

TFSEARCH: This website searches input sequences with pre-computed weighted matrices of known transcription factors.

URL: http://biogrid-head.engr.uconn.edu/lasagna_search/

TF Model Input

Matrix-Derived Models: Enter matrix Use TRANSFAC Matrices Use JASPAR CORE Matrices Use UniPROBE Matrices

LASAGNA-Aligned Models: Enter known TFBSs Use TRANSFAC TFBSs Use ORegAnno TFBSs Use PAZAR TFBSs

Enter keywords to search for TFs Search

295 TF Models Selected Show Remove All

Promoter Sequence Input

Promoter sequences in FASTA: [Load Sample](#)

```
>seq_0
gttatgtatcacaacataggatcacataacatgatattaatgattatgaagctgaaagacattttctaaacaatcagaa
attaagaacaagattgatcaacatgctagaagacagattgaattatcttatatcctctttggagaaaatattacaaa
ttgtgtcacatgaagaaggatcaataagcatgtgggcaataatgtaggaaaaatacaaatgtgtggcaggcattatt
taataaaaatgttataccttttggaaagagataacatgagatgtacacattacagccattgtatcacacaaaaattga
atacccttttgttttcataacattgaaatttggagttcacgtcaggtgtttgtagattgcctacattttgaatacatctgat,
```

Retrieve promoter sequence:

Entrez Gene IDs, gene symbols, mRNA accession numbers Exact match? Search

Sample random promoters in Go

0 Promoters Selected Show Remove All

Result Filtering

Cutoff p-value:

Report top- scoring sites per promoter for each TF

Restore Defaults Start Searching

Click and choose vertebrate and all TF models.

Paste DNA sequence into form. The test data include promoter sequences which bind transcription factors.

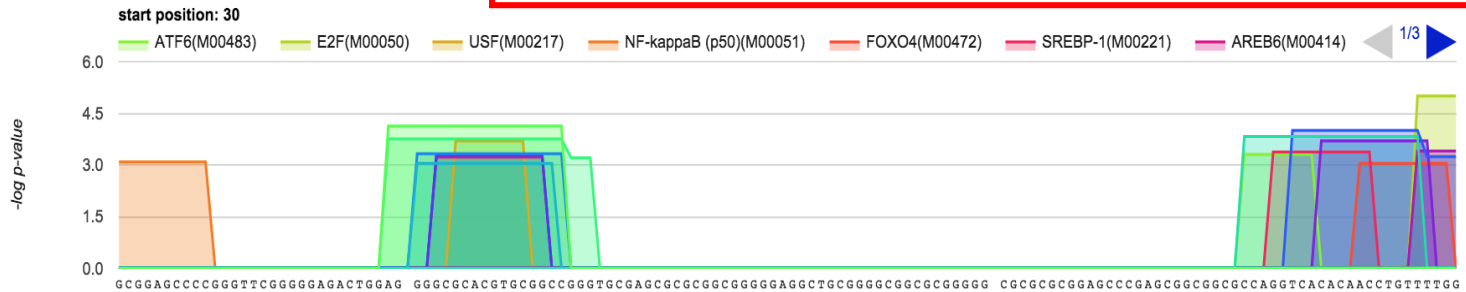
Click Exec to search.

EP_SAM

Display results in plain text (tab-delimited) Display results as images Visualize in UCSC Genome Browser

The boxes below indicate the nucleotides of the input sequence that match the particular TF weight matrix.

EP_SAM



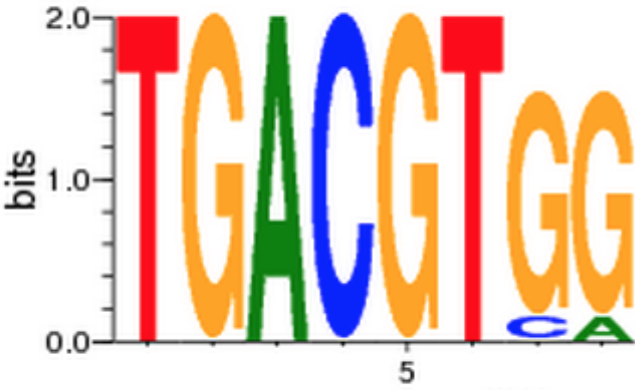
Information containing the accession number, TF binding sequence and score value.

Position offset: 0 Update position Prev Next Display the entire promoter Save image in PNG

Hits

EP_SAM						
Name	Sequence	Position (0-based)	Strand	Score	p-value	E-value
AML-1a (M00271)	AGCGGT	281	+	7.31	0	0
AML-1a (M00271)	AGCGGT	351	-	7.31	0	0
AML-1a (M00271)	TGCGGT	386	+	7.2	0.000125	0.075

Here we see more information on the TF matrix sequence for this particular sequence.

Species Group	Vertebrates
TRANSFAC Accession Number	M00483
Identifier	V\$ATF6_01
Name	ATF6
Number of Sites	20
K	0
 <p>bits</p> <p>2.0</p> <p>1.0</p> <p>0.0</p> <p>5</p> <p>WebLogo 3.2</p>	
References	10856300