

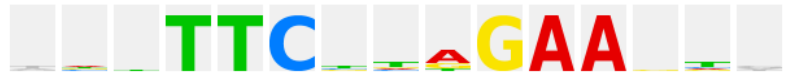
The matrix comparison tool uses the developed m2match algorithm (Stegmaier et al, article submitted) to compare an input matrix against the TRANSFAC® matrix library to find characterized motifs describing similar patterns. The application may be used to determine if a custom matrix represents a novel, newly identified motif or simply to compare a motif generated from newly identified binding sites for a characterized transcription factor to previously constructed matrices for the same or related factor.

**1** In this example, a subset of 11 STAT5 binding sites within the rat IGF1, GHRE1 and GHRE2 genes is identified (Laz et al, Mol Endocrinol 2009 23(8):1242-5).

```
>IGF1-1
tttttcttagaagta
>IGF1-2
aaattctaagaaact
>GHRE1-1
gccttcctggaagaa
>GHRE1-2
tgcttcttagaatga
>GHRE2-1
catttctttgaagtg
>GHRE2-2
gagttcctggaacct
>GHRE2-3
aagttctgagaactg
>GHRE2-4
tcttcagggaaatc
>GHRE2-5
ttttcgaagaattg
>GHRE2-6
aaattcgagaagtg
>GHRE2-7
tgattcctagaaaag
```

**2**

After opening the Tools -> Create and compare matrices menu, the "Create matrices" option is selected and used to create a matrix from the aligned binding sites.



**3**

The newly created matrix is then submitted for comparison using the "Compare matrices against TF library" option.

Query Matrix	Transfac Id	Matrix accession	Matrix class	Alignment	P-value	FDR
U00004	V\$STAT5A_01	<a href="#">M00457</a>	STAT	<a href="#">View</a>	8.6597E-15	1.2375E-11
U00004	V\$STAT5B_01	<a href="#">M00459</a>	STAT	<a href="#">View</a>	3.9080E-14	2.7903E-11
U00004	V\$STAT1_05	<a href="#">M01260</a>	STAT	<a href="#">View</a>	1.4189E-13	6.7538E-11
U00004	V\$STAT5A_Q6	<a href="#">M01890</a>	STAT	<a href="#">View</a>	7.9108E-12	2.8241E-9



**4**

The V\$STAT5A\_Q6 matrix, among others, is identified as similar to our input matrix. The linked Matrix Report describes how the V\$STAT5A\_Q6 matrix was created from 46 genomic binding sites collected from 100 publications.

Matrix Report: V\$STAT5A\_Q6 - STAT5A

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Sequence	Transcription factors	Bound Gene	Experimental evidence	Experimental source	References
aaaTTTCAGGAA	STAT5A(h)	IFNG(h)	CT DM FA FO GS SS TP SE OT	PBMC	<a href="#">21</a>
AAATTTCTAATTC	STAT5A(b)	CSN1S1(b)	CT DM FA FO GS SS TP SE OT	HC11 [more...]	<a href="#">13</a>
AACTTCTGGGAA	STAT5A(r)	Ins1(r)	CT DM FA FO GS SS TP SE OT	INS-1 + PRL	<a href="#">51</a>