Tomtom
Motif Comparison Tool

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

If you use TOMTOM in your research, please cite the following paper:
Shobhit Gupta, JA Stamatoyannopolous, 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 NEW | RESULTS IN XML FORMAT

QUERY MOTIFS

Next Top

Database	ID	Alt. ID	Preview	Matches	List
query_motifs	ATGYWAAT			31	POU2F3_DBD_1, POU5F1P1_DBD_1,

TARGET DATABASES

Previous Next Top

Database	Used	Matched
jolma2013	843	14
JASPAR2018_CORE_vertebrates_non-redundant	579	14
uniprobe_mouse	386	3

MATCHES TO ATGYWAAT

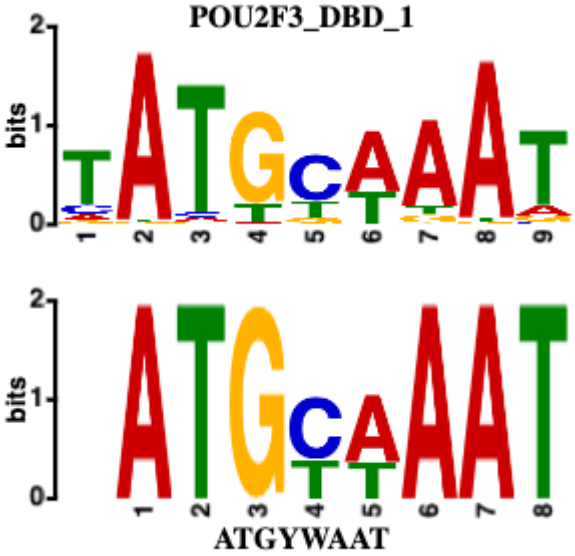
Previous Next Top

Summary

Name	POU2F3_DBD_1
Database	jolma2013
***p*-value**	3.87e-08
***E*-value**	6.99e-05
***q*-value**	4.64e-05
Overlap	8
Offset	1
Orientation	Normal

Show logo download options

Optimal Alignment

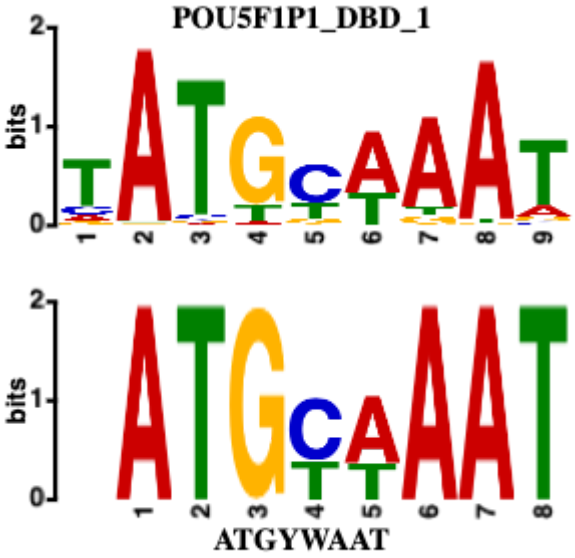


Summary

Optimal Alignment

Name	POU5F1P1_DBD_1
Database	jolma2013
***p*-value**	3.87e-08
***E*-value**	6.99e-05
***q*-value**	4.64e-05
Overlap	8
Offset	1
Orientation	Normal

Show logo download options

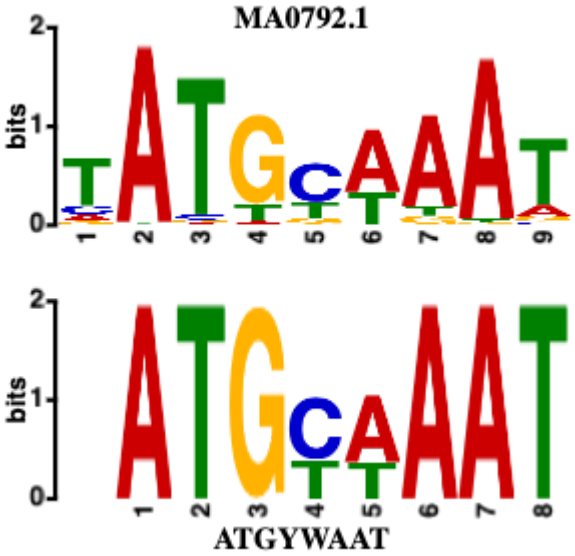


Summary

Name	MA0792.1 (POU5F1B)
Database	JASPAR2018_CORE_vertebrates_non-redundant
***p*-value**	3.87e-08
***E*-value**	6.99e-05
***q*-value**	4.64e-05
Overlap	8
Offset	1
Orientation	Normal

Show logo download options

Optimal Alignment

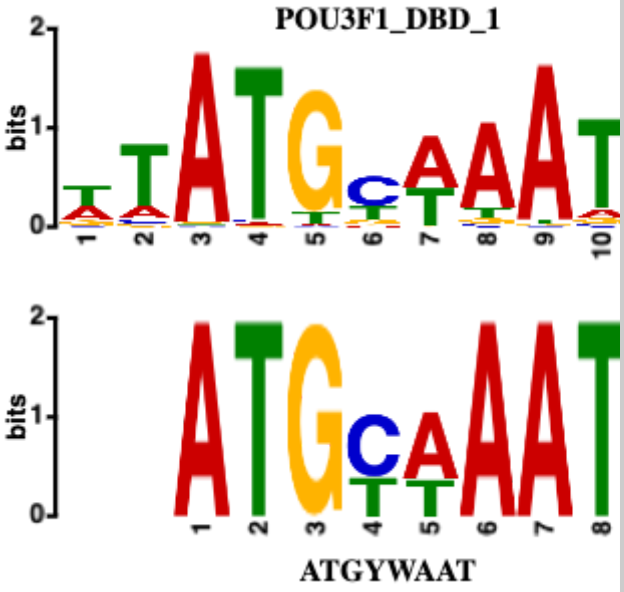


Summary

Name	POU3F1_DBD_1
Database	jolma2013
***p*-value**	9.67e-08
***E*-value**	1.75e-04
***q*-value**	5.27e-05
Overlap	8
Offset	2
Orientation	Normal

Show logo download options

Optimal Alignment

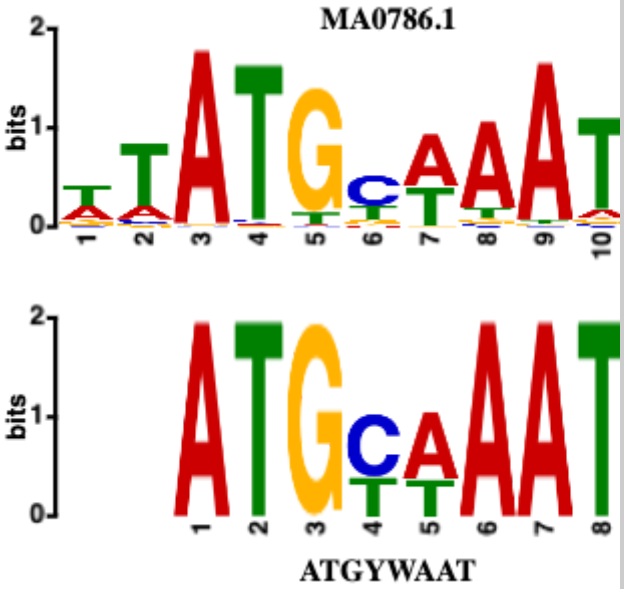


Summary

Name	MA0786.1 (POU3F1)
Database	JASPAR2018_CORE_vertebrates_non-redundant
***p*-value**	9.67e-08
***E*-value**	1.75e-04
***q*-value**	5.27e-05
Overlap	8
Offset	2
Orientation	Normal

Show logo download options

Optimal Alignment

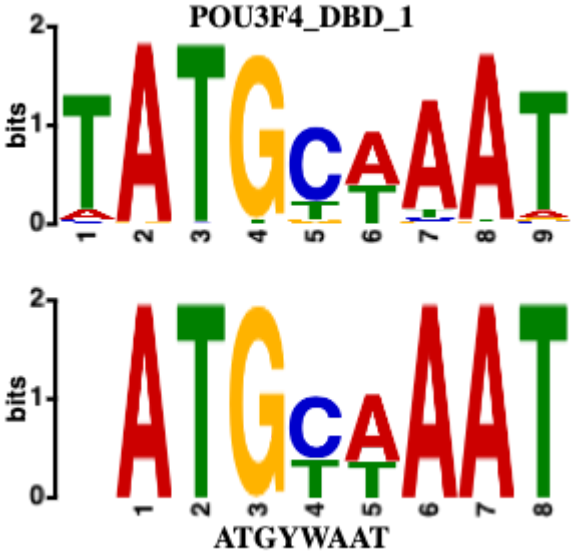


Summary

Name	POU3F4_DBD_1
Database	jolma2013
***p*-value**	1.02e-07
***E*-value**	1.85e-04
***q*-value**	5.27e-05
Overlap	8
Offset	1
Orientation	Normal

Show logo download options

Optimal Alignment

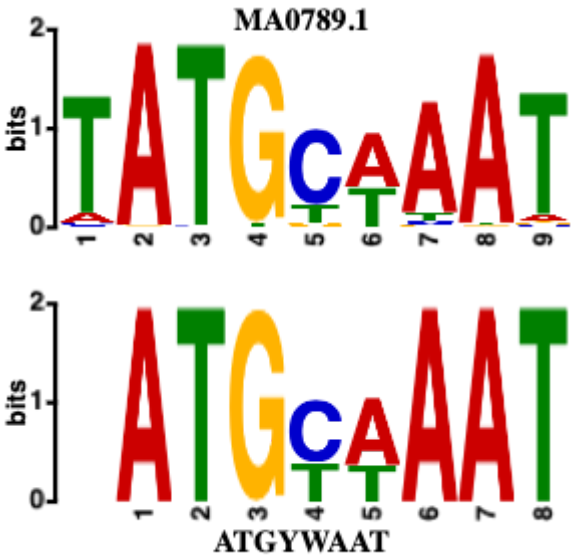


Summary

Name	MA0789.1 (POU3F4)
Database	JASPAR2018_CORE_vertebrates_non-redundant
***p*-value**	1.02e-07
***E*-value**	1.85e-04
***q*-value**	5.27e-05
Overlap	8
Offset	1
Orientation	Normal

Show logo download options

Optimal Alignment

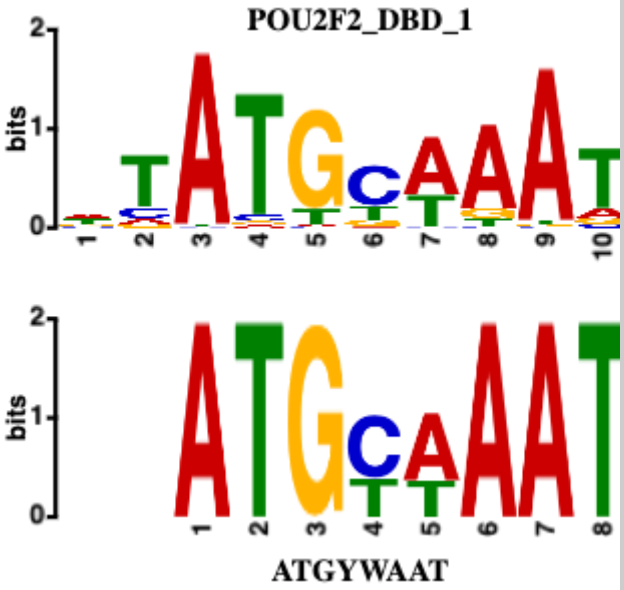


Summary

Name	POU2F2_DBD_1
Database	jolma2013
***p*-value**	2.05e-07
***E*-value**	3.71e-04
***q*-value**	9.23e-05
Overlap	8
Offset	2
Orientation	Normal

Show logo download options

Optimal Alignment

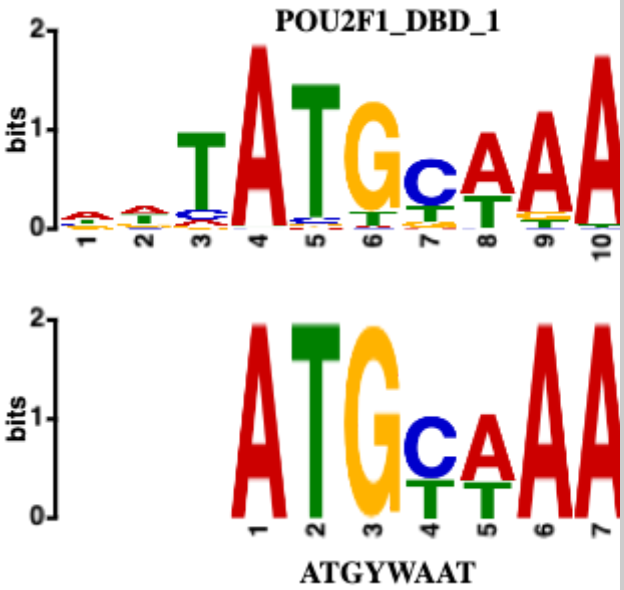


Summary

Name	POU2F1_DBD_1
Database	jolma2013
***p*-value**	2.56e-07
***E*-value**	4.63e-04
***q*-value**	9.23e-05
Overlap	8
Offset	3
Orientation	Normal

Show logo download options

Optimal Alignment

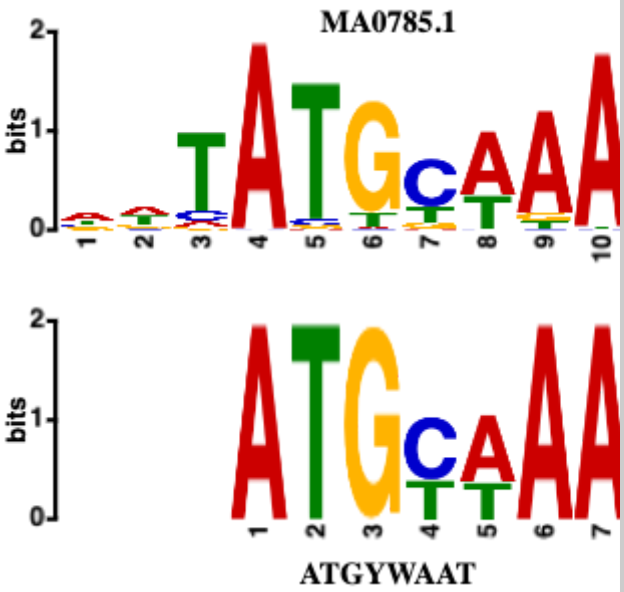


Summary

Name	MA0785.1 (POU2F1)
Database	JASPAR2018_CORE_vertebrates_non-redundant
***p*-value**	2.56e-07
***E*-value**	4.63e-04
***q*-value**	9.23e-05
Overlap	8
Offset	3
Orientation	Normal

Show logo download options

Optimal Alignment



Summary

Name	POU1F1_DBD_2
Database	jolma2013
***p*-value**	3.59e-07
***E*-value**	6.49e-04
***q*-value**	1.08e-04
Overlap	8
Offset	3
Orientation	Normal

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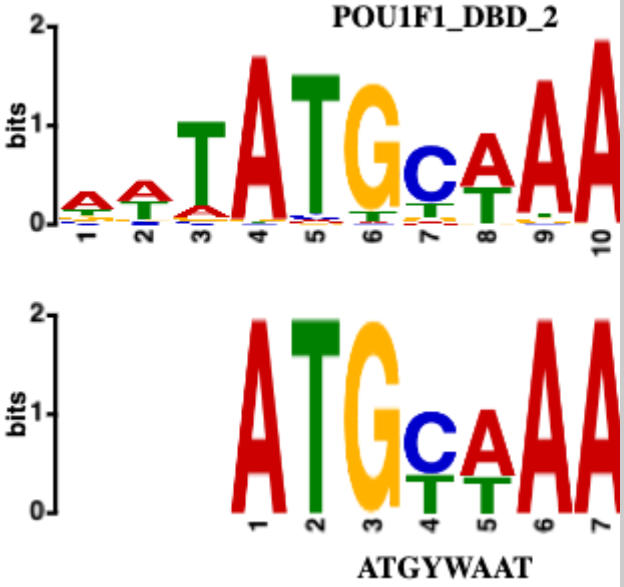
Optimal Alignment



Summary

Name	MA0784.1 (POU1F1)
Database	JASPAR2018_CORE_vertebrates_non-redundant
***p*-value**	3.59e-07
***E*-value**	6.49e-04
***q*-value**	1.08e-04
Overlap	8
Offset	3
Orientation	Normal

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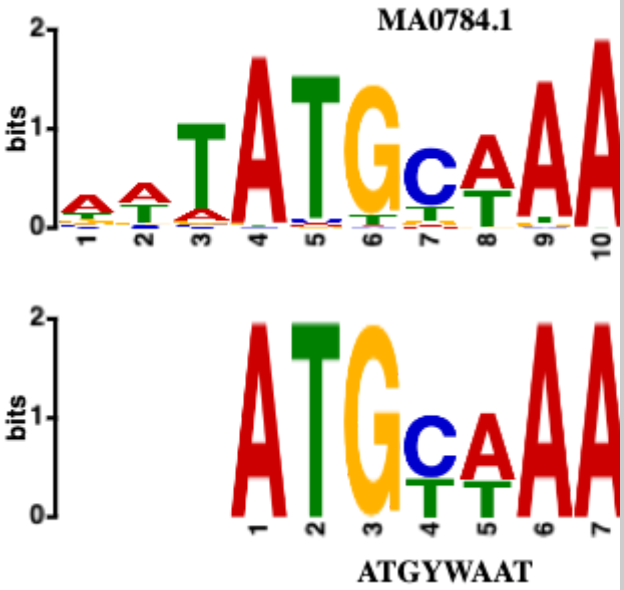
Optimal Alignment

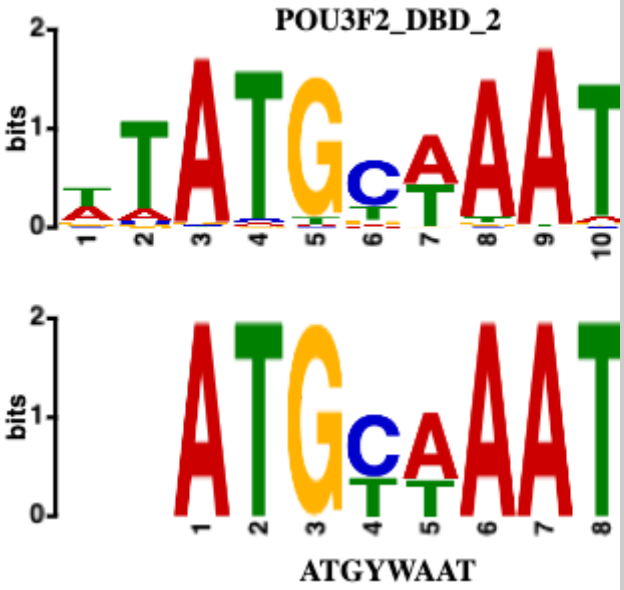


Summary

Name	POU3F2_DBD_2
Database	jolma2013
***p*-value**	5.46e-07
***E*-value**	9.88e-04
***q*-value**	1.41e-04
Overlap	8
Offset	2
Orientation	Normal

Show logo download options

Optimal Alignment

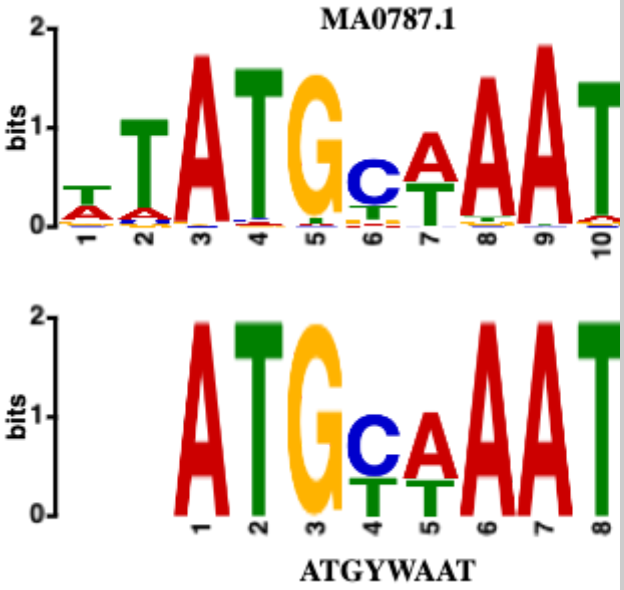


Summary

Name	MA0787.1 (POU3F2)
Database	JASPAR2018_CORE_vertebrates_non-redundant
***p*-value**	5.46e-07
***E*-value**	9.88e-04
***q*-value**	1.41e-04
Overlap	8
Offset	2
Orientation	Normal

Show logo download options

Optimal Alignment



Summary

Name	Pou2f2_DBD_2
Database	jolma2013
***p*-value**	1.73e-06
***E*-value**	3.14e-03
***q*-value**	4.17e-04
Overlap	8
Offset	1
Orientation	Normal

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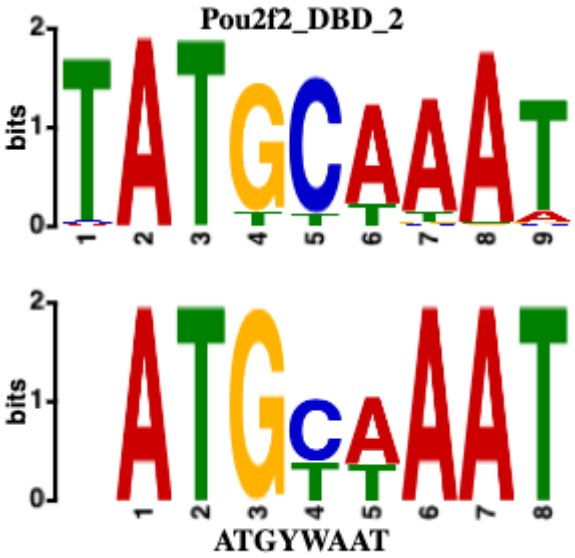
Optimal Alignment



Summary

Name	POU3F3_DBD_1
Database	jolma2013
***p*-value**	2.89e-06
***E*-value**	5.22e-03
***q*-value**	6.12e-04
Overlap	8
Offset	3
Orientation	Normal

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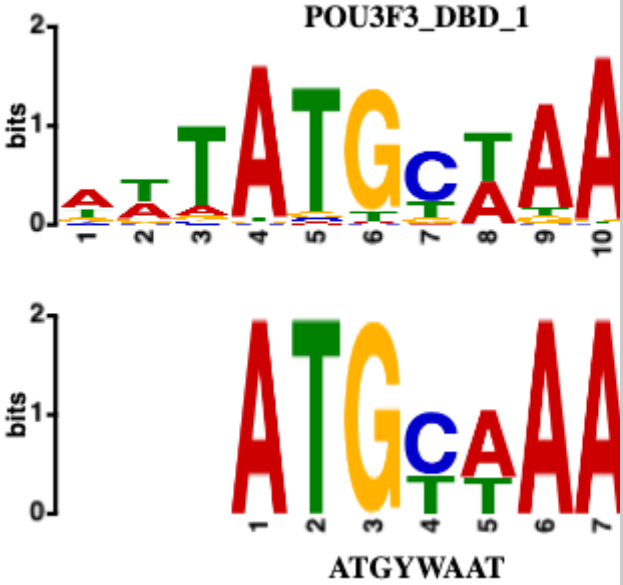
Optimal Alignment

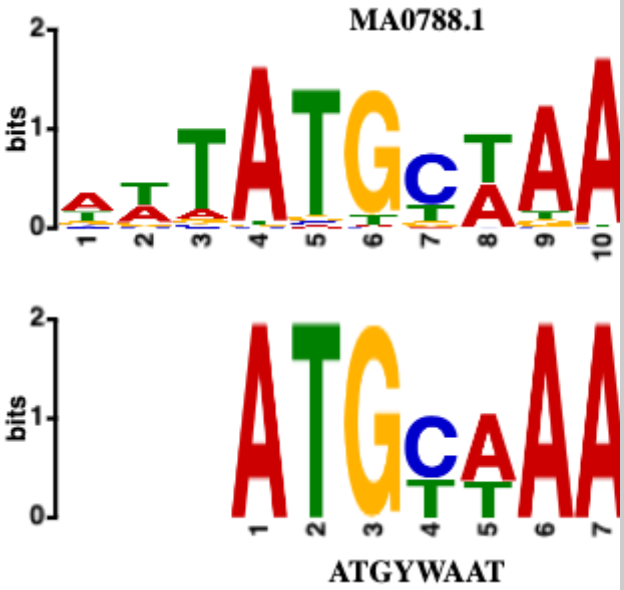


Summary

Name	MA0788.1 (POU3F3)
Database	JASPAR2018_CORE_vertebrates_non-redundant
***p*-value**	2.89e-06
***E*-value**	5.22e-03
***q*-value**	6.12e-04
Overlap	8
Offset	3
Orientation	Normal

Show logo download options

Optimal Alignment



Summary

Name	MA0627.1 (Pou2f3)
Database	JASPAR2018_CORE_vertebrates_non-redundant
***p*-value**	4.33e-06
***E*-value**	7.83e-03
***q*-value**	7.80e-04
Overlap	8
Offset	4
Orientation	Normal

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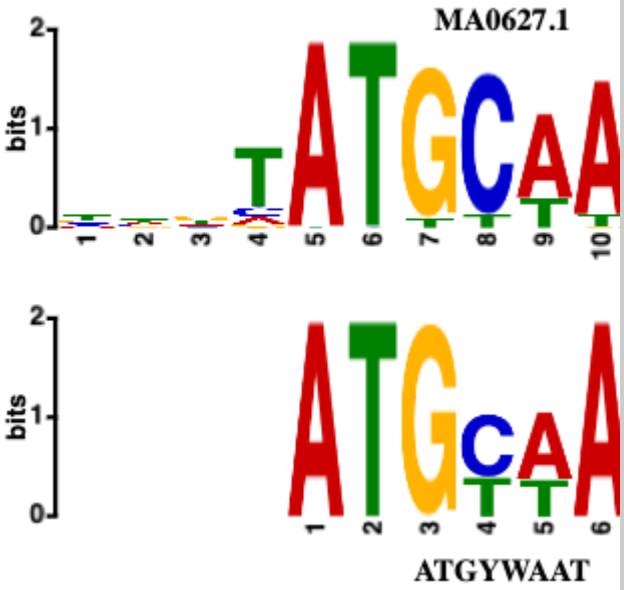
Optimal Alignment

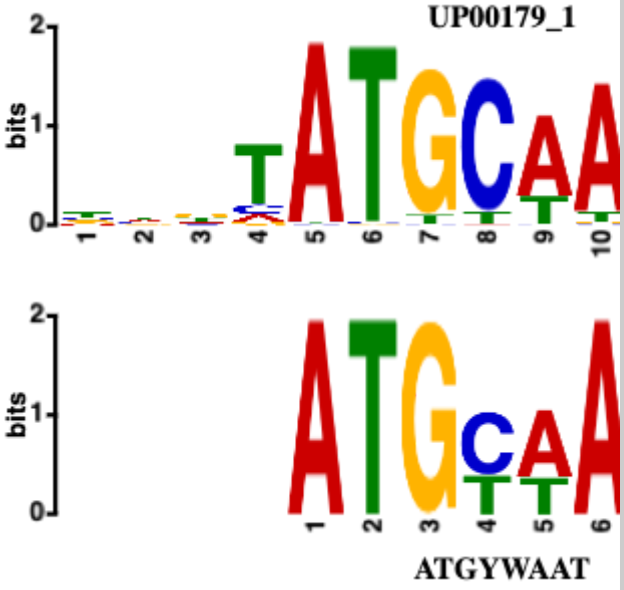


Summary

Name	UP00179_1 (Pou2f3_3986.2)
Database	uniprobe_mouse
***p*-value**	4.33e-06
***E*-value**	7.83e-03
***q*-value**	7.80e-04
Overlap	8
Offset	4
Orientation	Normal

Show logo download options

Optimal Alignment

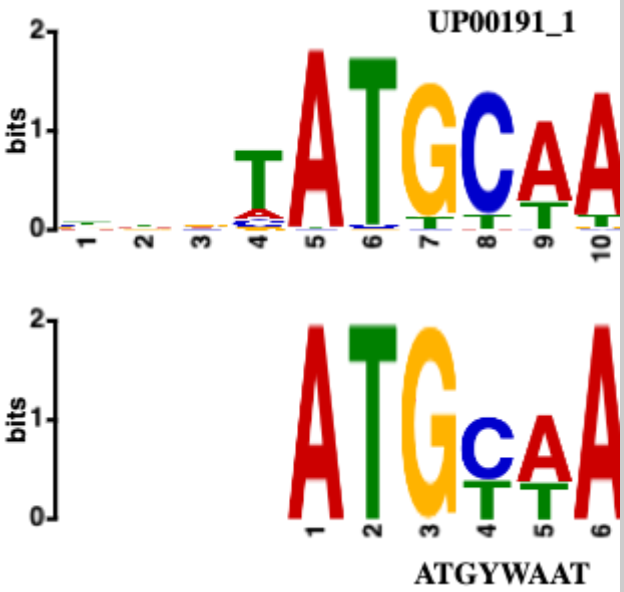


Summary

Name	UP00191_1 (Pou2f2_3748.1)
Database	uniprobe_mouse
***p*-value**	4.33e-06
***E*-value**	7.83e-03
***q*-value**	7.80e-04
Overlap	8
Offset	4
Orientation	Normal

Show logo download options

Optimal Alignment



Summary

Name	MA1115.1 (POU5F1)
Database	JASPAR2018_CORE_vertebrates_non-redundant
***p*-value**	5.63e-06
***E*-value**	1.02e-02
***q*-value**	9.67e-04
Overlap	8
Offset	2
Orientation	Normal

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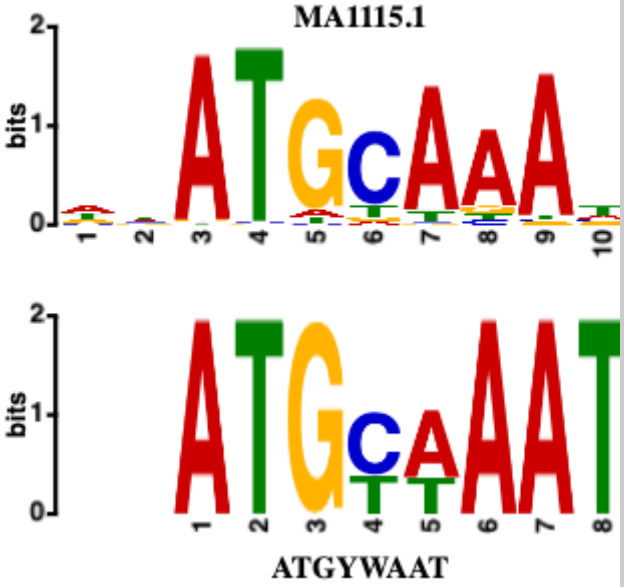
Optimal Alignment

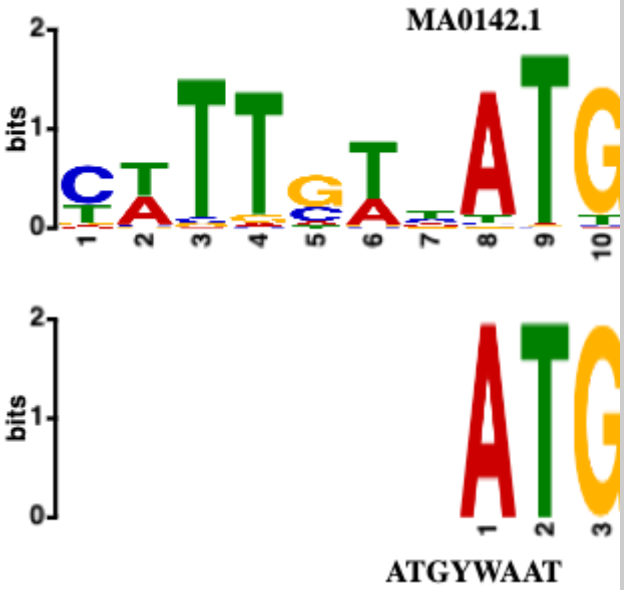


Summary

Name	MA0142.1 (Pou5f1::Sox2)
Database	JASPAR2018_CORE_vertebrates_non-redundant
***p*-value**	6.94e-06
***E*-value**	1.25e-02
***q*-value**	1.14e-03
Overlap	8
Offset	7
Orientation	Normal

Show logo download options

Optimal Alignment

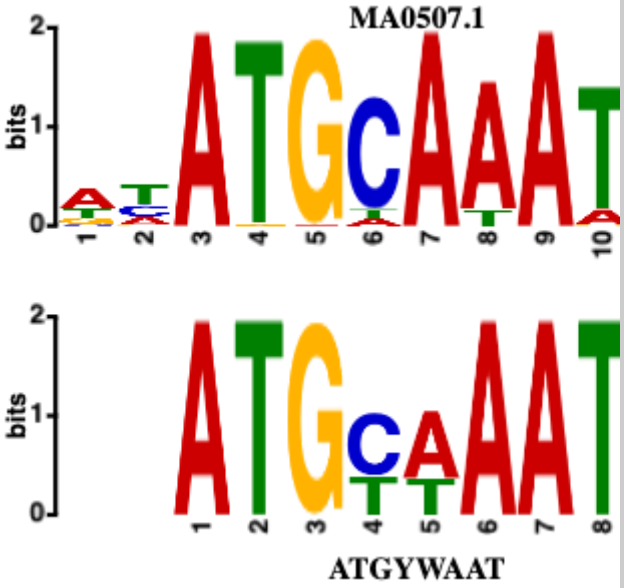


Summary

Name	MA0507.1 (POU2F2)
Database	JASPAR2018_CORE_vertebrates_non-redundant
***p*-value**	1.89e-05
***E*-value**	3.42e-02
***q*-value**	2.96e-03
Overlap	8
Offset	2
Orientation	Reverse Complement

Show logo download options

Optimal Alignment

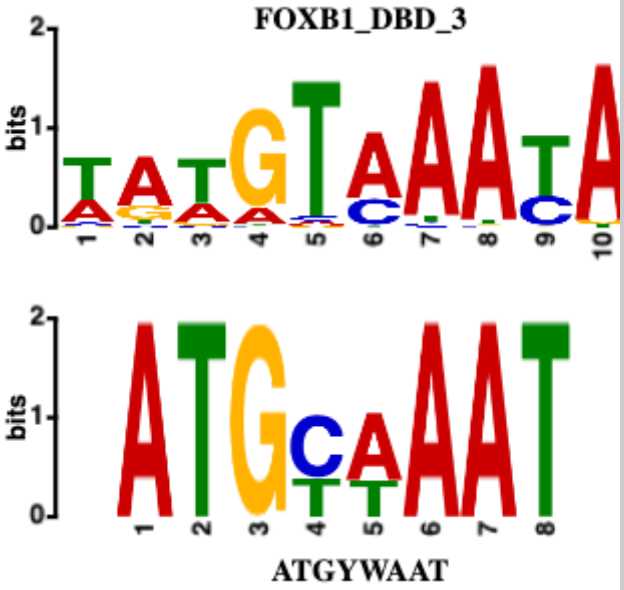


Summary

Name	FOXB1_DBD_3
Database	jolma2013
***p*-value**	6.42e-04
***E*-value**	1.16e+00
***q*-value**	9.25e-02
Overlap	8
Offset	1
Orientation	Normal

Show logo download options

Optimal Alignment

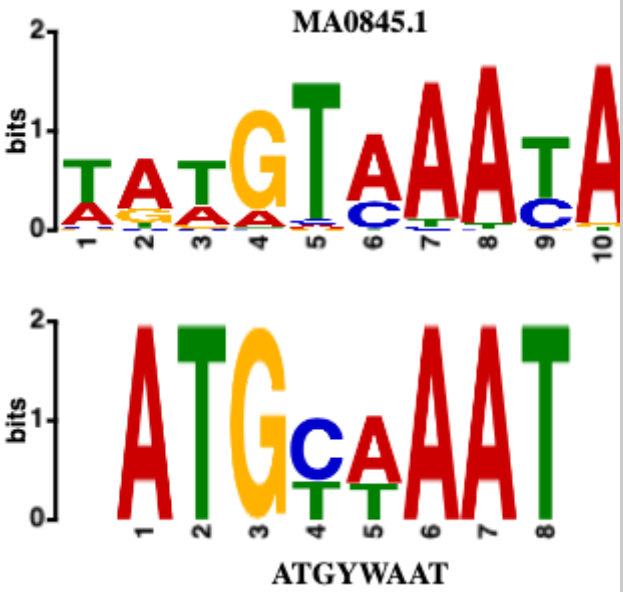


Summary

Name	MA0845.1 (FOXB1)
Database	JASPAR2018_CORE_vertebrates_non-redundant
***p*-value**	6.42e-04
***E*-value**	1.16e+00
***q*-value**	9.25e-02
Overlap	8
Offset	1
Orientation	Normal

Show logo download options

Optimal Alignment

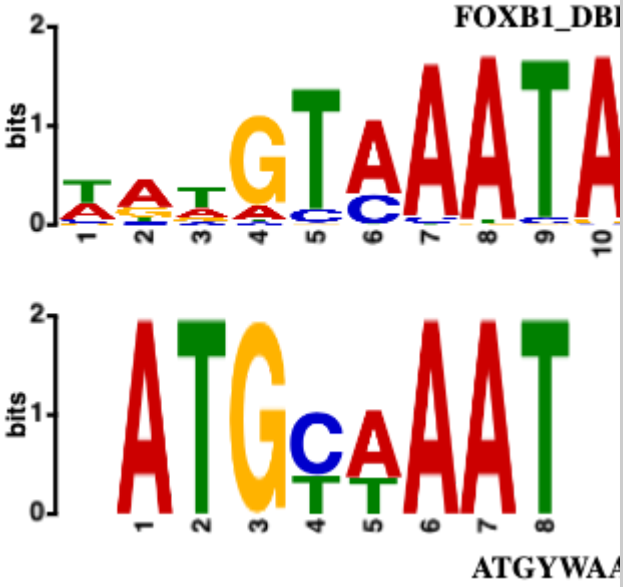


Summary

Name	FOXB1_DBD_2
Database	jolma2013
***p*-value**	9.75e-04
***E*-value**	1.76e+00
***q*-value**	1.35e-01
Overlap	8
Offset	1
Orientation	Normal

Show logo download options

Optimal Alignment

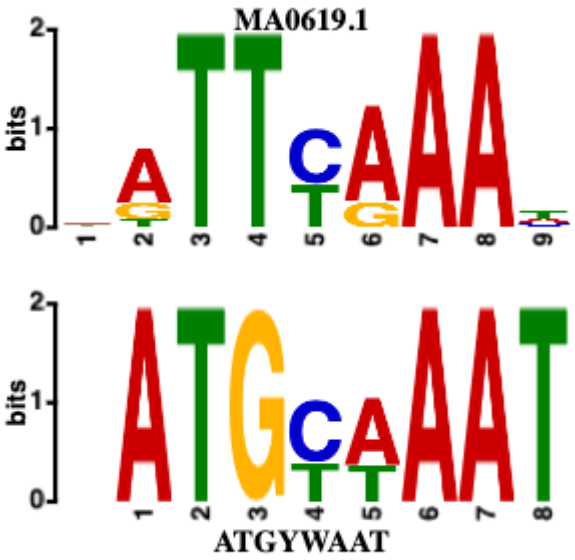


Summary

Name	MA0619.1 (LIN54)
Database	JASPAR2018_CORE_vertebrates_non-redundant
***p*-value**	1.55e-03
***E*-value**	2.80e+00
***q*-value**	2.07e-01
Overlap	8
Offset	1
Orientation	Reverse Complement

Show logo download options

Optimal Alignment

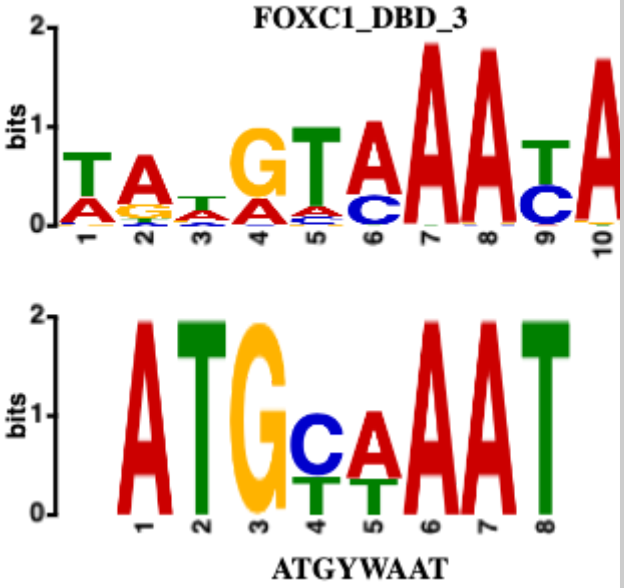


Summary

Name	FOXC1_DBD_3
Database	jolma2013
***p*-value**	2.23e-03
***E*-value**	4.03e+00
***q*-value**	2.77e-01
Overlap	8
Offset	1
Orientation	Normal

Show logo download options

Optimal Alignment

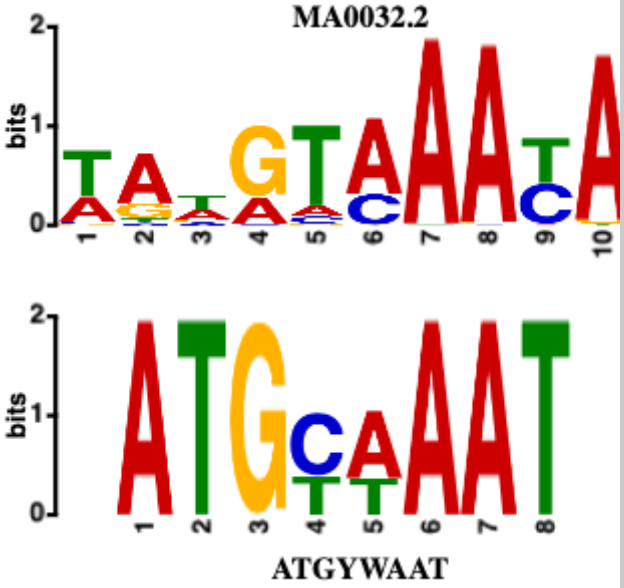


Summary

Name	MA0032.2 (FOXC1)
Database	JASPAR2018_CORE_vertebrates_non-redundant
***p*-value**	2.23e-03
***E*-value**	4.03e+00
***q*-value**	2.77e-01
Overlap	8
Offset	1
Orientation	Normal

Show logo download options

Optimal Alignment



Summary

Name	SOX18_full_2
Database	jolma2013
***p*-value**	3.21e-03
***E*-value**	5.81e+00
***q*-value**	3.86e-01
Overlap	8
Offset	4
Orientation	Reverse Complement

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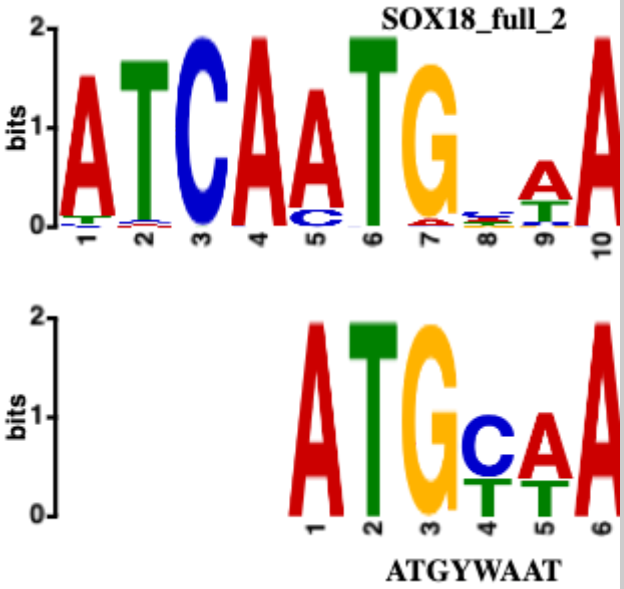
Optimal Alignment



Summary

Name	UP00236_1 (Irx2_0900.3)
Database	uniprobe_mouse
***p*-value**	4.00e-03
***E*-value**	7.24e+00
***q*-value**	4.65e-01
Overlap	8
Offset	7
Orientation	Normal

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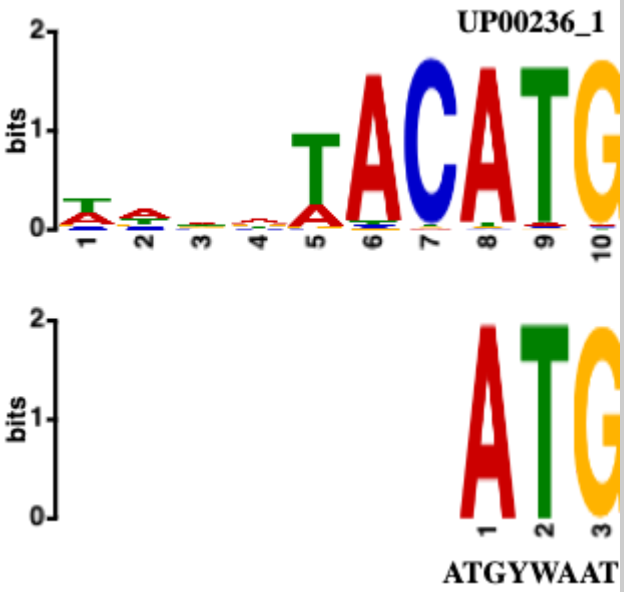
Optimal Alignment



SETTINGS

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Alphabet

Source: the query file

Name	Bg.				Bg.	Name
Adenine	0.243	A	~	T	0.243	Thymine
Cytosine	0.257	C	~	G	0.257	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 *E*-value of 10 or smaller.

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TOMTOM version
5.0.5 (Release date: Mon Mar 18 20:12:19 2019 -0700)

Reference
Shobhit Gupta, JA Stamatoyannopolous, Timothy Bailey and William Stafford Noble, "Quantifying similarity between motifs", *Genome Biology*, **8**(2):R24, 2007.

Command line

```
tomtom -no-ssc -oc . -verbosity 1 -min-overlap 5 -mi 1 -dist pearson -evalue -thresh 10.0 query_motifs
```

Result calculation took 1.536 seconds