# MEME-ChIP
### Motif Analysis of Large Nucleotide Datasets

For further information on how to interpret these results please access http://meme-suite.org/doc/meme-chip-output-format.html.
To get a copy of the MEME software please access http://meme-suite.org.

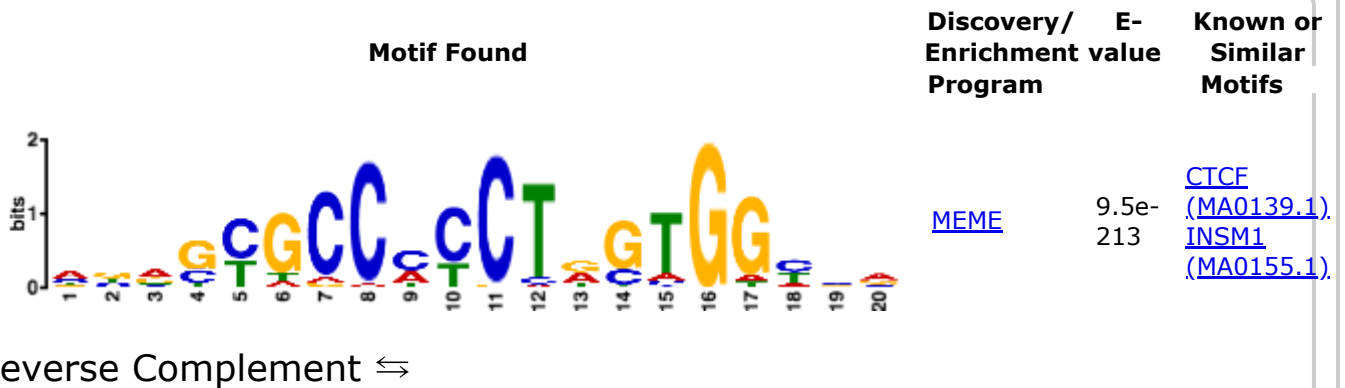If you use MEME-ChIP in your research, please cite the following paper:
Philip Machanick and Timothy L. Bailey, "MEME-ChIP: motif analysis of large DNA datasets", *Bioinformatics*, **27**12, 1696-1697, 2011. [full text]

**MOTIFS** | **PROGRAMS** | **INPUT FILES** | **PROGRAM INFORMATION** | **SUMMARY IN TSV FORMAT** 🆕 | **MOTIFS IN MEME TEXT FORMAT** 🆕

## MOTIFS

The significant motifs (E-value ≤ 0.05) found by the programs MEME, DREME and CentriMo; clustered by similarity and ordered by E-value.

Expand All Clusters        Collapse All Clusters

| Motif Found | Discovery/ Enrichment Program | E-value | Known or Similar Motifs |
|---|---|---|---|
|  | MEME | 9.5e-213 | CTCF (MA0139.1) INSM1 (MA0155.1) |

Reverse Complement ⇆

## PROGRAMS

| Command | Running Time | Status | Outputs |
|---|---|---|---|
| **getsize** memechip_out/ER4_fasta_meme_100.fa 1> $metrics | 0.02s | Success | |
| **fasta-most** -min 50 < memechip_out/ER4_fasta_meme_100.fa 1> $metrics | 0.07s | Success | |
| **fasta-center** -dna -len 100 < memechip_out/ER4_fasta_meme_100.fa 1> memechip_out/seqs-centered | 0.09s | Success | • seqs-centered |

| Command | Running Time | Status | Outputs |
|---|---|---|---|
| **fasta-shuffle-letters** memechip_out/seqs-centered memechip_out/seqs-shuffled -kmer 2 -tag -dinuc -dna -seed 1 | 0.02s | Success | • seqs-shuffled |
| **fasta-get-markov** -nostatus -nosummary -dna -m 1 memechip_out/ER4_fasta_meme_100.fa memechip_out/background | 0.01s | Success | • Background |
| **meme** memechip_out/seqs-centered -oc memechip_out/meme_out -mod zoops -nmotifs 3 -minw 6 -maxw 20 -bfile memechip_out/background -dna -revcomp -nostatus | 14.28s | Success | • MEME HTML<br>• MEME text<br>• MEME XML |
| **dreme** -verbosity 1 -oc memechip_out/dreme_out -png -dna -p memechip_out/seqs-centered -n memechip_out/seqs-shuffled | 0.06s | Error 1 | |
| **centrimo** -seqlen 566 -verbosity 1 -oc memechip_out/centrimo_out -bfile memechip_out/background memechip_out/ER4_fasta_meme_100.fa memechip_out/meme_out/meme.xml motif_databases/JASPAR/JASPAR_CORE_2016_vertebrates.meme | 0.72s | Warnings | • CentriMo HTML |
| **tomtom** -verbosity 1 -oc memechip_out/meme_tomtom_out -min-overlap 5 -dist pearson -evalue -thresh 1 -no-ssc memechip_out/meme_out/meme.xml motif_databases/JASPAR/JASPAR_CORE_2016_vertebrates.meme | 3.18s | Success | • Tomtom HTML<br>• Tomtom TSV<br>• Tomtom XML |
| **tomtom** -verbosity 1 -text -thresh 0.1 memechip_out/combined.meme memechip_out/combined.meme 1> memechip_out/motif_alignment.txt | 0.05s | Success | • Motif Alignment |
| **spamo** -verbosity 1 -oc memechip_out/spamo_out_1 -bgfile memechip_out/background -keepprimary -primary ABRGYGCCMCCTRGTGGYVR memechip_out/ER4_fasta_meme_100.fa memechip_out/meme_out/meme.xml memechip_out/meme_out/meme.xml motif_databases/JASPAR/JASPAR_CORE_2016_vertebrates.meme | 2.52s | Success | • SpaMo HTML |
| **fimo** --parse-genomic-coord --verbosity 1 --oc memechip_out/fimo_out_1 --bgfile memechip_out/background --motif ABRGYGCCMCCTRGTGGYVR memechip_out/meme_out/meme.xml memechip_out/ER4_fasta_meme_100.fa | 0.12s | Success | • FIMO GFF<br>• FIMO HTML<br>• FIMO TSV |

## INPUT FILES

### Alphabet

**Background source:** built from the (primary) sequences

| Name | Bg. | | | Bg. | Name |
|------|-----|---|---|-----|------|
| Adenine | 0.2538 | A | ~ T | 0.2538 | Thymine |
| Cytosine | 0.2462 | C | ~ G | 0.2462 | Guanine |

## Primary Sequences

| Database | Source | Sequence Count |
|----------|--------|----------------|
| ER4 fasta meme 100 | ER4_fasta_meme_100.fa | 100 |

## Motifs

| Database | Source | Motif Count |
|----------|--------|-------------|
| JASPAR CORE 2016 vertebrates | motif_databases/JASPAR/JASPAR_CORE_2016_vertebrates.meme | 519 |

**MEME-ChIP version**
5.0.2 (Release date: Thu Aug 30 14:26:08 2018 -0700)

**Reference**
Philip Machanick and Timothy L. Bailey, "MEME-ChIP: motif analysis of large DNA datasets", *Bioinformatics*, **27**12, 1696-1697, 2011.

**Command line summary**
meme-chip -db motif_databases/JASPAR/JASPAR_CORE_2016_vertebrates.meme -meme-maxw 20 ER4_fasta_meme_100.fa