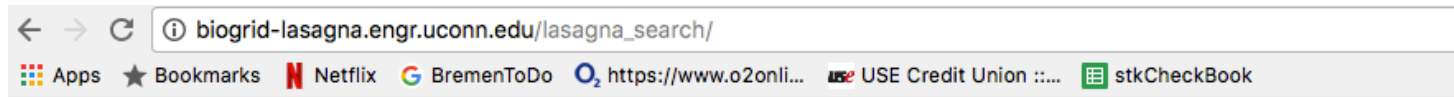


**TFSEARCH:** The Transcription Factor binding site search program detailed here is called LASAGNA:

[http://biogrid-lasagna.engr.uconn.edu/lasagna\\_search/](http://biogrid-lasagna.engr.uconn.edu/lasagna_search/)



### LASAGNA-Search 2.0: Searching for transcription factor binding sites (TFBSs)

Search for TFBSs

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Choose the TRANSFAC transcription matrices button. These are all vertebrate transcription factors.

Click here to open a window for copy and pasting sequences.

**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

295 TF Models Selected

**Promoter Sequence Input**

- Promoter sequences in FASTA: [Load Sample](#)
- Retrieve promoter sequence:

Entrez Gene IDs, gene symbols, mRNA accession numt  Exact match?

Sample  random promoters in

0 Promoters Selected

**Result Filtering**

- Cutoff p-value:
- Report top- scoring sites per promoter for each TF

### 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

**295 TF Models Selected**

### Promoter Sequence Input

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

```
>EP_1
GAGAGCGGGCAGGAGGCGGGTTGGGAGGGCGCGGAGCCCCGGGTTCTGGGGGAGA
CTGGAG
GGGCGCACGTGCGGCCGGGTGCGAGCGCGCGGGCGGGGGAGGCTGCGGGGCGGC
GCGGGGG
CGCGCGCGGAGCCCGAGCGGCCGGCGCCAGGTCACACAACCTGTTTTGGCGCCTGC
```

- Retrieve promoter sequence:

Entrez Gene IDs, gene symbols, mRNA accession numt  Exact match?  ?

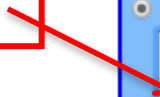
Sample  random promoters in

**0 Promoters Selected**

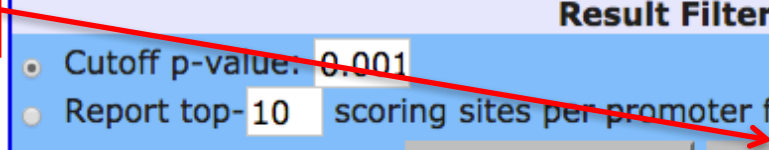
### Result Filtering

- Cutoff p-value:
- Report top-  scoring sites per promoter for each TF

Enter sequence for analysis.



CLICK to search promoter sequence with Transfac Binding site matrices.



Name	Sequence	Position (0-based)	Strand	Score	p-value	E-value
<a href="#">AML-1a (M00271)</a>	AGCGGT	281	+	7.31	0	0
<a href="#">AML-1a (M00271)</a>	AGCGGT	351	-	7.31	0	0
<a href="#">AML-1a (M00271)</a>	TGCGGT	386	+	7.2	0.000125	0.075
<a href="#">AML-1a (M00271)</a>	TGCGGT	233	+	7.2	0.000125	0.075
<a href="#">CdxA (M00100)</a>	CTTTCTG	370	+	6.11	0.000475	0.286
<a href="#">STAT6 (M00500)</a>	GACTTCC	551	-	8.69	7.5E-5	0.045
<a href="#">STAT6 (M00500)</a>	GACTTCCC	550	-	8.51	0.00015	0.090
<a href="#">STAT6 (M00500)</a>	GACTTC	552	-	8.17	0.00095	0.57
<a href="#">ATF6 (M00483)</a>	TGACCTGG	147	-	7.93	0.0005	0.301
<a href="#">E2F (M00050)</a>	TTTGCGC	165	+	10.78	0	0

**Results:** The name of the transcription factor is in the left column. The Position indicates where the TF has a good match in the sequence being searched. The higher the Score, the better the match and the lower the probability (p-value).

Clicking on the name link will pull up information about the transcription factor.

<a href="#">AML-1a (M00271)</a>	TGCGGT	386
<a href="#">AML-1a (M00271)</a>	TGCGGT	233
<a href="#">AML-1a (M00271)</a>	TGCGGT	370
<a href="#">AML-1a (M00271)</a>	TGCGGT	551
<a href="#">AML-1a (M00271)</a>	TGCGGT	550
<a href="#">AML-1a (M00271)</a>	TGCGGT	552
<a href="#">AML-1a (M00271)</a>	TGCGGT	147
<a href="#">AML-1a (M00271)</a>	TGCGGT	165
<a href="#">STAT6 (M00499)</a>	GACTTCCC	550
<a href="#">USF</a>		

Species Group	Vertebrates
TRANSFAC Accession Number	<a href="#">M00050</a>
Identifier	VSE2F_02
Name	E2F
Number of Sites	12
K	0
References	<a href="#">1411535</a>