



MAST

Motif Alignment & Search Tool

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

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

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

Timothy L. Bailey and Michael Gribskov, "Combining evidence using p-values: application to sequence homology searches", *Bioinformatics*, **14**(1):48-54, 1998. [\[full text\]](#)

[MOTIFS](#) | [SEARCH RESULTS](#) | [INPUTS & SETTINGS](#) | [PROGRAM INFORMATION](#) | [RESULTS IN TEXT FORMAT](#) | [RESULTS IN XML FORMAT](#)

MOTIFS

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

Motifs with a pale red background are very similar to other earlier specified motifs and may be biasing the results. It is recommended that you re-run MAST and request it to remove redundant motifs.

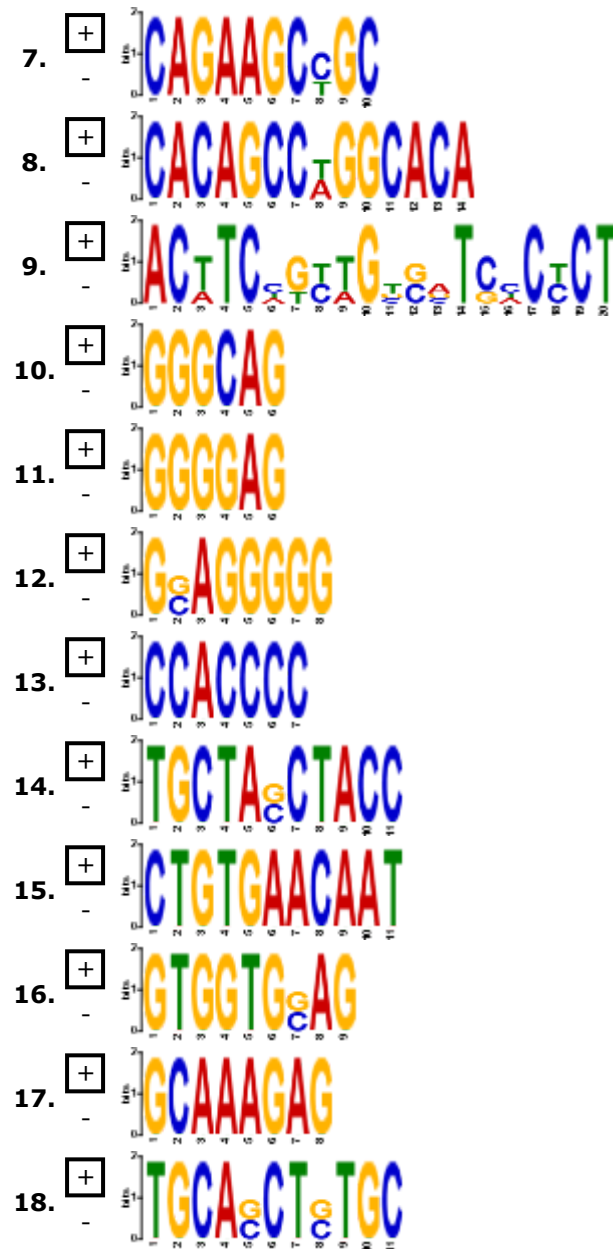
Logo

Name

| | | |
|----|--|--|
| 1. | | CMTKTRCWRRSAGGGMTGRGKGGCRGCARRGAGGCSWRAGAI |
| 2. | | TYTGACATRSCTKSTAWGACTKRAAAWKKGCMCRTCYTTA |
| 3. | | GYCTCCMCNYGGYTSTMASYMCCMWMTYYCYRAA |
| 4. | | AASCAGVRAAAVCAG |
| 5. | | TGGSARHMCTGTSWGMAKAC |
| 6. | | ATGCAAATCTGGCAAGTCATT |

Logo

Name



CAGAAGCYGC

CACAGCCWGGCACA

ACTTCHGYTGBSVTCHCYCT

GGGCAG

GGGGAG

GSAGGGGG

CCACCCC

TGCTASCTACC

CTGTGAACAAT

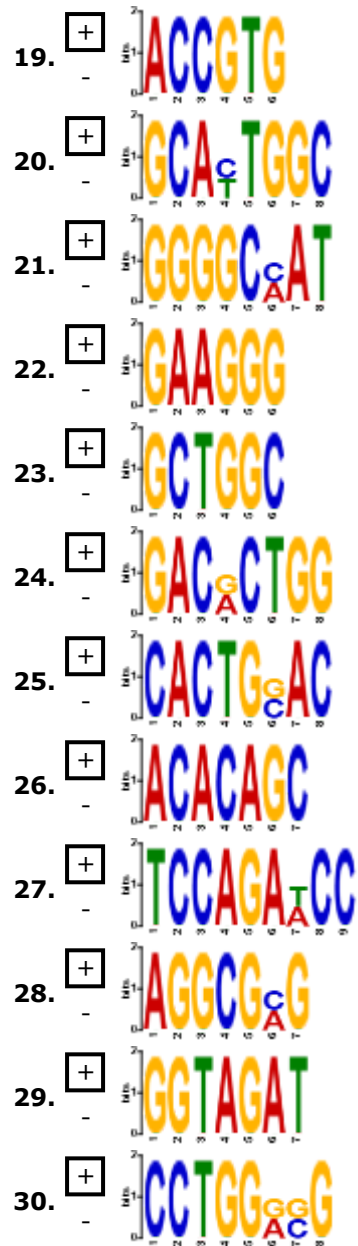
GTGGTGSAG

GCAAAGAG

TGCASCTSTGC

Logo

Name



ACCGTG

GCAYTGGC

GGGGCMAT

GAAGGG

GCTGGC

GACRCTGG

CACTGSAC

ACACAGC

TCCAGAWCC

AGGCGMG

GGTAGAT

CCTGGRSG

Top Scoring Sequences

Each of the following 12 sequences has an *E*-value less than 10.
The motif matches shown have a position *p*-value less than 0.0001.
Hover the cursor over the sequence name to view more information about a sequence.
Hover the cursor over a motif for more information about the match.
Click on the arrow (↕) next to the *E*-value to see the sequence surrounding each match.

CMTKTRCWRRSAGGGMTGRGKGGCRGCARRGAGGCSWRAGAKRAGSTT

TYTGACATRSTCKSTAWGACTKRAAAWKKGCMCRTCYTTA

GYCTCCMCNYGGYTSTMASYMCCMWMTYYCYRAA

AASCAGVRAAAVCAG

TGGSARHMCTGTSWGMATKAC

ATGCAAATCTGGCAAGTCATT

CAGAAGCYGC

CACAGCCWGGCACA

ACTTCHGYTGBSVTCHCYCT

GGGCAG

GGGGAG

GSAGGGGG

CCACCCC

TGCTASCTACC

CTGTGAACAAT

GTGGTGSAG

GCAAAGAG

TGCASCTSTGC

ACCGTG

GCAYTGGC

GGGGCMAT

GAAGGG

GCTGGC

GACRCTGG

CACTGSAC

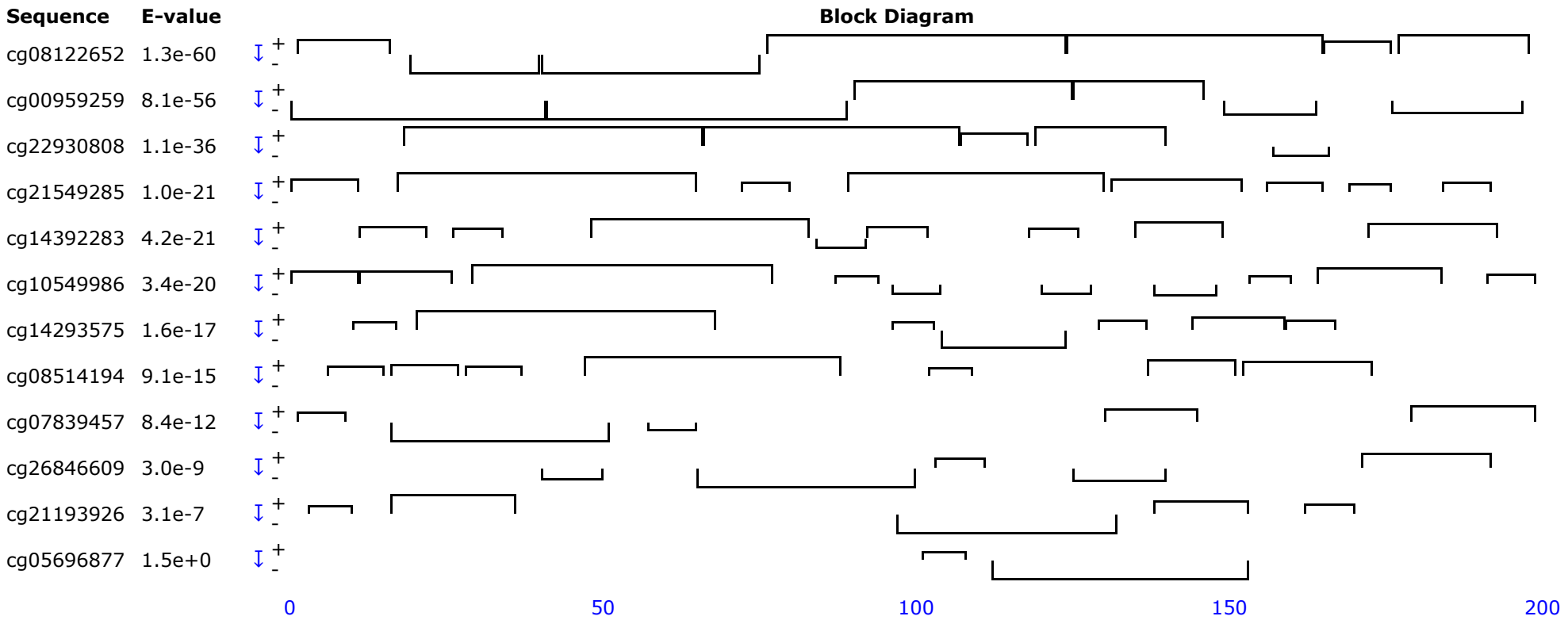
ACACAGC

TCCAGAWCC

AGGCGMG

GGTAGAT

CCTGGRSG



☐ CMTKTRCWRRSAGGGMTGRGKGGCRGCARRGAGGCSWRAGAKRAGSTT ☐ TYTGACATRSTKSTAWGACTKRAAAWKKGCMCRTCYTTA
☐ GYYCTCCMCNYGGYTSTMASYMCCMWMTYYCYRAA ☐ AASCAGVRAAAVCAG ☐ TGGSARHMCTGTSWGMAKAC ☐ ATGCAAATCTGGCAAGTCATT
☐ CAGAAGCYGC ☐ CACAGCCWGGCACA ☐ ACTTCHGYTGBSVTCHCYCT ☐ GGGCAG ☐ GGGGAG ☐ GSAGGGGG ☐ CCACCCC ☐ TGCTASCTACC
☐ CTGTGAACAAT ☐ GTGGTGSAG ☐ GCAAAGAG ☐ TGCASCTSTGC ☐ ACCGTG ☐ GCAYTGGC ☐ GGGGCMAT ☐ GAAGGG ☐ GCTGGC
☐ GACRCTGG ☐ CACTGSAC ☐ ACACAGC ☐ TCCAGAWCC ☐ AGGCGMG ☐ GGTAGAT ☐ CCTGGRSG

INPUTS & SETTINGS

[Prev](#) [Next](#) [Top](#)

Alphabet

Background Source: an old version of the NCBI non-redundant database

| Name | Bg. | | | Bg. | Name |
|----------|----------|---|---|-----|---------|
| Adenine | 0.274262 | A | ~ | T | Thymine |
| Cytosine | 0.22521 | C | ~ | G | Guanine |

Sequences

The following sequence database was supplied to MAST.

| Database | Sequence Count | Residue Count | Last Modified |
|-----------------------------|----------------|---------------|--------------------------|
| SLE_dmp_cpg_sequences.fasta | 12 | 2412 | Sat Jun 21 08:09:21 2025 |
| Total | 12 | 2412 | |

Motifs

The following motif database was supplied to MAST.

| Database | Last Modified |
|----------|--------------------------|
| meme.xml | Sat Jun 21 08:09:38 2025 |

Other Settings

Strand Handling

The result of scanning both strands is **combined**. When matches overlap the non-overlapping combination with the best p-value is shown.

Max Correlation

Motifs with a correlation greater than **0.6** are marked for potential removal dependant on the --remcorr option.

Remove Correlated
Max Sequence E -
value
Adjust Hit p -value
Displayed Hits
Displayed Weak Hits

Correlated motifs exceeding the threshold are **highlighted** and their removal is recommended.
Sequences with an E -value less than **10** are included in the output.
The hit p -value is **not adjusted** for the length of the sequence.
The p -value of a hit must be less than **0.0001** to be shown in the output.
Weak hits are **not displayed**.

[Prev](#) [Top](#)

MAST version 5.5.8

(Release date: Thu May 15 15:01:46 2025 -0700)

Reference

Timothy L. Bailey and Michael Gribskov, "Combining evidence using p -values: application to sequence homology searches", *Bioinformatics*, **14**(1):48-54, 1998. [\[full text\]](#)

Command line summary

```
mast -oc . -nostatus meme.xml SLE_dmp_cpg_sequences.fasta
```

Ran in 0.04 seconds on Sat Jun 21 08:09:38 2025 on noble-meme.grid.gs.washington.edu