



For further information on how to interpret these results or to get a copy of the MEME software please access <http://meme.nbcrc.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. [\[full text\]](#)

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QUERY MOTIFS

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| Database | ID | Alt. |
|---------------------------------|---|-----------------------------|
| newseq.Noonan.motif of interest | pattern/Type1/motif_visualization/pwm_Motif_125.feather | pattern/Type1/motif_visuali |
| newseq.Noonan.motif of interest | pattern/Type1/motif_visualization/pwm_Motif_133.feather | pattern/Type1/motif_visuali |
| newseq.Noonan.motif of interest | pattern/Type1/motif_visualization/pwm_Motif_143.feather | pattern/Type1/motif_visuali |
| newseq.Noonan.motif of interest | pattern/Type1/motif_visualization/pwm_Motif_154.feather | pattern/Type1/motif_visuali |
| newseq.Noonan.motif of interest | pattern/Type1/motif_visualization/pwm_Motif_168.feather | pattern/Type1/motif_visuali |
| newseq.Noonan.motif of interest | pattern/Type1/motif_visualization/pwm_Motif_214.feather | pattern/Type1/motif_visuali |
| newseq.Noonan.motif of interest | pattern/Type1/motif_visualization/pwm_Motif_22.feather | pattern/Type1/motif_visuali |
| newseq.Noonan.motif of interest | pattern/Type1/motif_visualization/pwm_Motif_222.feather | pattern/Type1/motif_visuali |
| newseq.Noonan.motif of interest | pattern/Type1/motif_visualization/pwm_Motif_278.feather | pattern/Type1/motif_visuali |
| newseq.Noonan.motif of interest | pattern/Type1/motif_visualization/pwm_Motif_6.feather | pattern/Type1/motif_visuali |

| Database | ID | Alt. |
|---------------------------------|--|-----------------------------|
| newseq.Noonan.motif of interest | pattern/Type1/motif_visualization/pwm_Motif_9.feather | pattern/Type1/motif_visuali |
| newseq.Noonan.motif of interest | pattern/Type1/motif_visualization/pwm_Motif_99.feather | pattern/Type1/motif_visuali |

TARGET DATABASES

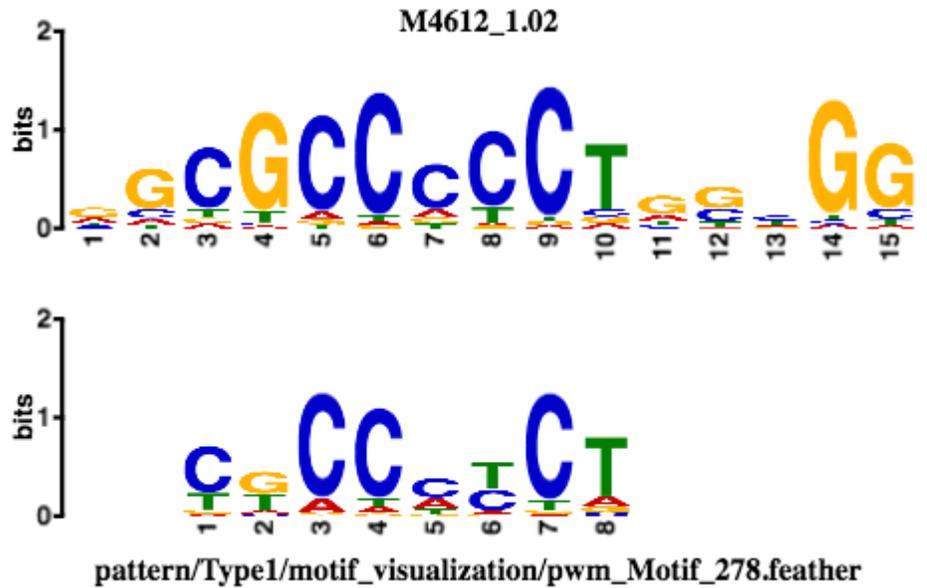
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| Database | Used | Matched |
|--------------|------|---------|
| Homo sapiens | 733 | 5 |

MATCHES TO PATTERN/TYPE1/MOTIF_VISUALIZATION/PWM_MOTIF_278.FEATHER (PATTERN/TYPE1/MOTIF_VISUALIZATION/PWM_MOTIF_278.FEATHER)

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| Summary | Alignment |
|--|--|
| <p>Name M4427_1.02 (CTCF)</p> <p>Database Homo sapiens</p> <p>p-value 1.57e-06</p> <p>E-value 1.15e-03</p> <p>q-value 2.28e-03</p> <p>Overlap 8</p> <p>Offset 4</p> <p>Orientation Reverse Complement</p> <p>Show logo download options</p> | <p>M4427_1.02</p> <p>bits</p> <p>1 2 3 4 5 6 7 8 9 10 11 12 13 14 15</p> <p>bits</p> <p>1 2 3 4 5 6 7 8</p> <p>pattern/Type1/motif_visualization/pwm_Motif_278</p> |
| Summary | Alignment |
| <p>Name M4612_1.02 (CTCFL)</p> <p>Database Homo sapiens</p> <p>p-value 2.56e-05</p> <p>E-value 1.88e-02</p> <p>q-value 1.86e-02</p> <p>Overlap 8</p> <p>Offset 2</p> <p>Orientation Reverse Complement</p> <p>Show logo download options</p> | |

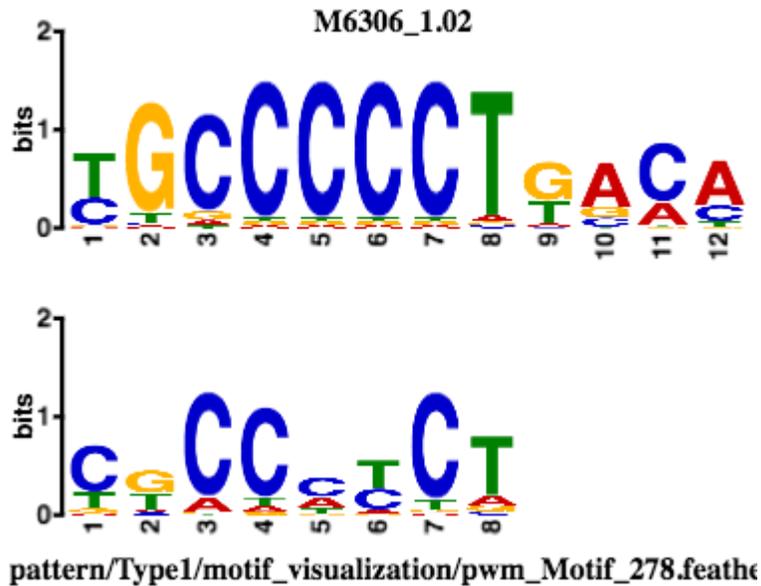


Summary

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 |

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MATCHES TO PATTERN/TYPE1/MOTIF_VISUALIZATION/PWM_MOTIF_6.FEATHER (PATTERN/TYPE1/MOTIF_VISUALIZATION/PWM_MOTIF_6.FEATHER)

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Summary

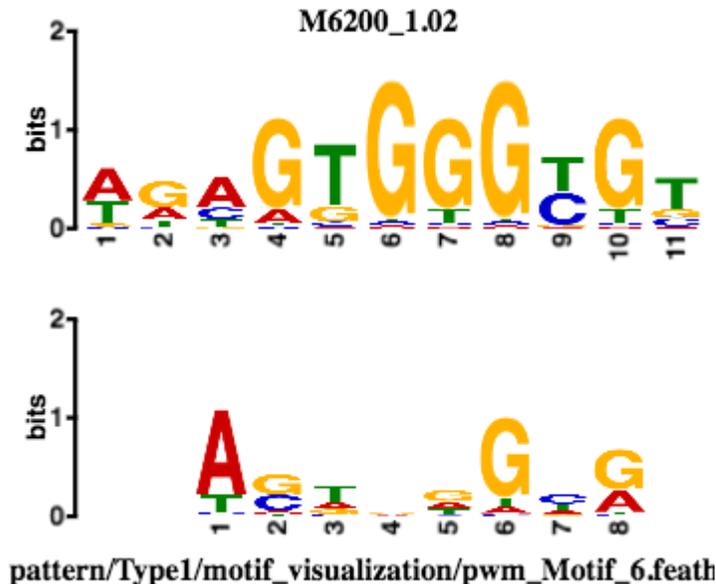
Alignment

| | |
|-----------------|-----------------------------------|
| Name | M6200_1.02 (EGR3) |
| Database | Homo sapiens |
| p-value | 3.02e-05 |
| E-value | 2.21e-02 |
| q-value | 4.42e-02 |
| Overlap | 8 |
| Offset | 2 |



Orientation Normal

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**MATCHES TO PATTERN/TYPE1/MOTIF_VISUALIZATION/PWM_MOTIF_9.FEATHER
(PATTERN/TYPE1/MOTIF_VISUALIZATION/PWM_MOTIF_9.FEATHER)**

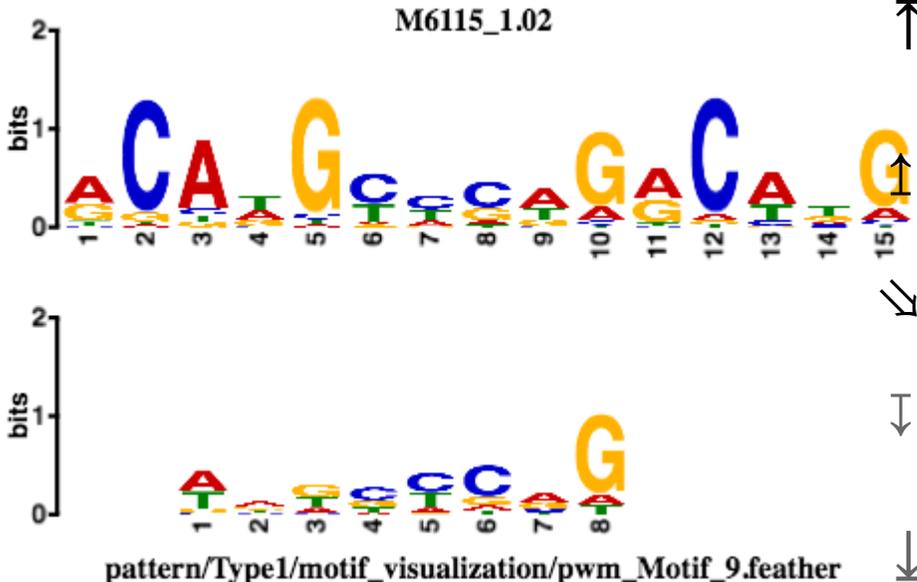
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Summary

Alignment

| | |
|--------------------|-----------------------------------|
| Name | M6115_1.02 (TP73) |
| Database | Homo sapiens |
| p-value | 6.00e-05 |
| E-value | 4.40e-02 |
| q-value | 8.79e-02 |
| Overlap | 8 |
| Offset | 2 |
| Orientation | Reverse Complement |

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SETTINGS

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Background

| Name | Bg. | | | Bg. | Name |
|----------|-------|---|---|-----|---------|
| Adenine | 0.250 | A | ~ | T | Thymine |
| Cytosine | 0.250 | 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 q-value of 0.1 or smaller.

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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.Noonan.motif_of_interest.meme db/CIS-
```

Result calculation took 3.502 seconds