



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

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

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

Shobhit Gupta, JA Stamatoyannopoulos, Timothy Bailey and William Stafford Noble, "Quantifying similarity between motifs", *Genome Biology*, 8(2):R24, 2007. [\[full text\]](#)

[QUERY MOTIFS](#) | [TARGET DATABASES](#) | [MATCHES](#) | [SETTINGS](#) | [PROGRAM INFORMATION](#) | [RESULTS IN TSV FORMAT](#) | [RESULTS IN XML FORMAT](#)

QUERY MOTIFS

[Next Top](#)

Database	ID	Alt. ID	Preview	Matches	List
streme.xml	1-CTGGGAY	STREME-1		0	
streme.xml	2-GCCTCRGCCTCCCAA	STREME-2		3	ZN770_HUMAN.H11MO.0.C , IKZF1_HUMAN.H11MO.0.C , CRX_HUMAN.H11MO.0.B
streme.xml	3-ACAGGCRGTGAGCCAC	STREME-3		3	FOS_HUMAN.H11MO.0.A , ZN257_HUMAN.H11MO.0.C , FOSB_HUMAN.H11MO.0.A
streme.xml	4-CCAGGCTGGWST	STREME-4		0	

TARGET DATABASES

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

Database	Used	Matched
HOCOMOCov11_core_HUMAN_mono_meme_format	401	6

MATCHES TO 2-GCCTCRGCCTCCCAA (STREME-2)

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

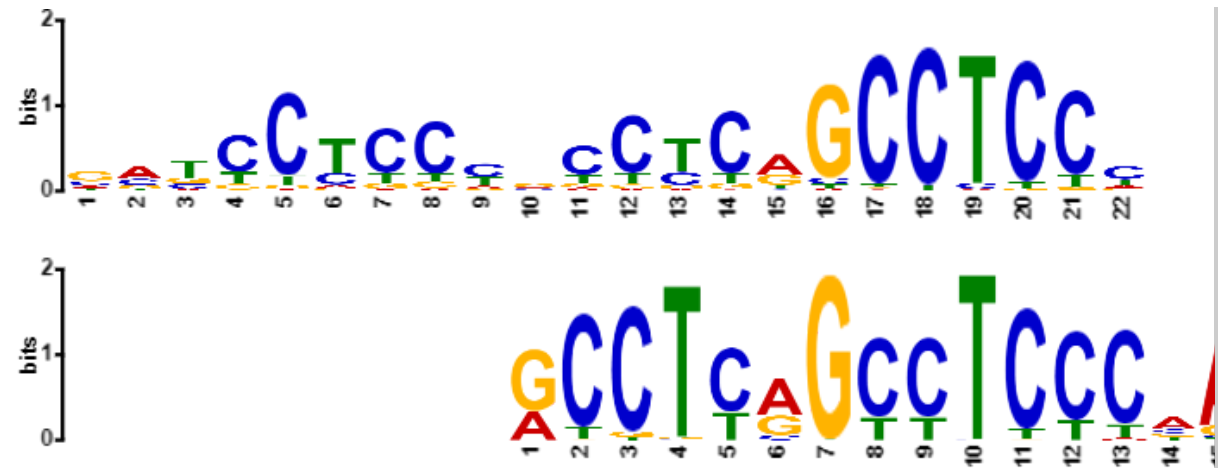
Summary	Optimal Alignment

Name [ZN770_HUMAN.H11MO.0.C](#)
Database HOCOMOCov11_core_HUMAN_mono_meme_format
p-value 2.13e-06
E-value 8.53e-04
q-value 1.71e-03

Overlap 13
Offset 9
Orientation Reverse Complement

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Tomtom Results



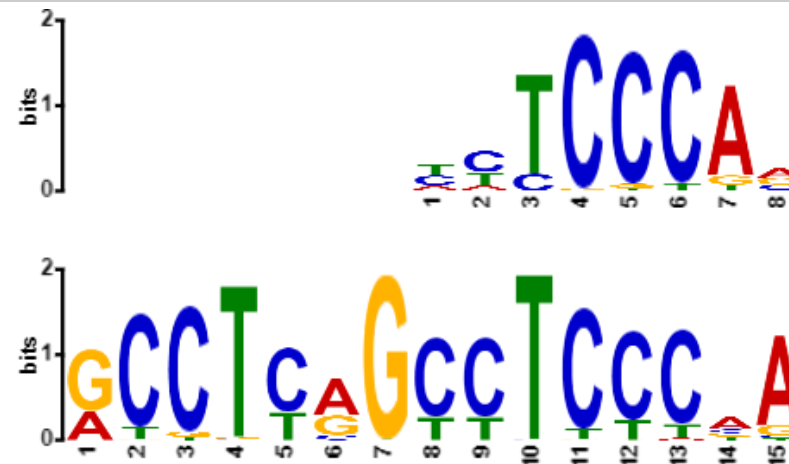
Summary

Name [IKZF1_HUMAN.H11MO.0.C](#)
Database HOCOMOCov11_core_HUMAN_mono_meme_format
p-value 6.98e-05
E-value 2.80e-02
q-value 2.80e-02

Overlap 8
Offset -7
Orientation Reverse Complement

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Optimal Alignment



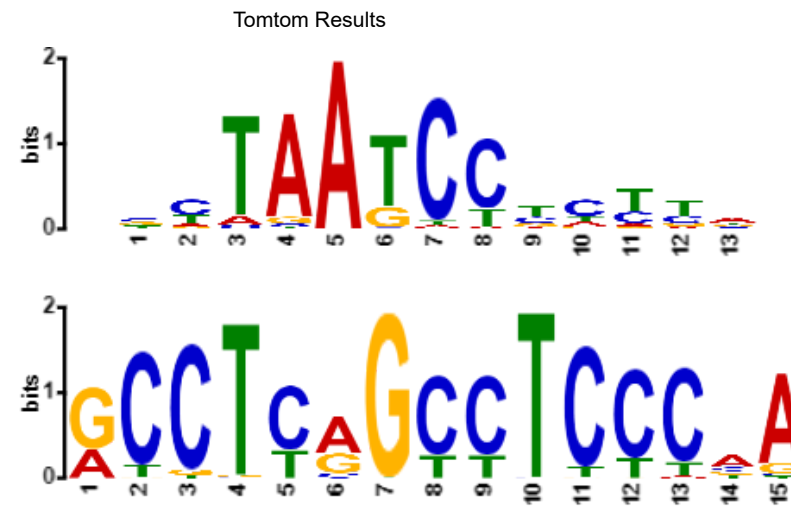
Summary

Optimal Alignment

Name [CRX_HUMAN.H11MO.0.B](#)
Database HOCOMOCov11_core_HUMAN_mono_meme_format
p-value 1.24e-03
E-value 4.97e-01
q-value 3.31e-01

Overlap 13
Offset -1
Orientation Reverse Complement

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MATCHES TO 3-ACAGGCGTGAGCCAC (STREME-3)

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

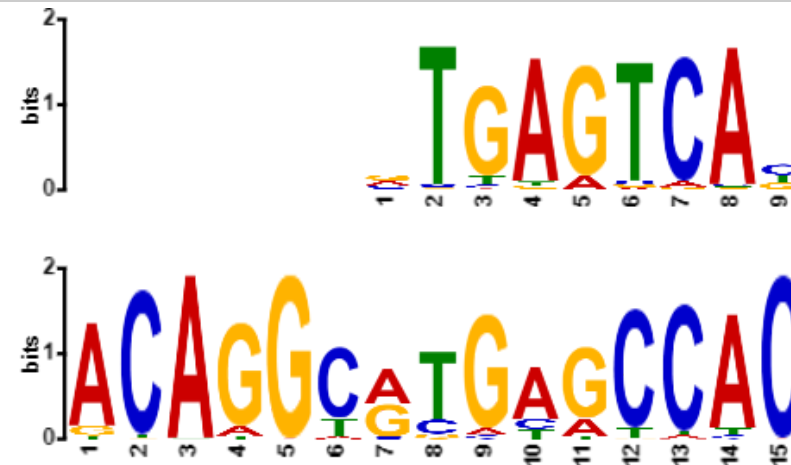
Summary

Name [FOS_HUMAN.H11MO.0.A](#)
Database HOCOMOCov11_core_HUMAN_mono_meme_format
p-value 3.80e-04
E-value 1.53e-01
q-value 2.63e-01

Overlap 9
Offset -6
Orientation Normal

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Optimal Alignment

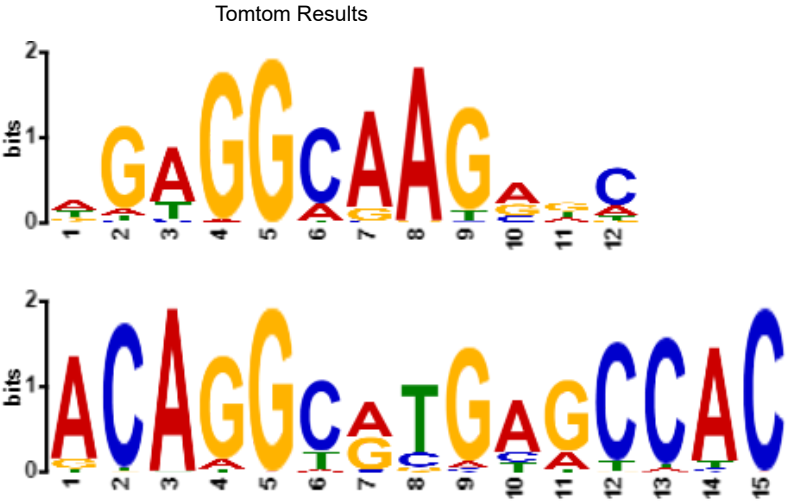


Summary

Optimal Alignment

Name [ZN257_HUMAN.H11MO.0.C](#)
Database HOCOMOCov11_core_HUMAN_mono_meme_format
p-value 9.19e-04
E-value 3.69e-01
q-value 2.63e-01

Overlap 12
Offset 0
Orientation Reverse Complement
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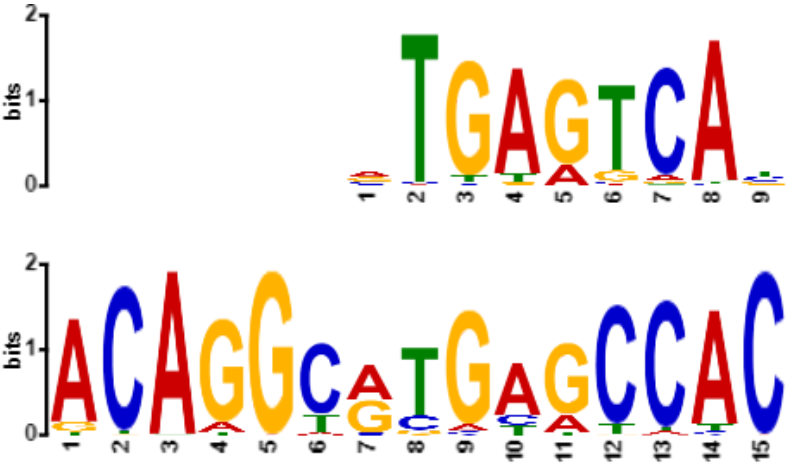


Summary

Name [FOSB_HUMAN.H11MO.0.A](#)
Database HOCOMOCov11_core_HUMAN_mono_meme_format
p-value 9.85e-04
E-value 3.95e-01
q-value 2.63e-01

Overlap 9
Offset -6
Orientation Normal
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Optimal Alignment



SETTINGS

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

Alphabet

Source: the query file

Name	Bg.			Bg.	Name
Adenine	0.25	A	~	0.25	Thymine
Cytosine	0.25	C	~	0.25	Guanine

Other Settings

Strand Handling	Motifs may be reverse complemented before comparison to find a better match.
Distance Measure	Pearson correlation coefficient
Match Threshold	Matches must have a <i>E</i> -value of 1 or smaller.

[Previous Top](#)**Tomtom version**

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

ReferenceShobhit Gupta, JA Stamatoyannopolous, Timothy Bailey and William Stafford Noble, "Quantifying similarity between motifs", *Genome Biology*, 8(2):R24, 2007. [\[full text\]](#)**Command line**

```
tomtom -verbosity 1 -oc streme_tomtom_out -min-overlap 5 -dist pearson -evaluate -thresh 1 -no-ssc streme_out/streme.xml
```

Result calculation took 2.196 seconds

