



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. [\[full text\]](#)

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QUERY MOTIFS

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Database	ID	Alt. ID	Preview	Matches	List
meme.xml	AAWAAAAAWAAAAA	MEME-1		15	FOXJ3_HUMAN.H11MO.0.A , PRDM6_HUMAN.H11MO.0.C , ANDR_HUMAN.H11MO.0.A , GATA3_HUMAN.H11MO.0.A ,
meme.xml	CCTYRGCTCCCRAR	MEME-3		2	ZN770_HUMAN.H11MO.0.C , IKZF1_HUMAN.H11MO.0.C
meme.xml	GCTGGGATTACAGGC	MEME-2		1	ZN264_HUMAN.H11MO.0.C

TARGET DATABASES

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Database	Used	Matched
HOCOMOCov11_core_HUMAN_mono_meme_format	401	18

MATCHES TO AAWAAAAAWAAAAA (MEME-1)

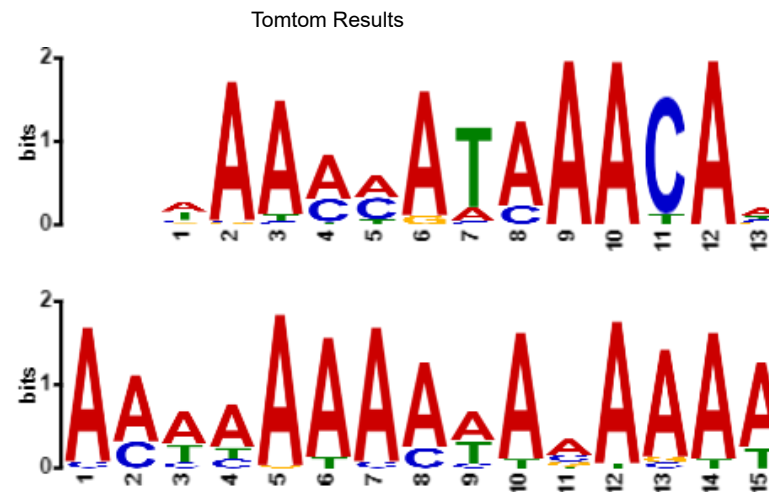
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Summary	Optimal Alignment

Name [FOX13_HUMAN.H11MO.0.A](#)
Database HOCOMOCov11_core_HUMAN_mono_meme_format
p-value 1.14e-06
E-value 4.57e-04
q-value 8.88e-04

Overlap 13
Offset -2
Orientation Reverse Complement

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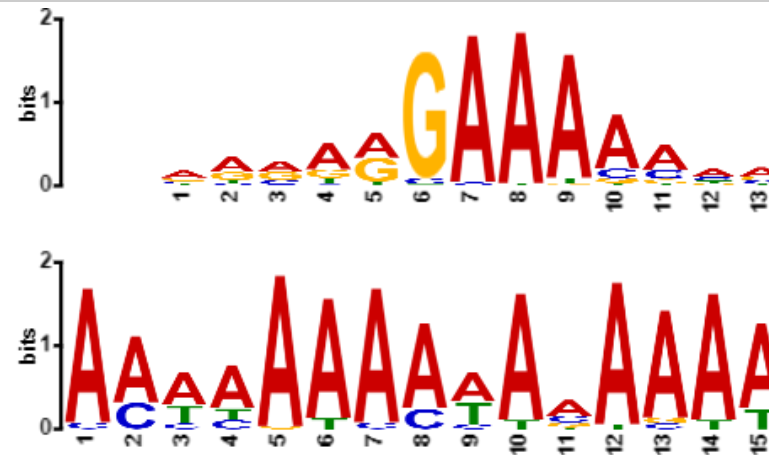
Summary

Name [PRDM6_HUMAN.H11MO.0.C](#)
Database HOCOMOCov11_core_HUMAN_mono_meme_format
p-value 8.42e-06
E-value 3.38e-03
q-value 3.28e-03

Overlap 13
Offset -2
Orientation Normal

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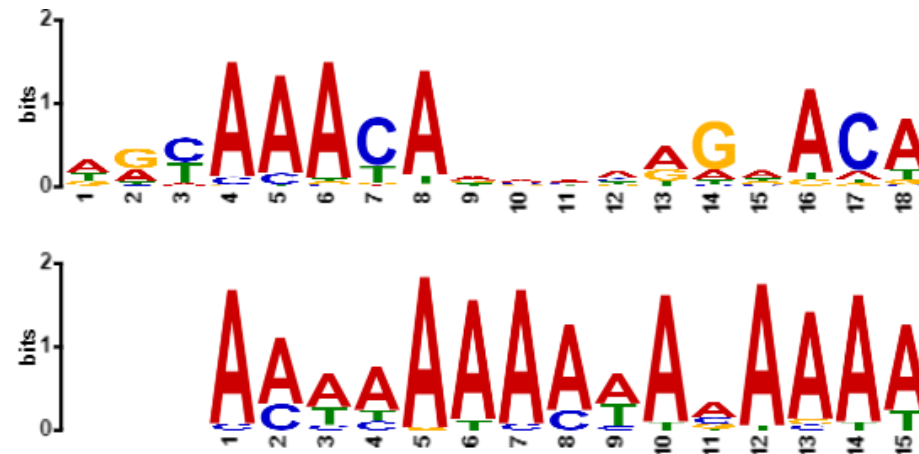
Optimal Alignment



Summary

Optimal Alignment

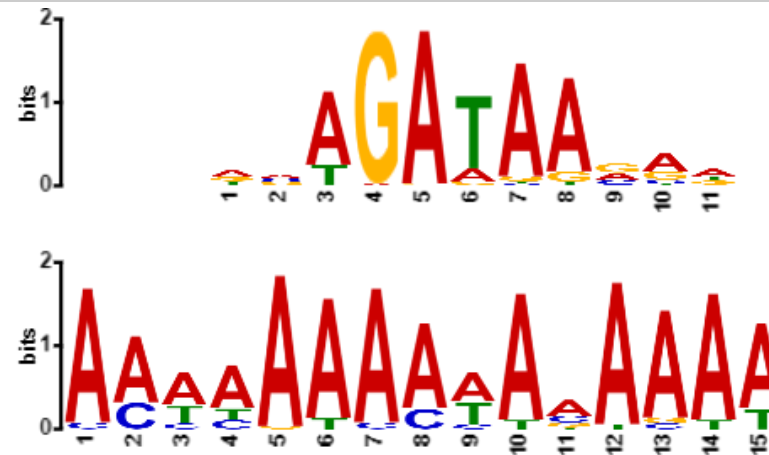
Name	ANDR_HUMAN.H11MO.0.A
Database	HOCOMOCov11_core_HUMAN_mono_meme_format
p-value	1.32e-05
E-value	5.30e-03
q-value	3.43e-03
Overlap	15
Offset	3
Orientation	Reverse Complement
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Summary

Name	GATA3_HUMAN.H11MO.0.A
Database	HOCOMOCov11_core_HUMAN_mono_meme_format
p-value	3.86e-04
E-value	1.55e-01
q-value	6.86e-02
Overlap	11
Offset	-3
Orientation	Normal
	Show logo download options

Optimal Alignment



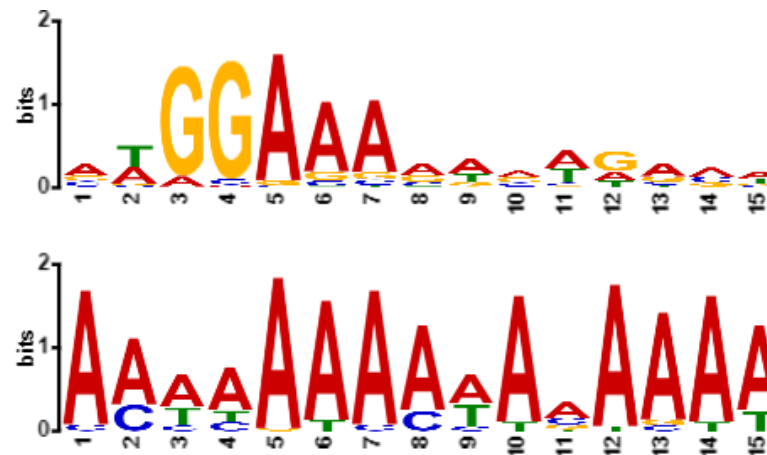
Summary

Optimal Alignment

Name [NFAC1_HUMAN.H11MO.0.B](#)
Database HOCOMOCov11_core_HUMAN_mono_meme_format
p-value 4.62e-04
E-value 1.85e-01
q-value 6.86e-02

Overlap 15
Offset 0
Orientation Normal

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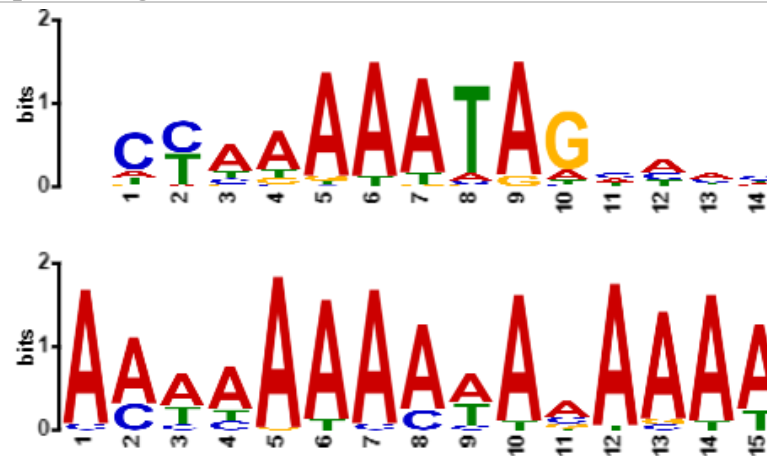
Summary

Name [MEF2B_HUMAN.H11MO.0.A](#)
Database HOCOMOCov11_core_HUMAN_mono_meme_format
p-value 5.28e-04
E-value 2.12e-01
q-value 6.86e-02

Overlap 14
Offset -1
Orientation Reverse Complement

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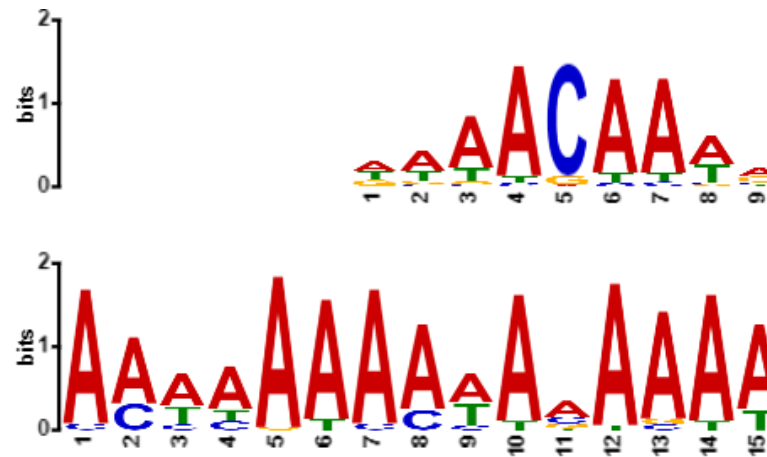
Optimal Alignment



Summary

Optimal Alignment

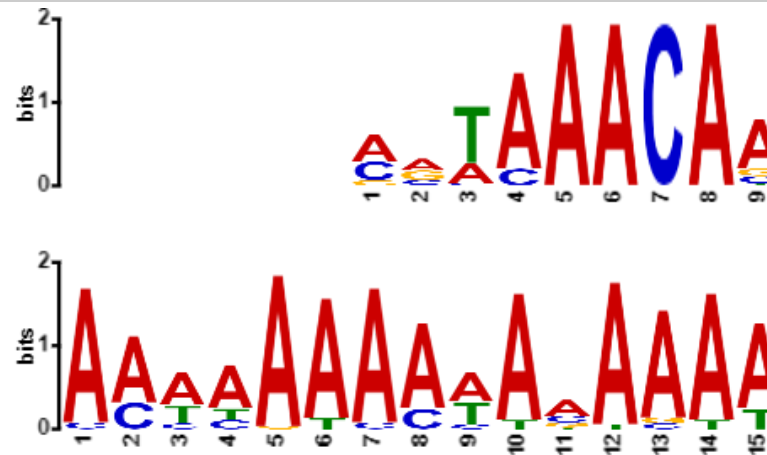
Name	SRY_HUMAN.H11MO.0.B
Database	HOCOMOCov11_core_HUMAN_mono_meme_format
p-value	6.51e-04
E-value	2.61e-01
q-value	7.24e-02
Overlap	9
Offset	-6
Orientation	Reverse Complement
	Show logo download options



Summary

Name	FOXO4_HUMAN.H11MO.0.C
Database	HOCOMOCov11_core_HUMAN_mono_meme_format
p-value	8.28e-04
E-value	3.32e-01
q-value	8.05e-02
Overlap	9
Offset	-6
Orientation	Reverse Complement
	Show logo download options

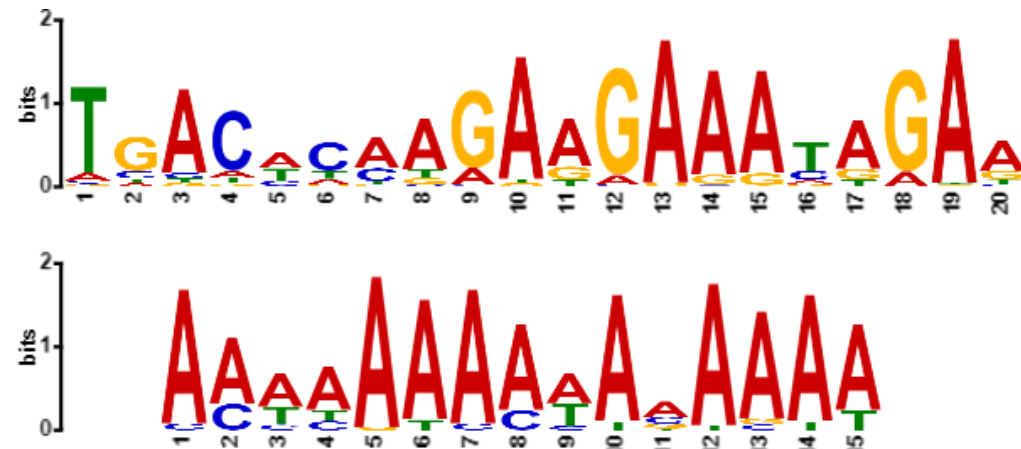
Optimal Alignment



Summary

Optimal Alignment

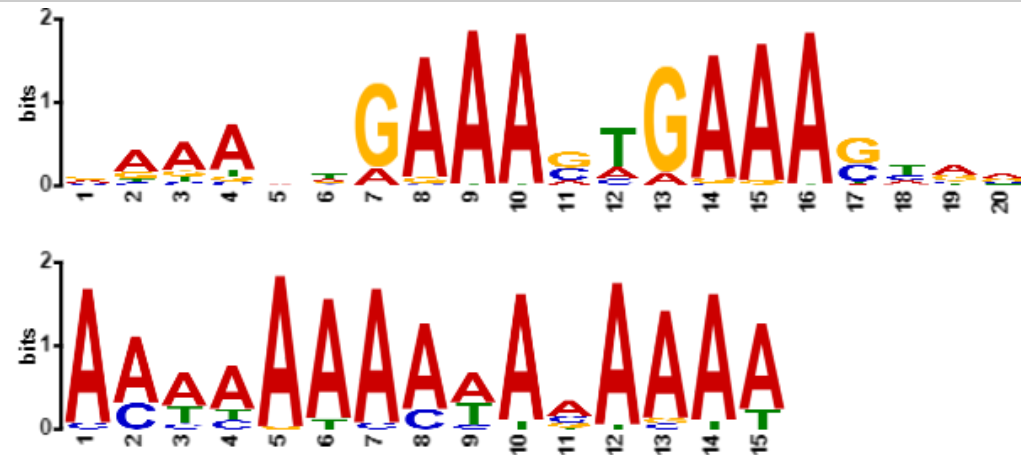
Name	ZFP28_HUMAN.H11MO.0.C
Database	HOCOMOCov11_core_HUMAN_mono_meme_format
p-value	1.12e-03
E-value	4.50e-01
q-value	9.00e-02
Overlap	15
Offset	2
Orientation	Reverse Complement
	Show logo download options



Summary

Name	IRF1_HUMAN.H11MO.0.A
Database	HOCOMOCov11_core_HUMAN_mono_meme_format
p-value	1.17e-03
E-value	4.69e-01
q-value	9.00e-02
Overlap	15
Offset	0
Orientation	Normal
	Show logo download options

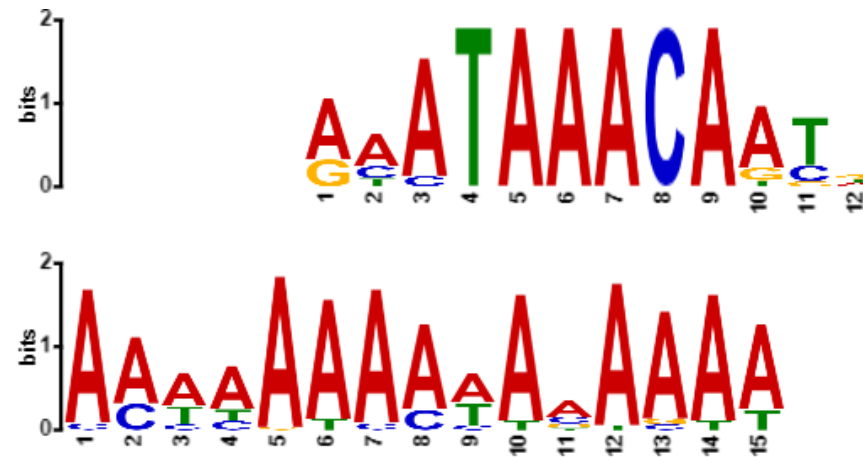
Optimal Alignment



Summary

Optimal Alignment

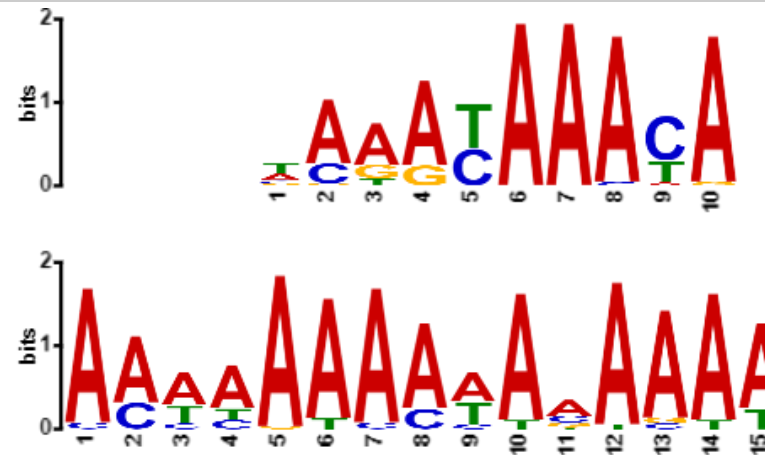
Name	FOXQ1_HUMAN.H11MO.0.C
Database	HOCOMOCov11_core_HUMAN_mono_meme_format
p-value	1.27e-03
E-value	5.10e-01
q-value	9.00e-02
Overlap	10
Offset	-5
Orientation	Reverse Complement
	Show logo download options



Summary

Name	FOXJ2_HUMAN.H11MO.0.C
Database	HOCOMOCov11_core_HUMAN_mono_meme_format
p-value	1.91e-03
E-value	7.68e-01
q-value	1.18e-01
Overlap	10
Offset	-4
Orientation	Reverse Complement
	Show logo download options

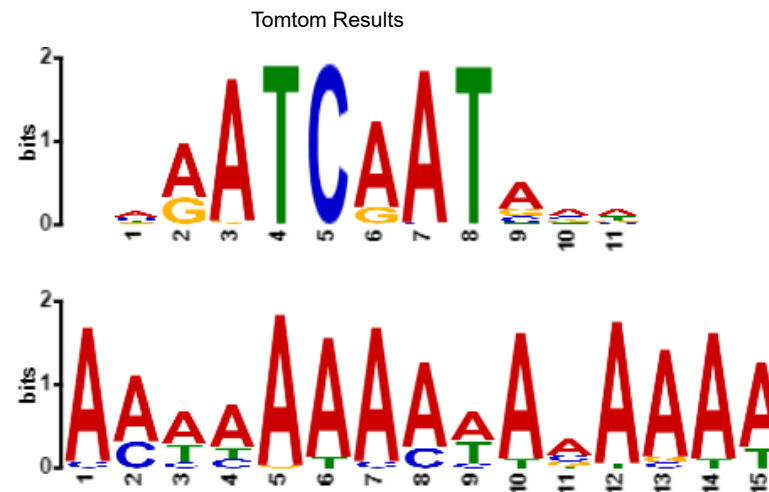
Optimal Alignment



Summary

Optimal Alignment

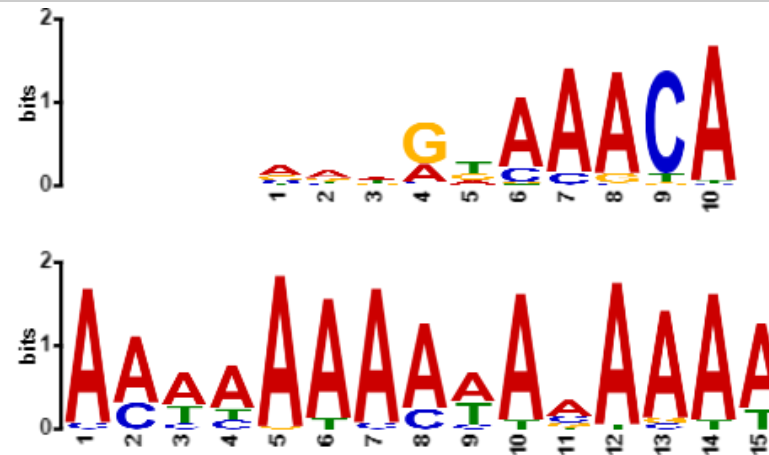
Name	HNF6_HUMAN.H11MO.0.B
Database	HOCOMOCov11_core_HUMAN_mono_meme_format
p-value	2.09e-03
E-value	8.38e-01
q-value	1.18e-01
Overlap	11
Offset	-1
Orientation	Reverse Complement
	Show logo download options



Summary

Name	FOXK1_HUMAN.H11MO.0.A
Database	HOCOMOCov11_core_HUMAN_mono_meme_format
p-value	2.12e-03
E-value	8.51e-01
q-value	1.18e-01
Overlap	10
Offset	-4
Orientation	Reverse Complement
	Show logo download options

Optimal Alignment

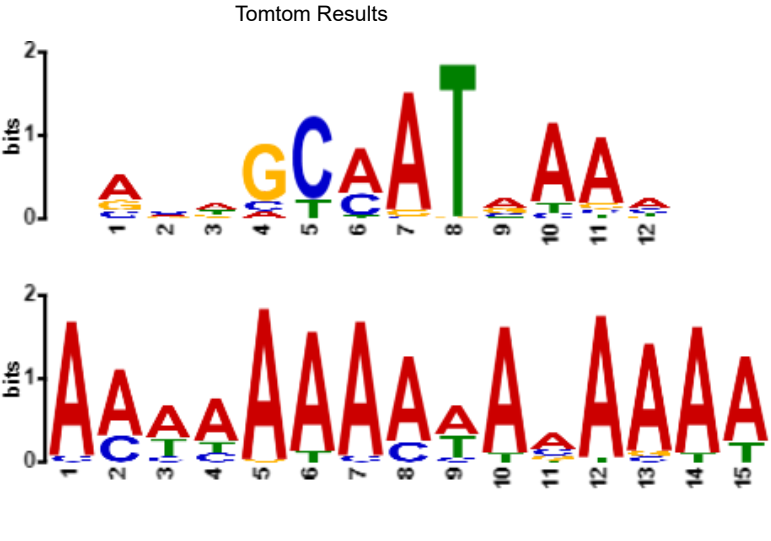


Summary

Optimal Alignment

Name	CDX2_HUMAN.H11MO.0.A
Database	HOCOMOCov11_core_HUMAN_mono_meme_format
p-value	2.40e-03
E-value	9.61e-01
q-value	1.23e-01
Overlap	12
Offset	-1
Orientation	Reverse Complement

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MATCHES TO GCTGGGATTACAGGC (MEME-2)

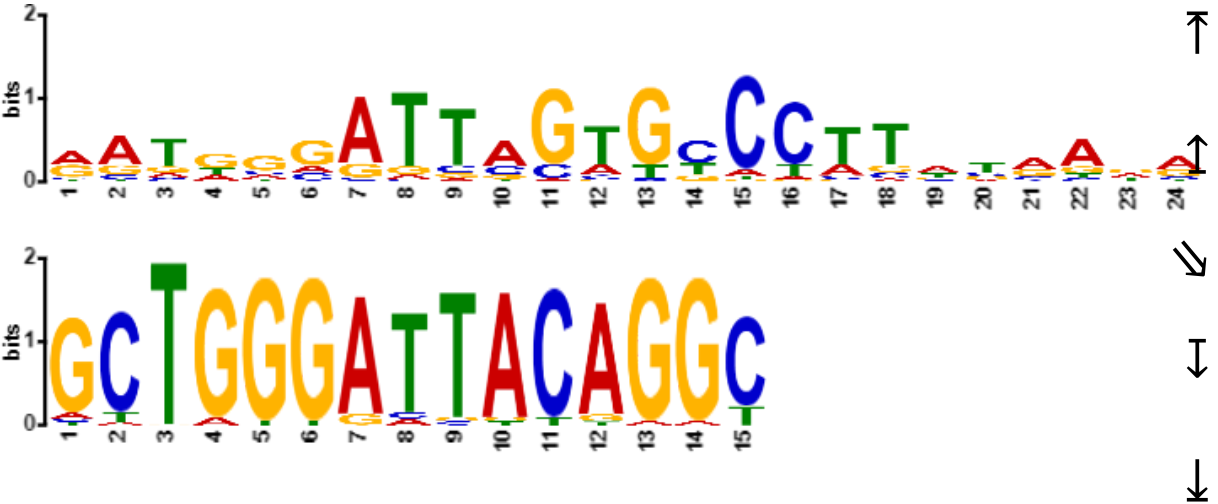
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Summary

Name	ZN264_HUMAN.H11MO.0.C
Database	HOCOMOCov11_core_HUMAN_mono_meme_format
p-value	1.26e-03
E-value	5.05e-01
q-value	1.00e+00
Overlap	15
Offset	0
Orientation	Reverse Complement

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Optimal Alignment



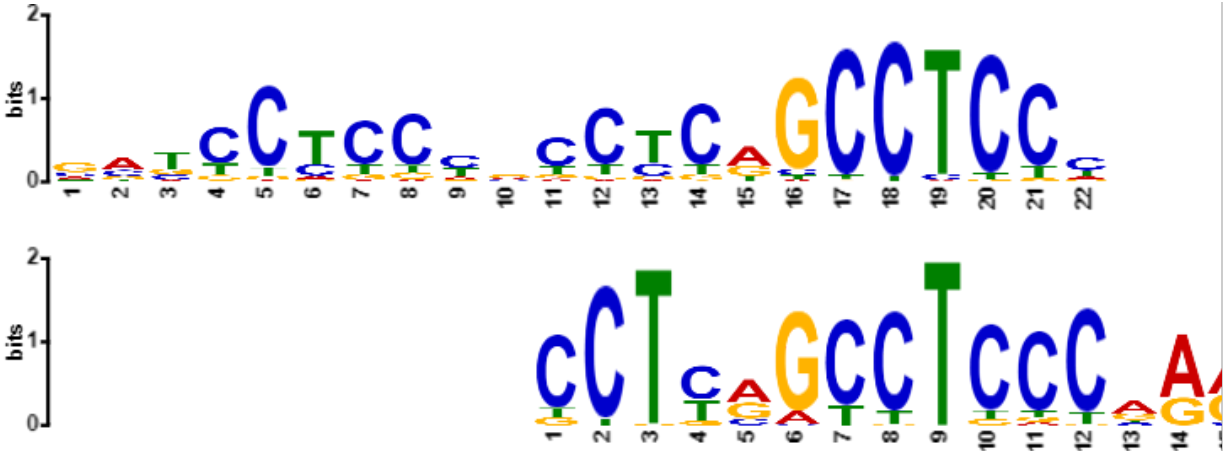
MATCHES TO CCTYRGCTCCCRAR (MEME-3)

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Summary

Optimal Alignment

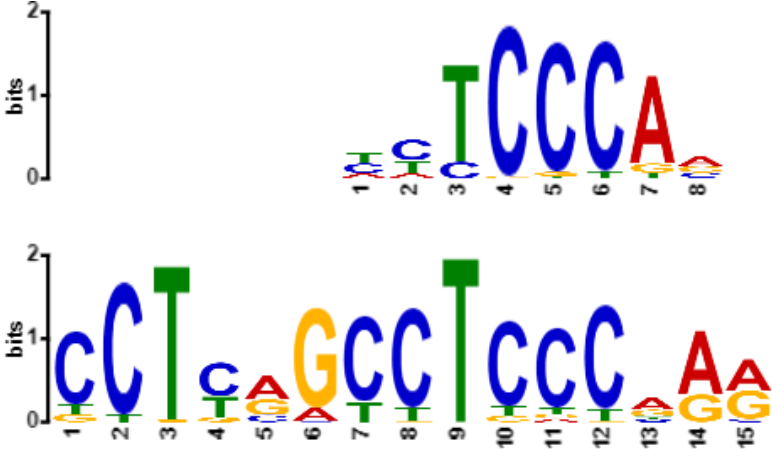
Name	ZN770_HUMAN.H11MO.0.C
Database	HOCOMOCov11_core_HUMAN_mono_meme_format
p-value	9.23e-06
E-value	3.70e-03
q-value	7.40e-03
Overlap	12
Offset	10
Orientation	Reverse Complement
	Show logo download options



Summary

Name	IKZF1_HUMAN.H11MO.0.C
Database	HOCOMOCov11_core_HUMAN_mono_meme_format
p-value	1.09e-04
E-value	4.38e-02
q-value	4.38e-02
Overlap	8
Offset	-6
Orientation	Reverse Complement
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Optimal Alignment



SETTINGS

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Alphabet

Source: the query file

Name	Bg.			Bg.	Name
Adenine	0.228	A	~	T	Thymine
Cytosine	0.272	C	~	G	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 meme_tomtom_out -min-overlap 5 -dist pearson -evaluate -thresh 1 -no-ssc meme_out/meme.xml
```

Result calculation took 2.403 seconds

