



For further information on how to interpret these results or to get a copy of the MEME software please access <http://meme.nbcr.net>.

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](#)

QUERY MOTIFS

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

Database	ID	Alt. I
newseq.E081.motif of interest	pattern/Type1/motif_visualization/pwm_Motif_0.feather	pattern/Type1/motif_visualizat
newseq.E081.motif of interest	pattern/Type1/motif_visualization/pwm_Motif_125.feather	pattern/Type1/motif_visualizat
newseq.E081.motif of interest	pattern/Type1/motif_visualization/pwm_Motif_143.feather	pattern/Type1/motif_visualizat
newseq.E081.motif of interest	pattern/Type1/motif_visualization/pwm_Motif_154.feather	pattern/Type1/motif_visualizat
newseq.E081.motif of interest	pattern/Type1/motif_visualization/pwm_Motif_278.feather	pattern/Type1/motif_visualizat

TARGET DATABASES

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

Database	Used	Matched
Homo sapiens	733	3

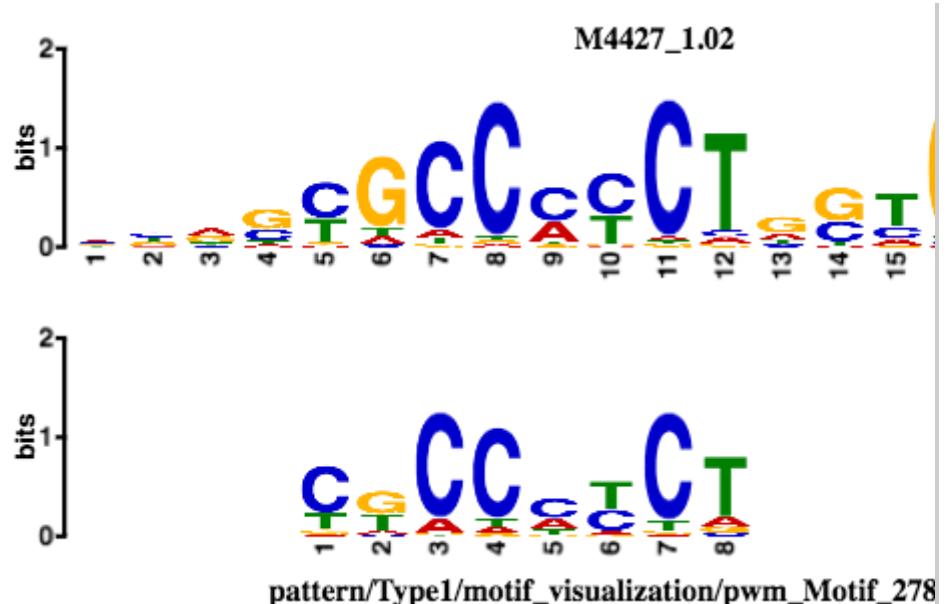
MATCHES TO PATTERN/TYPE1/MOTIF_VISUALIZATION/PWM_MOTIF_278.FEATHER

(PATTERN/TYPE1/MOTIF_VISUALIZATION/PWM_MOTIF_278.FEATHER)

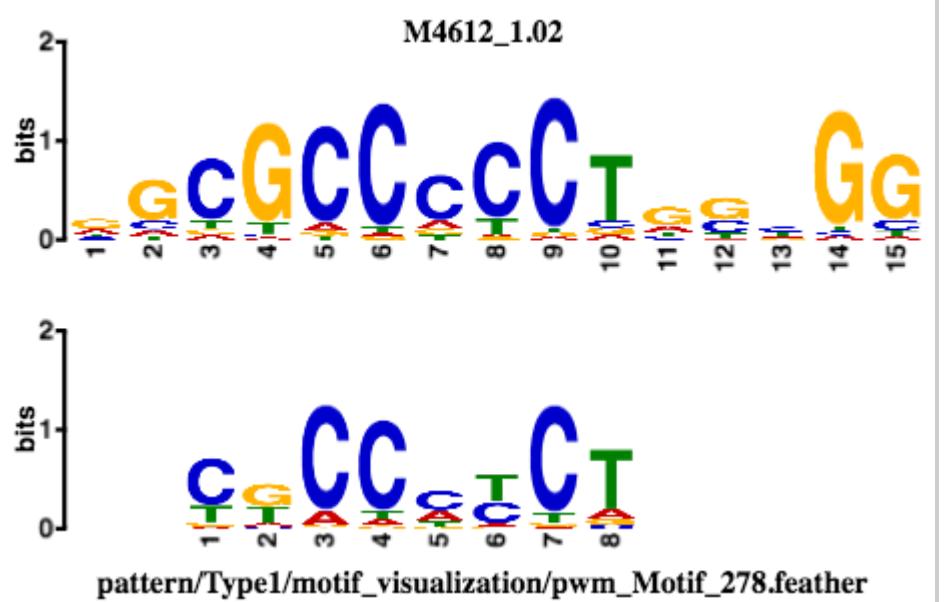
[Previous](#) [Next](#) [Top](#)

Summary	Alignment
Name	M4427_1.02 (CTCF)
Database	Homo sapiens
p-value	1.57e-06

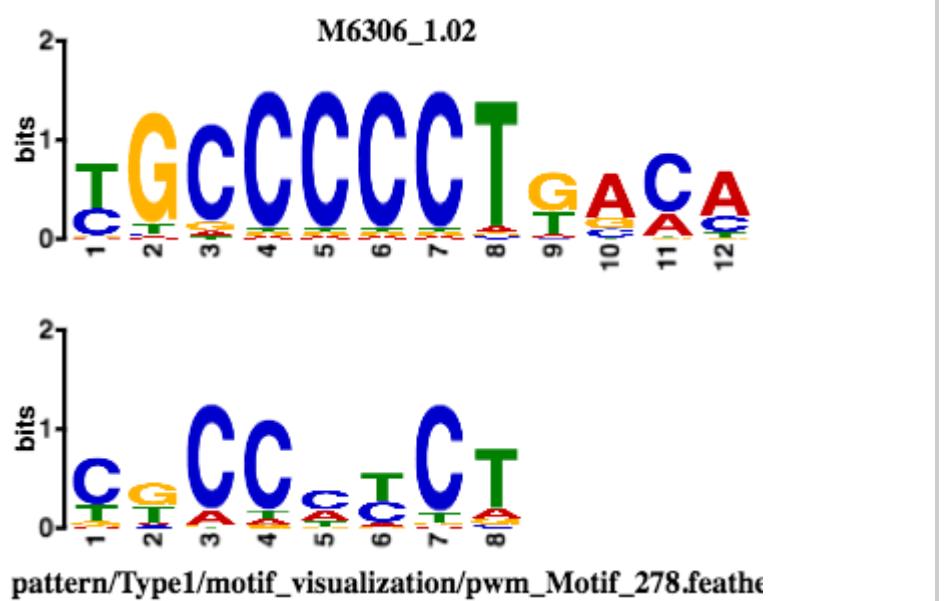
E-value	1.15e-03
q-value	2.28e-03
Overlap	8
Offset	4
Orientation	Reverse Complement

[Show logo download options](#)**Summary****Alignment**

Name	M4612_1.02 (CTCF)
Database	Homo sapiens
p-value	2.56e-05
E-value	1.88e-02
q-value	1.86e-02
Overlap	8
Offset	2
Orientation	Reverse Complement

[Show logo download options](#)**Summary****Alignment**

Name	M6306_1.02 (INSM1)
Database	Homo sapiens
p-value	1.83e-04
E-value	1.34e-01
q-value	8.85e-02
Overlap	8
Offset	0
Orientation	Reverse Complement

[Show logo download options](#)

SETTINGS[Previous](#) [Next](#) [Top](#)**Background**

Name	Bg.		Bg.	Name
Adenine	0.250	A	~	T
Cytosine	0.250	C	~	G

0.250 Thymine
0.250 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 q-value of 0.1 or smaller.

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

4.11.4 (Release date: Thu May 18 17:37:13 2017 -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 -dist pearson -thresh 0.1 newseq.E081.motif_of_interest.meme db/CIS-
```

Result calculation took 1.611 seconds

