→		
22-GTGACRWA			2.4e-001	5.4e+000	253 (5.1%)	↓	→		

Stopped because 3 consecutive motifs exceeded the p-value threshold (0.05).
STREME ran for 1667.29 seconds.

Motif

Logo

RC Logo

P-value

E-value

Sites

More

Submit/Download

Positional Distribution

Matches per Sequence

23-ACAAGT

2.8e-001

6.5e+000

422 (8.5%)

↓

→

Stopped because 3 consecutive motifs exceeded the p-value threshold (0.05).
STREME ran for 1667.29 seconds.

INPUTS & SETTINGS

[Previous](#) [Next](#) [Top](#)

Sequences

Role	Source	Alphabet	Sequence Count	Total Size
Positive (primary) Sequences	regions-7.fasta	DNA	4939	480645
Negative (control) Sequences	prom-1500.fasta	DNA	32805	3198248

Background Model

Source: built from the negative (control) sequences

Order: 2 (only order-0 shown)

Name	Freq.	Bg.		Bg.	Freq.	Name
Adenine	0.351	0.33	A ~ T	0.33	0.351	Thymine
Cytosine	0.149	0.17	C ~ G	0.17	0.149	Guanine

Other Settings

Strand Handling	Both the given and reverse complement strands are processed.
Objective Function	Differential Enrichment
Statistical Test	Binomial Test
Minimum Motif Width	6
Maximum Motif Width	20
Test Set	10% of the input sequences were randomly assigned to the test set.
Word Evaluation	Up to 25 words of each width from 6 to 20 were evaluated to find seeds.
Seed Refinement	Up to 4 seeds of each width from 6 to 20 were further refined.
Refinement Iterations	Up to 20 iterations were allowed when refining a seed.
Random Number Seed	1
Total Length	The total length of the sequence set(s) was not limited.
Maximum Motif p-value	Stop when the p-value is greater than 0.05 for 3 consecutive motifs.
Maximum Motifs to Find	No maximum number of motifs.
Maximum Run Time	No maximum running time.

[Previous](#) [Top](#)

STREME version

5.4.1 (Release date: Sat Aug 21 19:23:23 2021 -0700)

Reference

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

Command line

streme --p regions-7.fasta --n prom-1500.fasta --o ./streme_out-7_005-1148 --dna --minw 6 --maxw 20 --seed 1