



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

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

Robert McLeay and Timothy L. Bailey, "Motif Enrichment Analysis: A unified framework and method evaluation", *BMC Bioinformatics*, **11**:165, 2010, doi:10.1186/1471-2105-11-165. [\[full text\]](#)

[ENRICHED MOTIFS](#) | [INPUT FILES](#) | [PROGRAM INFORMATION](#) | [RESULTS IN TSV FORMAT](#)  | [POSITIVE SEQUENCES FOR EACH MOTIF](#) 

## ENRICHED MOTIFS

Sequence motif score: avg\_odds

Background model source: letter frequencies in (primary) sequences file (G4NN\_finetune\_min\_seq.fa)

Background model frequencies: 0.265796,0.234204,0.234204,0.265796











Total pseudocount added to a motif column: 0.1

Statistical test: Fisher's exact test (optimized over motif scores)

Labeling positives: all 100 primary sequences are labeled as 'positive'; all 1100 control sequences are labeled as 'negative'




Classifying positives: sequences with the motif scores  $\geq$  'TP Thresh' are classified as positive

E-value threshold for reporting results: 10

Logo	Database	ID	Alt ID	p-value	E-value	TP Thresh	TP (%)
	JASPAR2018 CORE vertebrates non-redundant	<a href="#">MA0660.1</a>	MEF2B	1.80e-8	1.04e-5	7.70	11 (11.0%)
	JASPAR2018 CORE vertebrates non-redundant	<a href="#">MA0773.1</a>	MEF2D	2.79e-8	1.62e-5	1.64	13 (13.0%)
	JASPAR2018 CORE vertebrates non-redundant	<a href="#">MA0052.3</a>	MEF2A	2.41e-6	1.39e-3	4.41	13 (13.0%)
	JASPAR2018 CORE vertebrates non-redundant	<a href="#">MA0497.1</a>	MEF2C	2.65e-6	1.54e-3	1.83	27 (27.0%)
	JASPAR2018 CORE vertebrates non-redundant	<a href="#">MA0778.1</a>	NFKB2	5.18e-6	3.00e-3	6.63	12 (12.0%)
	JASPAR2018 CORE vertebrates non-redundant	<a href="#">MA0019.1</a>	Ddit3::Cebpa	3.94e-5	2.28e-2	3.15	18 (18.0%)
	JASPAR2018 CORE vertebrates non-redundant	<a href="#">MA0814.1</a>	TFAP2C(var.2)	5.99e-5	3.47e-2	6.13	19 (19.0%)
	JASPAR2018 CORE vertebrates non-redundant	<a href="#">MA0111.1</a>	Spz1	1.01e-4	5.86e-2	8.29	16 (16.0%)
	JASPAR2018 CORE vertebrates non-redundant	<a href="#">MA0693.2</a>	VDR	1.01e-3	5.85e-1	7.30	15 (15.0%)
	JASPAR2018 CORE vertebrates non-redundant	<a href="#">MA0799.1</a>	RFX4	1.06e-3	6.14e-1	1.29	11 (11.0%)

23/03/2021

AME results

Logo	Database	ID	Alt ID	p-value	E-value	TP Thresh	TP (%)
	JASPAR2018 CORE vertebrates non-redundant	<a href="#">MA1125.1</a>	ZNF384	4.57e-3	2.65e0	257.53	6 (6.0%)
	JASPAR2018 CORE vertebrates non-redundant	<a href="#">MA0041.1</a>	Foxd3	5.65e-3	3.27e0	8.20	16 (16.0%)
	JASPAR2018 CORE vertebrates non-redundant	<a href="#">MA0006.1</a>	Ahr::Arnt	1.22e-2	7.04e0	1.35	16 (16.0%)

INPUT FILES

Alphabet

Background source: built from the (primary) sequences

Name	Bg.			Bg.	Name
Adenine	0.265796	A	~	T	Thymine
Cytosine	0.234204	C	~	G	Guanine

Sequences

Primary Sequences	Number	Control Sequences	Number
G4NN_finetune_min_seq.fa	100	primary sequences shuffled conserving 2-mer frequencies	1100

Motifs

Database	Source	Motif Count
JASPAR2018 CORE vertebrates non-redundant	motif_databases/JASPAR/JASPAR2018_CORE vertebrates_non-redundant.meme	579

AME version

5.1.1 (Release date: Wed Feb 12 17:20:50 2020 -0800)

Copyright © Robert McLeay & Timothy Bailey [meme-suite@uw.edu](mailto:meme-suite@uw.edu), 2009.

Command line summary

```
ame --oc G4NN_finetune_minseq_JasparCore --scoring avg --method fisher --hit-lo-fraction 0.25 --evaluate-report-threshold 10.0 --control --shuffle-- --kmer 2 G4NN_finetune_min_seq.fa motif_databases/JASPAR/JASPAR2018_CORE vertebrates_non-redundant.meme
```

