



## RSAT - matrix-scan result

```
$RSAT/perl-scripts/convert-seq -i $RSAT/public_html/tmp/www-data/2021/03/05/tmp_sequence_2021-03-05.001855_K8oi0A.fasta
```

### Server command

```
$RSAT/perl-scripts/matrix-scan -v 1 -matrix_format transfac -m $RSAT/public_html/tmp/www-data/2021/03/05/matrix-scan_2021-03-05.001855_SdIpwS.matrix
```

**Information:** One or several button(s) will appear at the bottom of this page, allowing you to send the result as input for a subsequent query.

```
matrix-scan -v 1 -matrix_format transfac -m $RSAT/public_html/tmp/www-data/2021/03/05/matrix-scan_2021-03-05.001855_SdIpwS.matrix
Slow counting mode
Input files
  input  $RSAT/public_html/tmp/www-data/2021/03/05/tmp_sequence_2021-03-05.001855_K8oi0A.fasta
  bg     $RSAT/public_html/data/genomes/Candida_glabrata/oligo-frequencies/2nt_upstream-noorf_Candida_glabrata.fasta
Matrix files
  matrix 1 $RSAT/public_html/tmp/www-data/2021/03/05/matrix-scan_2021-03-05.001855_SdIpwS.matrix
Sequence format      fasta
Pseudo counts       1
Background model
  Method      file
  Markov order  1
  Strand      sensitive
  Background pseudo-frequency 0.01
Residue probabilities
  a  0.32183
  c  0.18541
  g  0.17996
  t  0.31280
Thresholds
  lower upper
  pval  NA  0.0001
  score 1  NA
Output columns
  1 seq_id
  2 ft_type
  3 ft_name
  4 strand
  5 start
  6 end
  7 sequence
  8 weight
```

seq_id	ft_type	ft_name	strand	start	end	sequence	weight	Pval	ln_Pval	sig	rank
CgCTA1	limit	START_END	D	-1000	-1	.	0	0	0	0	
CgCTA1	site	Yap1p	R	-411	-404	AGGTAATT	8.2	5.3e-05	-9.838	4.273	1

### Matrices

matrix	name	ncol	nrow	pseudo	Wmin	Wmax	Wrange				
1	Yap1p	7	4	1	-32.400	8.600	41.000	a:0.322	c:0.185	g:0.180	t:0.313
2	Yap1p	7	4	1	-32.400	9.700	42.100	a:0.322	c:0.185	g:0.180	t:0.313
3	Yap1p	7	4	1	-32.400	9.100	41.500	a:0.322	c:0.185	g:0.180	t:0.313
4	Yap1p	7	4	1	-32.400	8.400	40.800	a:0.322	c:0.185	g:0.180	t:0.313
5	Yap1p	7	4	1	-32.400	9.100	41.500	a:0.322	c:0.185	g:0.180	t:0.313
6	Yap1p	9	4	1	-21.300	7.500	28.800	a:0.322	c:0.185	g:0.180	t:0.313
7	Yap1p	18	4	1	-54.200	15.700	69.900	a:0.322	c:0.185	g:0.180	t:0.313
8	Yap1p	8	4	1	-25.100	7.500	32.600	a:0.322	c:0.185	g:0.180	t:0.313
9	Yap1p	8	4	1	-29.000	8.200	37.200	a:0.322	c:0.185	g:0.180	t:0.313
10	Yap1p	8	4	1	-33.000	8.400	41.400	a:0.322	c:0.185	g:0.180	t:0.313
Number of sequences scanned				1							
Sum of sequence lengths				1000							

