

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 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 | RESULTS IN XML FORMAT

QUERY MOTIFS

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Database	ID	Alt. ID	Preview	Matches	List
meme.xml	GCTGGGATTACAGGC	MEME-3	¹] <mark>GCTGG</mark> &A _# ŢAçAGGC	1	PITX2 HUMAN.H11MO.0.D
meme.xml	GGGHGGCSGMGGSGG	MEME-2	j ggg_ggg	25	TBX15 HUMAN.H11MO.0.D, VEZF1 HUMAN.H11MO.0.C, SP1 HUMAN.H11MO.1.A
meme.xml	пппкпппп	MEME-1	֓֞֞֞֞֞֞֞֞֞֞֞֞֞֞֞֞֞֞֞֓֓֞֞֞֞֞֞֞֓֓֓֞֞֞֞֞֞֞	13	CPEB1 HUMAN.H11MO.0.D, PRDM6 HUMAN.H11MO.0.C, FOXJ3 HUMAN.H11MO.0.A, ANDR HUMAN.H11MO.0.A,

TARGET DATABASES

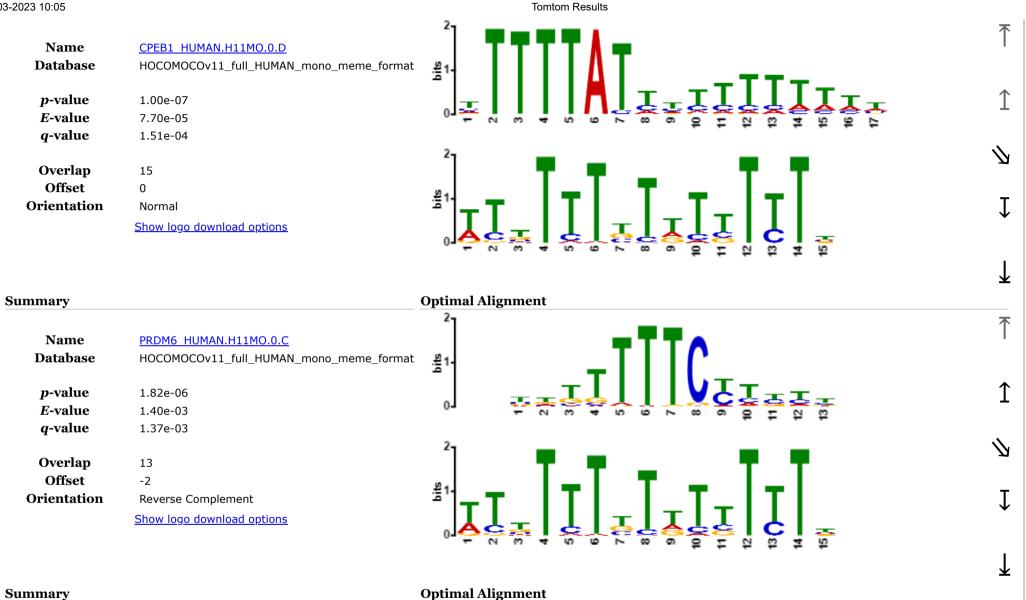
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Database	Used	Matched
HOCOMOCOv11_full_HUMAN_mono_meme_format	769	39

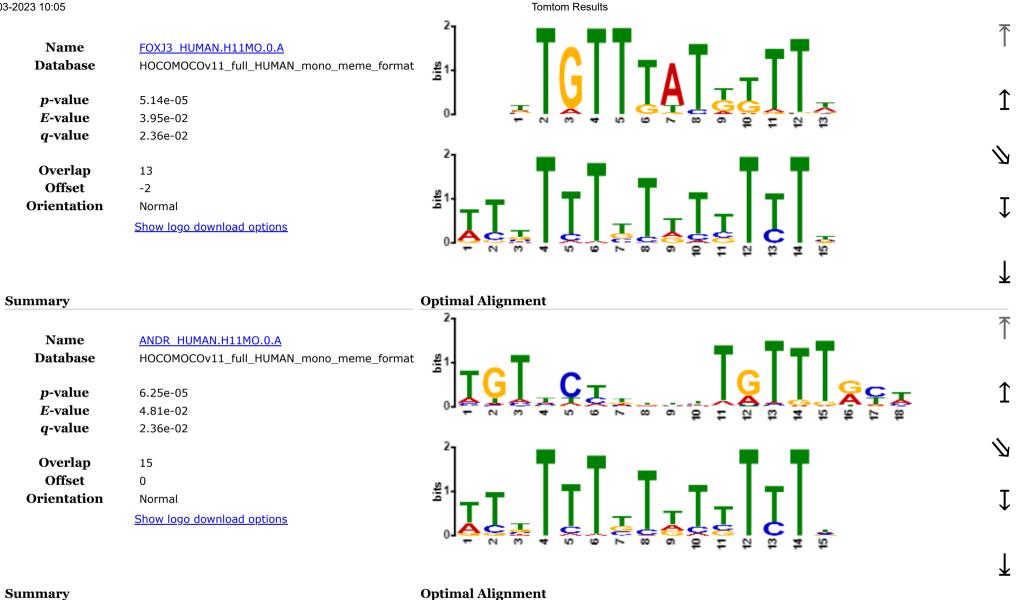
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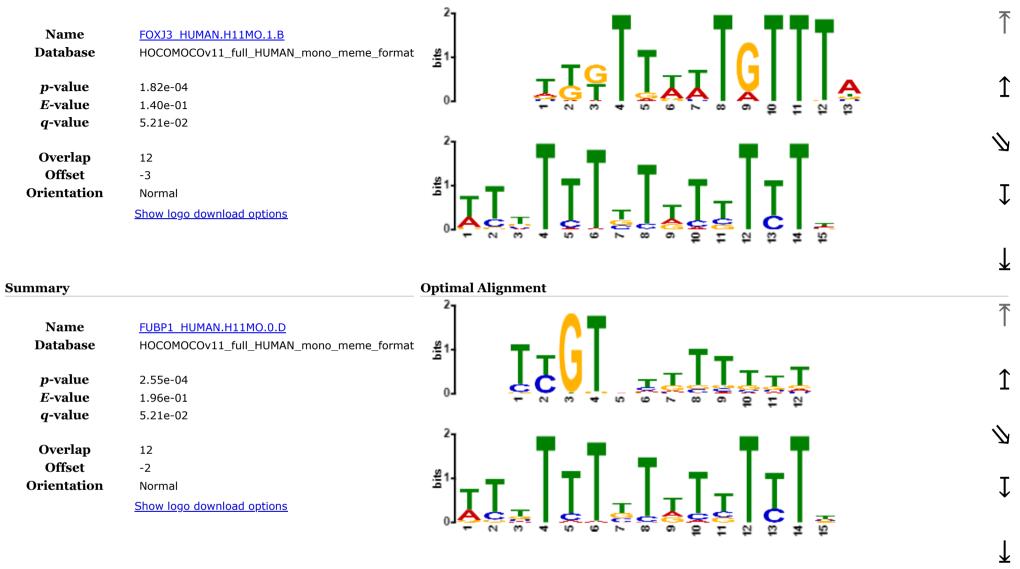
Summary	Optimal Alignment	

03-03-2023 10:05



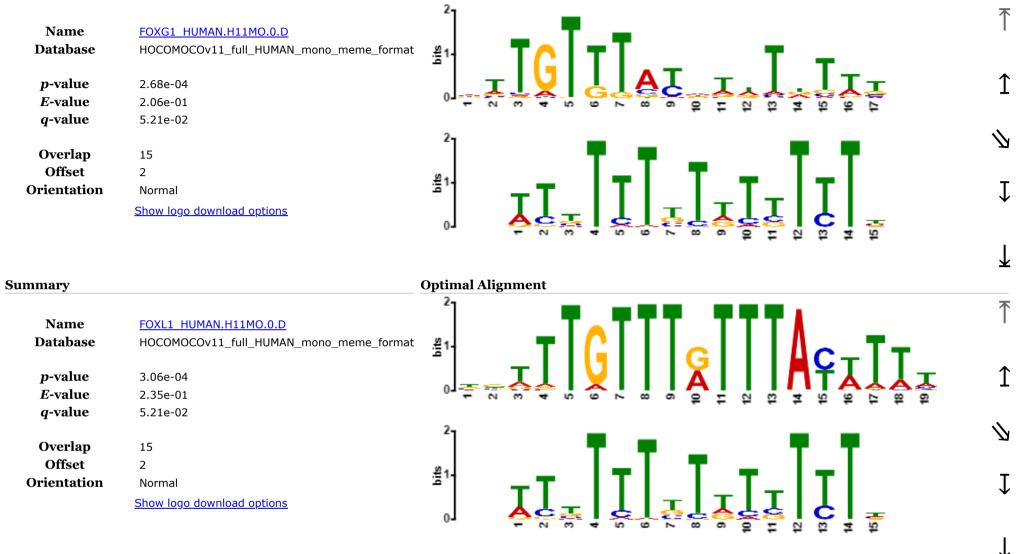
03-03-2023 10:05





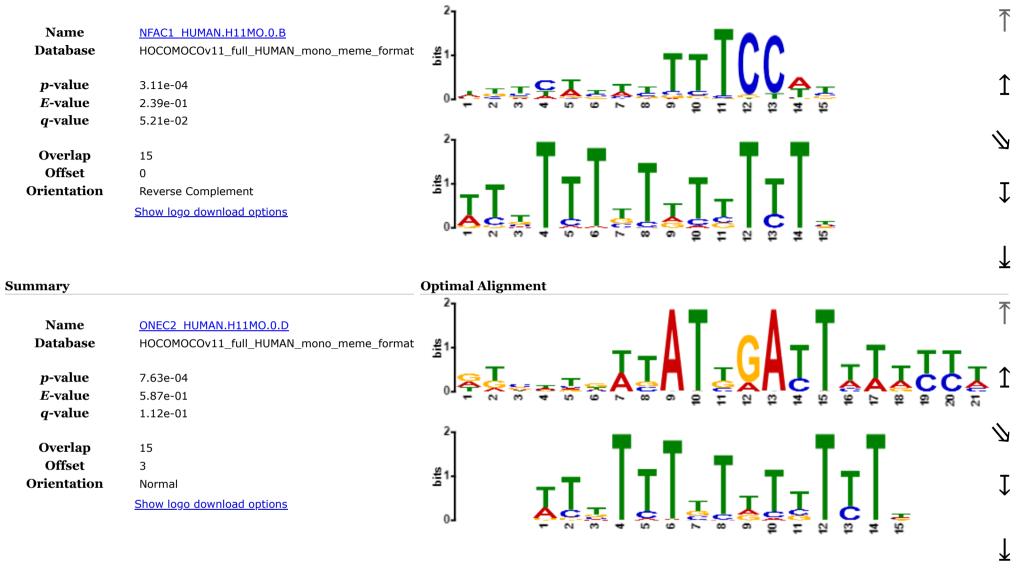
Optimal Alignment

03-03-2023 10:05

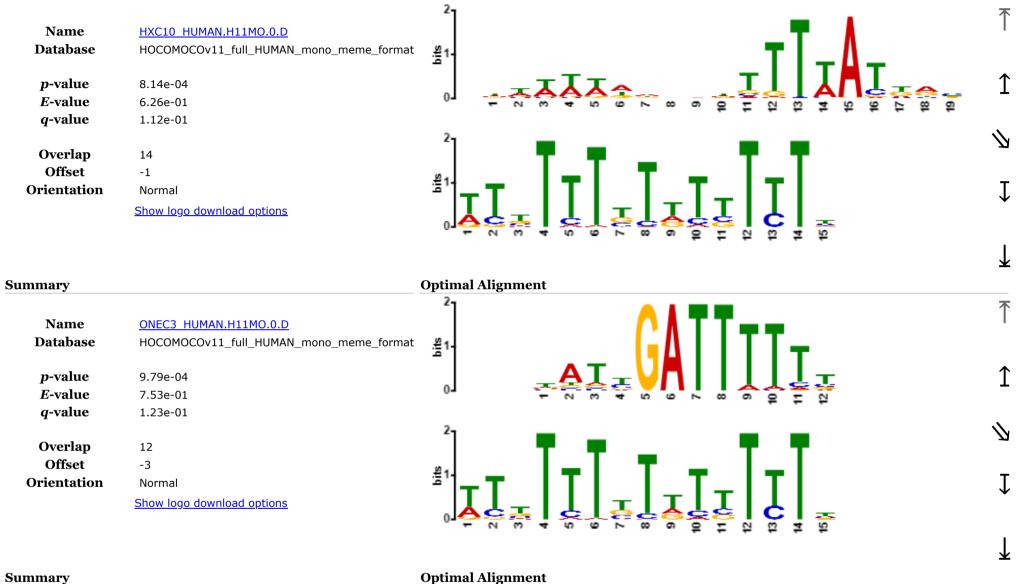


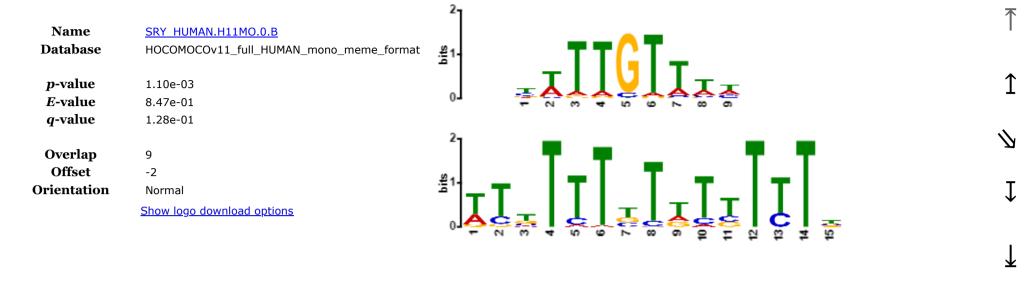
Optimal Alignment

Tomtom Results



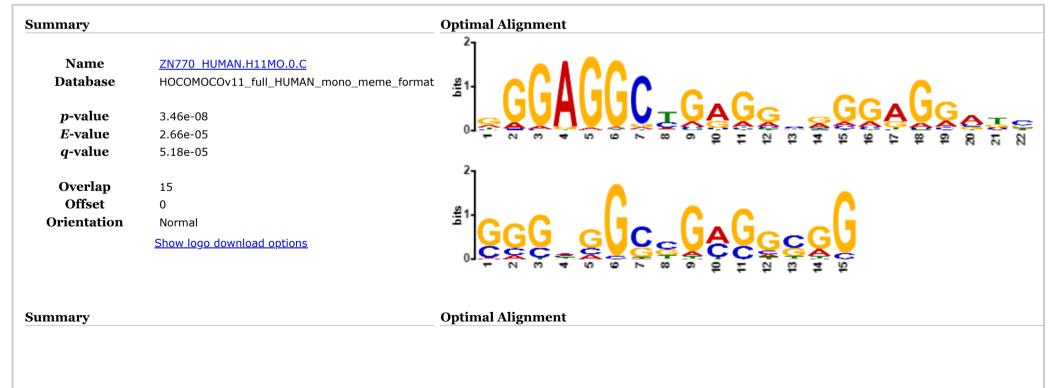
Optimal Alignment

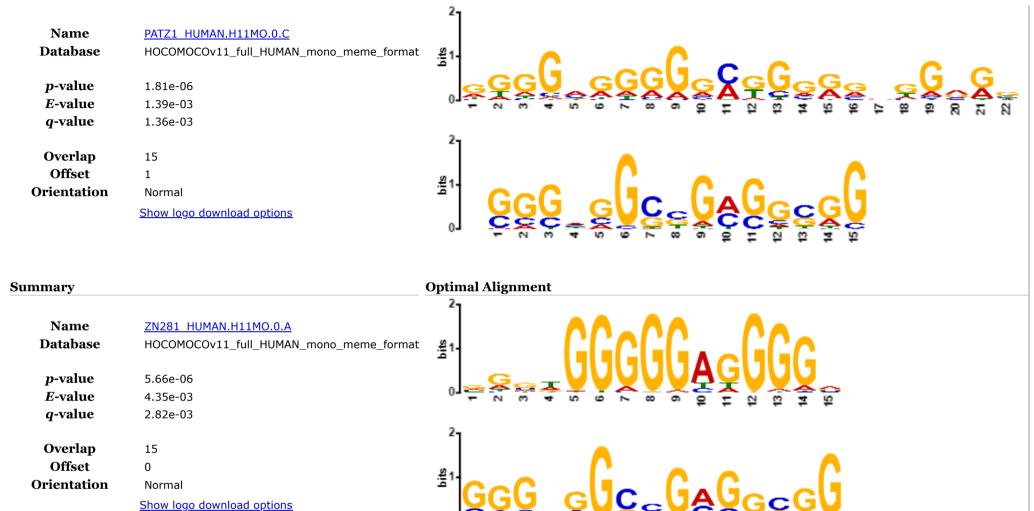


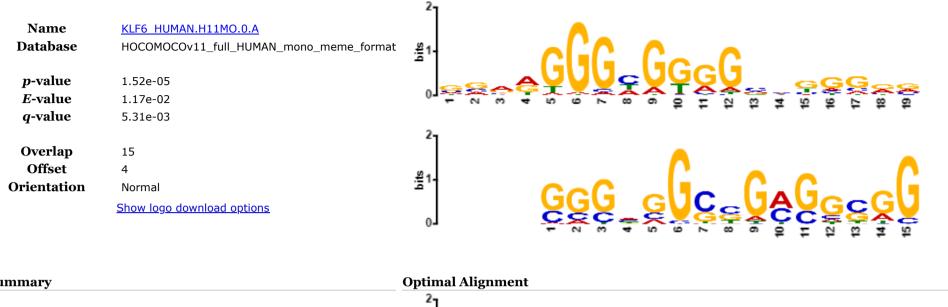


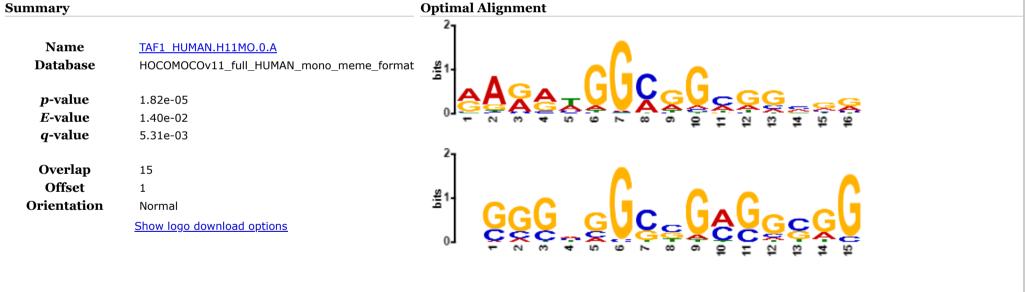
MATCHES TO GGGHGGCSGMGGSGG (MEME-2)

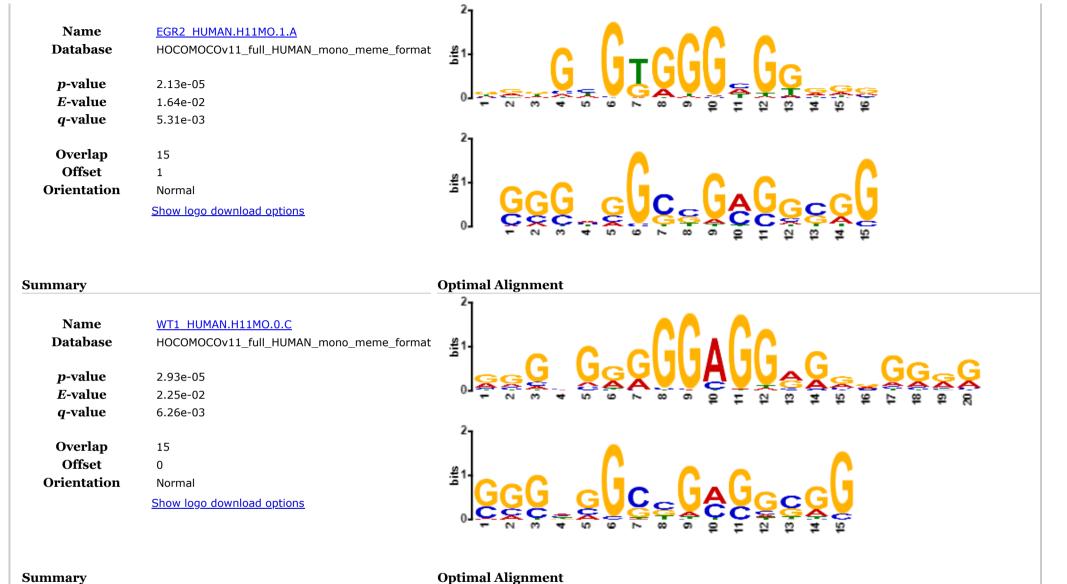
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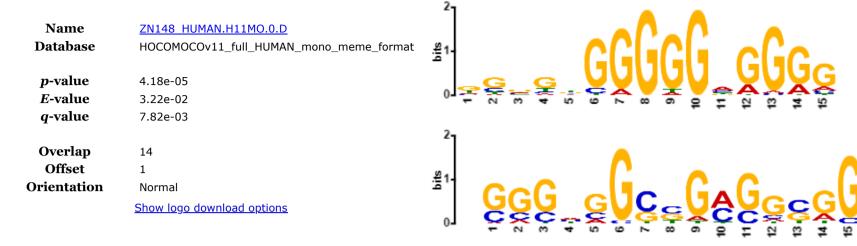












Summary	Optimal Alignment
·	

Name	ZN770 HUMAN.H11MO.1.C
Database	${\tt HOCOMOCOv11_full_HUMAN_mono_meme_format}$
<i>p</i> -value	4.95e-05

 p-value
 4.95e-05

 E-value
 3.81e-02

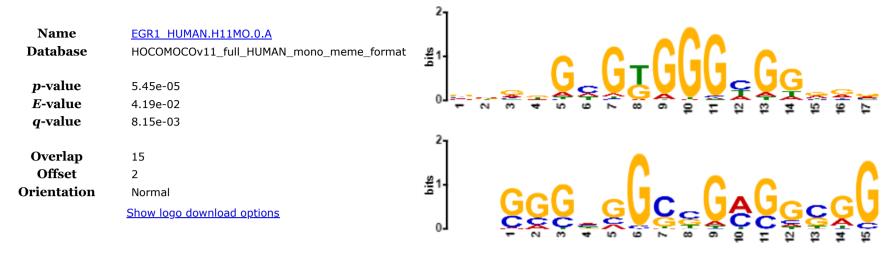
 q-value
 8.15e-03

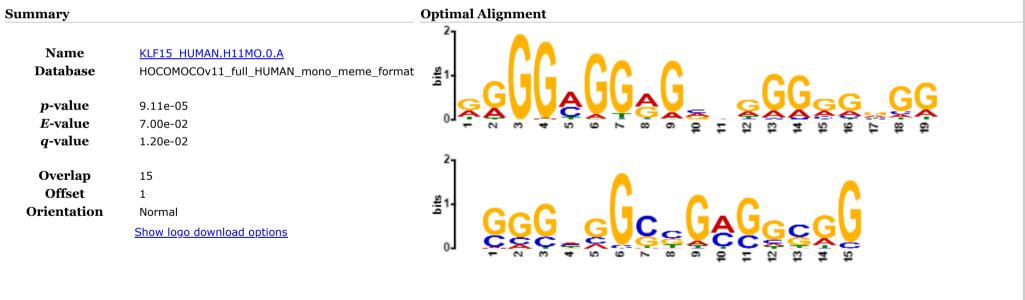
Overlap 11
Offset 0
Orientation Normal

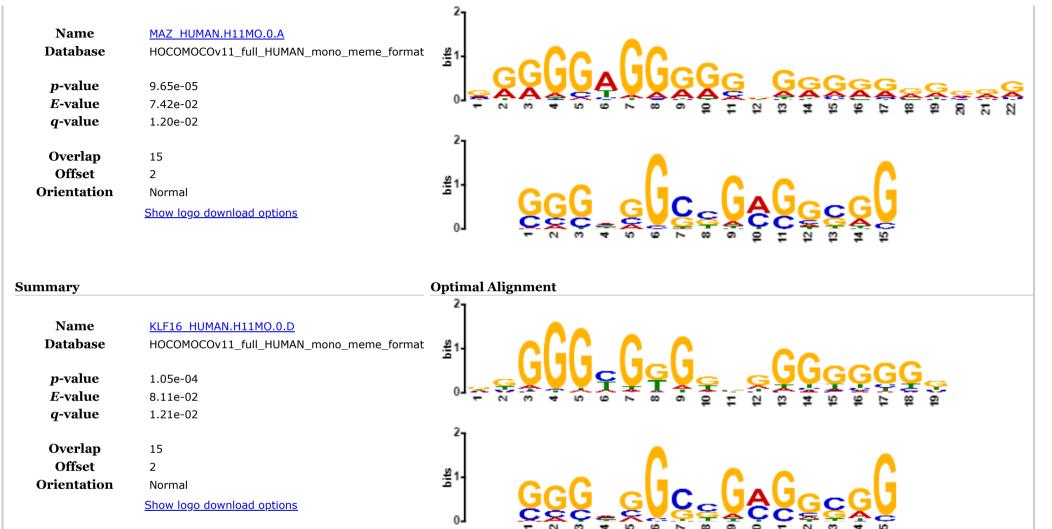
Show logo download options

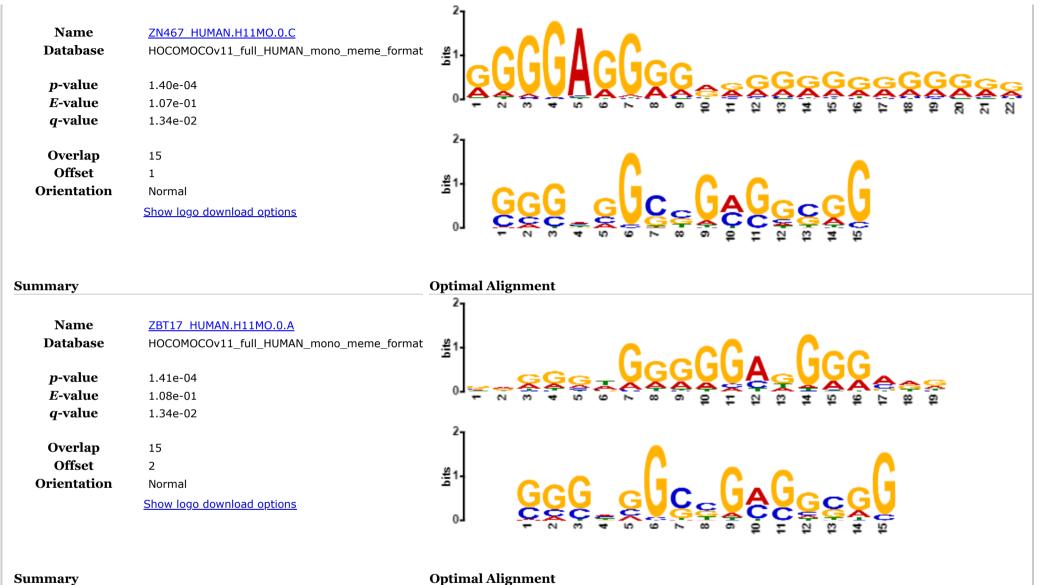


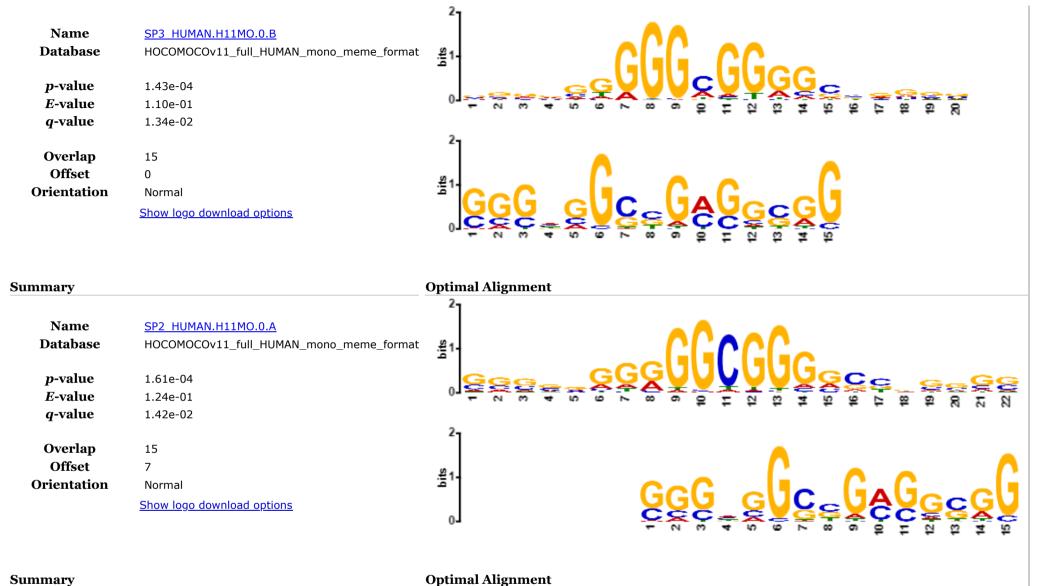


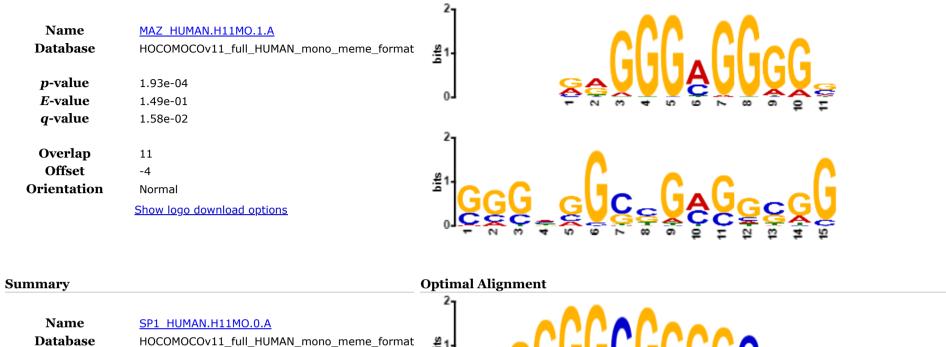


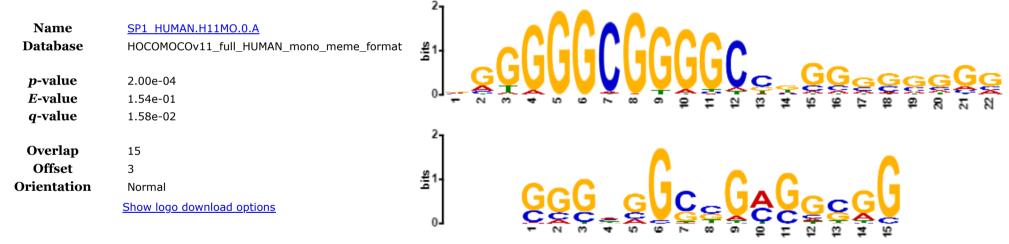


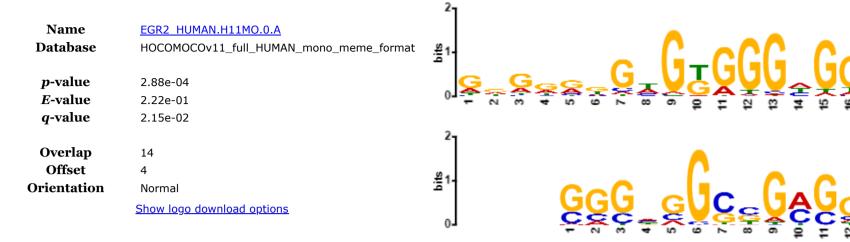












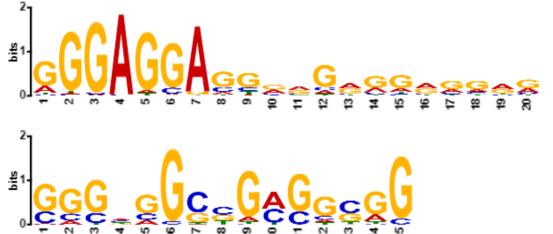
Name ZN263 HUMAN.H11MO.0.A Optimal Alignment

Database HOCOMOCOv11_full_HUMAN_mono_meme_format

p-value3.11e-04E-value2.39e-01q-value2.18e-02

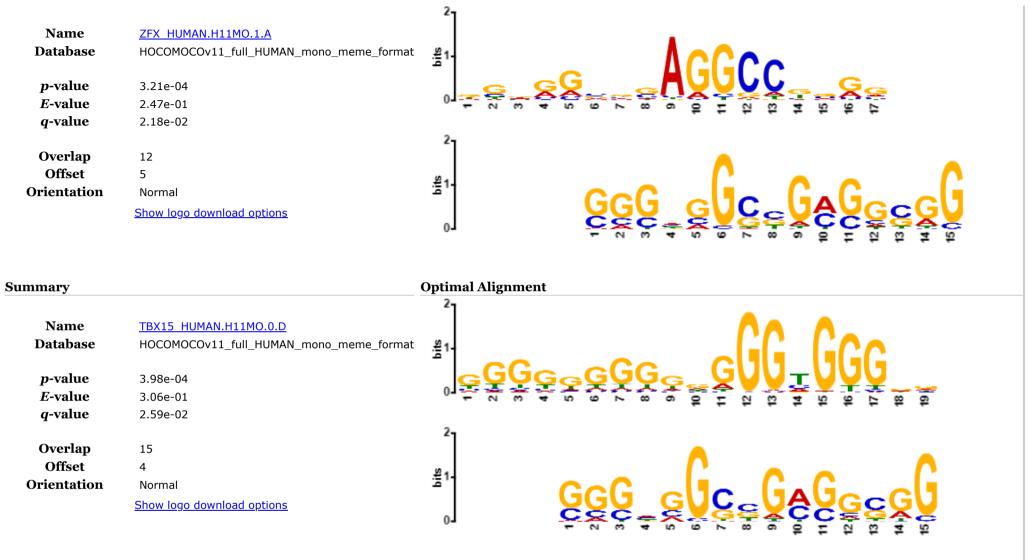
Overlap 15
Offset 0
Orientation Normal

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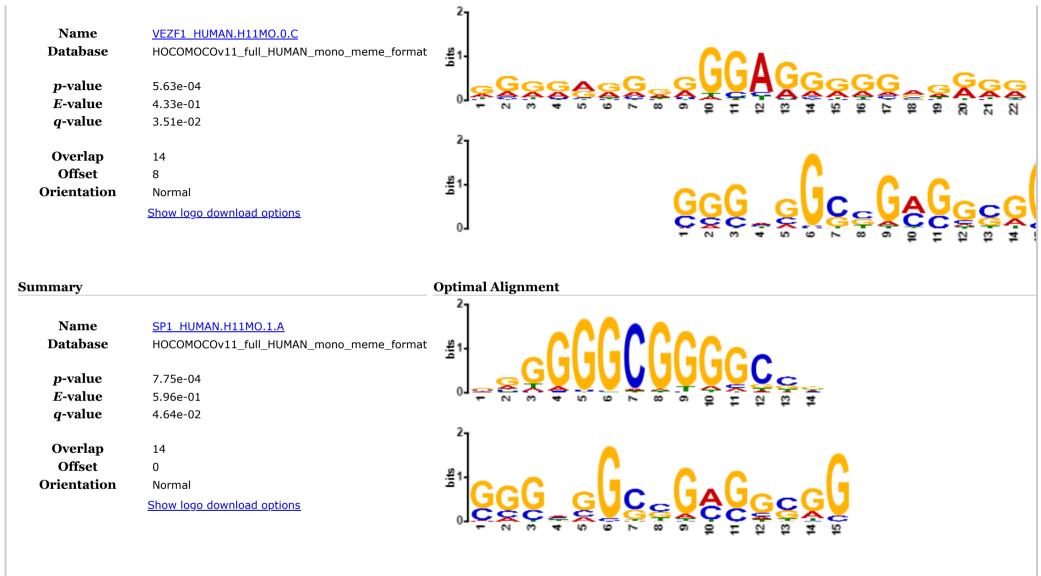


Summary

Optimal Alignment

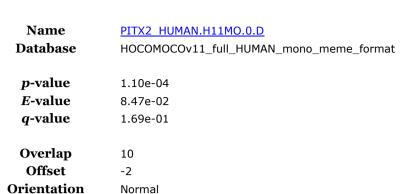


Optimal Alignment

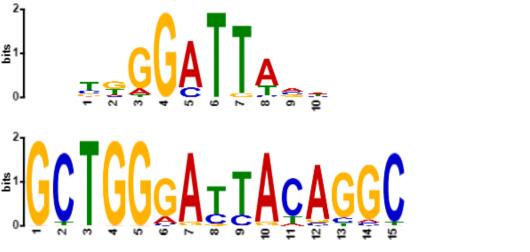


MATCHES TO GCTGGGATTACAGGC (MEME-3)

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SETTINGS Previous Next Top

Alphabet

Source: the query file

 Name
 Bg.
 Bg.
 Name

 Adenine
 0.267
 A
 ~
 T
 0.267
 Thymine

 Cytosine
 0.233
 C
 ~
 G
 0.233
 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 1 or smaller.

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Tomtom version

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

Reference

Shobhit 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 -evalue -thresh 1 -no-ssc meme_out/meme.xml

Result calculation took 4.397 seconds