

This Supplementary Material shows the Core Promoters of Complex III subunits/related genes identified by phylogenetic footprinting. The conserved regions are shown in color codes, which correspond to specific Transcription Factor Binding Sites (TFBS).

The description of the complete description of TFBS can be found in Supplementary Table S1 (in the “Matrix Family Library” Excel sheet).

**GEMS Launcher Task: *DiAlign TF*: Multiple alignment plus TF sites working on promoters.seq (3 seq.)**

[\[Alignment\]](#) [\[Pairwise similarities\]](#)

DiAlign professional TF Release 3.1 December 2004

Thu May 19 15:54:04 2005

**Solution parameters:**

**Sequence file:** [promoters.seq](#) (3 seq.)  
**Type of sequences:** nucleotide sequences  
**Threshold T:** 0.00  
**\*' signs below alignment denote:** diagonal similarity (max. similarity is represented by 10 '\*' signs)  
**Alignment output:** complete alignment is shown  
 # nucleic acids per line: 50  
**TF output:** common TF matches located in aligned regions (common to 3 (100.0 %) sequences)  
**Family matches:** yes  
**MatInspector library:** Matrix Family Library Version 5.0 (February 2005)  
 • ALL user\_defined.lib (0.75/Optimized)  
 • ALL vertebrates.lib (0.75/Optimized)  
**Selected groups**  
 (core/matrix sim):

**Aligned Sequences:**

No.	Sequence Name	Sequence Description	Length
1	P986561	sym=CYC1 loc=Loc1537 taxid=9606 spec=Homo sapiens chr=8 ctg=NT_023684 str=(+) start=1115192 end=1116211 len=1020 tss=501,520 comm=cytochrome c-1; (AK026633/517/gold;NM_001916/536/silver;)	1020 bp
2	P986563	sym=Cyc1 loc=Loc66445 taxid=10090 spec=Mus musculus chr=15 ctg=NT_039621 str=(+) start=37804647 end=37805670 len=1024 tss=501,524 comm=cytochrome c-1; (AK002815/524/gold;NM_025567/501/bronze;)	1024 bp
3	P986564	sym=na loc=Loc300047 taxid=10116 spec=Rattus norvegicus chr=7 ctg=NW_047780 str=(+) start=8996190 end=8997190 len=1001 tss=501 comm=similar to cytochrome c-1; (XM_216944/535/silver;)	1001 bp

**Alignment (DiAlign format):**

Please note that only **upper-case** letters are considered to be **aligned**. For more information, please have a look at the user guide.

[V\\$STAF](#)
[V\\$YYIF](#)
[V\\$AP2F](#)
[V\\$AREB](#)
[V\\$EREF](#)
[U\\$EREF](#)
[V\\$RORA](#)
[V\\$RARF](#)
[V\\$ZBPF](#)
[V\\$MZFI](#)
[V\\$HESF](#)
[V\\$SFIF](#)

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alignment
position      1 . . . . . 1 1 . . . . . 2 1 . . . . . 3 1 . . . . . 4 1 . . . . .
P986561      1 g c a t c a c g c g t c g g g c c a t g - - - - -
P986563      1 g g c a g c a c c a a g t g c c a c a g t g a t c a g t c c c t t a c a t c c a g a g g g a g c t g
P986564      1 - - - - -
    
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alignment position	5 1 . . . . .	6 1 . . . . .	7 1 . . . . .	8 1 . . . . .	9 1 . . . . .
<b>P986561</b>	21 - - - - -	- - - - -	- - - - -	- - - - -	- - - - -
<b>P986563</b>	51 c a g c t t a t c T	T T G T A A T G G A	C G G G T A C C C C	C A C T T A G A T A	T G C T C T C A t t
<b>P986564</b>	1 - - - - -	- T T T G T G A T G G A	C A G G T A C C C C	C A C T T A G T T A	T G T T C T C A g t
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alignment position	1 0 1 . . . . .	1 1 1 . . . . .	1 2 1 . . . . .	1 3 1 . . . . .	1 4 1 . . . . .
<b>P986561</b>	21 - - - - -	- - - - -	- - - - -	- - - - -	- - - - - A G T C
<b>P986563</b>	101 a A G A A A A T T G	A A T T A T G G A c	t T T A T A T G A G	G G T T T A A A A G	A A A G T T A G T C
<b>P986564</b>	42 g A G A A A A T T G	A A T T A T A G A a	c T T A T A T G A G	G G T T T A A A A G	A A A T T T A G T T
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alignment position	1 5 1 . . . . .	1 6 1 . . . . .	1 7 1 . . . . .	1 8 1 . . . . .	1 9 1 . . . . .
<b>P986561</b>	25 A A G G G A A t g a	a g g a g a a c a g	g g t g c t c a g c	c t g g g g g c c c	a g c c t c c c g c
<b>P986563</b>	151 A G G G G A A G T T	T C T A T G C T G G	G T C G C C T - - -	- - - - -	- - - - -
<b>P986564</b>	92 A G G G a g g G T T	T C T A T G C C C A	G T C G C C T - - -	- - - - -	- - - - -
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alignment position	2 0 1 . . . . .	2 1 1 . . . . .	2 2 1 . . . . .	2 3 1 . . . . .	2 4 1 . . . . .
<b>P986561</b>	75 t g t c a c g c g c	t g c c t g c g g c	c g a g a c c c c t	g c c c g c g c c c	t c t g c c g g g c
<b>P986563</b>	178 - - - - -	- - - - -	- - - - -	- - - - -	- - - - -
<b>P986564</b>	119 - - - - -	- - - - -	- - - - -	- - - - -	- - - - -
alignment position	2 5 1 . . . . .	2 6 1 . . . . .	2 7 1 . . . . .	2 8 1 . . . . .	2 9 1 . . . . .
<b>P986561</b>	125 t g c c c t c c a a	g c c g c c t t t	c t c t g g a g g t	c c t c a g c c t g	c a g g g g c a c c
<b>P986563</b>	178 - - - - -	- - - - -	- - - - -	- - - - -	- - - - -
<b>P986564</b>	119 - - - - -	- - - - -	- - - - -	- - - - -	- - - - -
alignment position	3 0 1 . . . . .	3 1 1 . . . . .	3 2 1 . . . . .	3 3 1 . . . . .	3 4 1 . . . . .
<b>P986561</b>	175 c t c c a c c c g g	c c a t c g c g c a	g c c t g g g a a g	G T G G A G A A A A	G G A G C G t c g g
<b>P986563</b>	178 - - - - -	- - - - -	- - - - -	G T G G A G C A G G	G G A G A G c t - -
<b>P986564</b>	119 - - - - -	- - - - -	- - - - -	G T A G A G C A G G	G G A G c t a c a t
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alignment position	3 5 1 . . . . .	3 6 1 . . . . .	3 7 1 . . . . .	3 8 1 . . . . .	3 9 1 . . . . .
<b>P986561</b>	225 g g t c t c g g a -	- - - - -	- - - - -	- - - - -	- - - - -
<b>P986563</b>	196 - - - - G C T G T	T A A T C C C A C A	C A G G c C A T G G	A T G A G C A A G C	t c - - - - -
<b>P986564</b>	139 a g a g a G C C G C	T T A C C C C T C A	C T G G - C A T G G	A T G G G C A A G C	c a c t c t t a a c
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alignment position	4 0 1 . . . . .	4 1 1 . . . . .	4 2 1 . . . . .	4 3 1 . . . . .	4 4 1 . . . . .
<b>P986561</b>	234 - - - - -	- - - - -	- - - - - G G C	G G C G T G G G A A	A C G C C G G G C G
<b>P986563</b>	233 - T C A G A A G A C	T A T C C A G T G G	C T C A A C T G G A	- G G G C G T G A T	T C G C G G G G C C
<b>P986564</b>	188 t T C A G A A G A C	T G T C C A G T A G	C T T A A C T G G A	C G A G C G G G A T	A C G C G G G G C C
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alignment position	4 5 1 . . . . .	4 6 1 . . . . .	4 7 1 . . . . .	4 8 1 . . . . .	4 9 1 . . . . .

<b>P986561</b>	257	GAGcggtggcgc	ctgtcaaggcc	aaacagagaga	cgcgacggggg	ccccgcccc	a
<b>P986563</b>	281	GAGGTGAAGG	AAC TGGGGAT	ATAGT AGAGA	Agccagaaa	ACAAA CAAAC	
<b>P986564</b>	238	AAGGTGAAGG	AAC TGGGAAT	ATAGT AGAGA	Agcag- -	AAA	AAAAGAAAA
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alignment position		501 . . . . .	511 . . . . .	521 . . . . .	531 . . . . .	541 . . . . .	
<b>P986561</b>	307	-----	-----	-----	-----	-----	-----
<b>P986563</b>	331	AAA CAAAGCA	ga - - - - -	- - - - -	- - - - -	TGT T	GT CAT TGTAA
<b>P986564</b>	286	AAA CAAAACA	ataagacaaa	aacaaaaaaa	tccag g	TGT T	AT TAT TGTAA
		*****				*****	*****
						*****	*****
						*****	*****
alignment position		551 . . . . .	561 . . . . .	571 . . . . .	581 . . . . .	591 . . . . .	
<b>P986561</b>	307	----- C	CGCCAGTTTC	CACGACAACC	CGAAGAGCGT	GGGGAGGCAg	
<b>P986563</b>	357	TTAGAGTTGC	GGCCAGGCTC	AACCCGGA CT	AGAGGAGCCG	GGCAAGGGAC	
<b>P986564</b>	336	TTAGAATTGC	AGCCAGACTC	AACcT - - - -	- - - - -	G	GGGAAGGTAC
		*****	*****	*****	*****	*****	*****
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alignment position		601 . . . . .	611 . . . . .	621 . . . . .	631 . . . . .	641 . . . . .	
<b>P986561</b>	348	g c g g t g c c c c	g g c c c c t g a c	t g a c g c g a c c	g g g a c c a g c g	c g c t t c g t c c	
<b>P986563</b>	407	AGT CCTGGTC	CAC TGA TGG A	CAG - - - - -	- - - - -	- - - - -	
<b>P986564</b>	372	AGC CCTGGTC	CAC TGA TGG A	CAG - - - - -	- - - - -	- - - - -	
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		*****	*****	*****		*****	*****
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alignment position		651 . . . . .	661 . . . . .	671 . . . . .	681 . . . . .	691 . . . . .	
<b>P986561</b>	398	ccgcccaccc	gacag gcCCC	GC CCCCGAGC	C CGGCCCCGC	CCCGCGCTC c	
<b>P986563</b>	430	-----	----- CT C	CCTACCCAGC	TCCGCC TAGG	TCCGCC CCACT	
<b>P986564</b>	395	-----	----- CT C	CCTATCCAGC	TGGGCGTAGG	CCCGGCCATT	
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			*****	*****		*****	*****
alignment position		701 . . . . .	711 . . . . .	721 . . . . .	731 . . . . .	741 . . . . .	
<b>P986561</b>	448	ccg - - GCTTT	C GC GAG GT t t	t g a CT CT C GT	GG	CG C C C C A G	GGG C C G A C G G
<b>P986563</b>	463	g t GTTGCTCT	C GC GT G GT C T	GAGCT CT C GT	CG	GC C C G C A G	GGG C C G A C G G
<b>P986564</b>	428	g g GTTGCTCT	C GC GT G GT C T	GAGTT CT C GT	CG	GC C C G C A A	GGG C C G A C G G
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alignment position		751 . . . . .	761 . . . . .	771 . . . . .	781 . . . . .	791 . . . . .	
<b>P986561</b>	496	GAGTG	GCGGC	C GC g c g g - A G	G A G G C C A A G A	T - - - G G C G G C	A G C T G C G G C T
<b>P986563</b>	513	G A A C G	G C G G C	C G C A C T A A A G	G G G G C C G A C A	T - - - G G C G G C	G G C G G C G G C T
<b>P986564</b>	478	G A A C G	G C G G C	C G C A C T A A A G	G A G G C C G A C A	t g g c G G C G G C	G G C G G C G G C T

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alignment position

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8 0 1 . . . . . 8 1 1 . . . . . 8 2 1 . . . . . 8 3 1 . . . . . 8 4 1 . . . . .

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P986561 542 TCGCTTCGCg g g g t a GTGT T GGGCCCGCGG GGCGCGGGGC TCCCGGGCGC
P986563 560 TCGCTTCGCC G g a CGGTAC T GGGCCCGCGG GGCGTGGGC TTCCAGGTGC
P986564 528 TCGCTTCGCC G a t CGGTGC T AGGCCCGCGG GGCATGGGC TTCCAGGTGC
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alignment position

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8 5 1 . . . . . 8 6 1 . . . . . 8 7 1 . . . . . 8 8 1 . . . . . 8 9 1 . . . . .

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P986561 592 g c GTGCCCGG GGTCTGCTGT GCAGCGCGC TCCCGGCAG CTc c c g c TAC
P986563 610 AAGTGCTCCG GGTCTGCTGG GC GGC GCGCG GTCCCGGCAG CT TCCATTGC
P986564 578 AAGTGCTCCG GGCCTGCTGG GC GGC GCGCG GCCCGGCAT CT TCCATTAC
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alignment position

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9 0 1 . . . . . 9 1 1 . . . . . 9 2 1 . . . . . 9 3 1 . . . . . 9 4 1 . . . . .

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P986561 642 GGACA CCTCA GGT GAG CGCT GGGCCGGGCC CCGGCTCCG CGCGGCCCCc g
P986563 660 GGACA CCGCA GGT GAG TCCT GCGCGGGGCC CCGACCATCG CGCGCCCTC
P986564 628 GGACA CCGCA GGT GAG TACT GGCACGGG a - CGGTCCATCG CGCGCCCTC
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alignment position

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9 5 1 . . . . . 9 6 1 . . . . . 9 7 1 . . . . . 9 8 1 . . . . . 9 9 1 . . . . .

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P986561 692 c a t ct CCGTG AAGTCACGG CGGGAGGCT GCGGGCGCGG GCCt g g g c a g
P986563 710 AG- - - CCCTG AAGTCACGG CGGGAGGCT C CGGGCGCGC GC CGGCATCG
P986564 677 AG- - - CCCTG AAGTCACGG CGGGAGGCT C CGGGCGCGC GC CAGCATCG
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alignment position

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1 0 0 1 . . . . . 1 0 1 1 . . . . . 1 0 2 1 . . . . . 1 0 3 1 . . . . . 1 0 4 1 . . . . .

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P986561 742 c g c g g a a g c g g t a c c g g c c a c c c a g c g t c c c e GG TCCAG CTGCC TGCCg
P986563 757 GTC TCCTGCG TTCCTCTAC AACTCGACGG - - GGTCCCCG CCGCCGGGCC
P986564 724 GTC ACCTACA TTCCTCTAC GACTCGGCAG - - GGTCCCCG CTGACCGGCC

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alignment position		1 0 5 1 . . . . .	1 0 6 1 . . . . .	1 0 7 1 . . . . .	1 0 8 1 . . . . .	1 0 9 1 . . . . .			
<b>P986561</b>	792	a c c t t g a g c g	t g t G G G A T C A	G G G C T G G G C G	C C C A C C T C T C	C G A A C G G C A G			
<b>P986563</b>	805	G G C A C A C c c a	g a - - A A G C C	G G T C T G G G T G	C C C A C G C C T T	G G A G T G G C A G			
<b>P986564</b>	772	G G C A C A C t c g	- - - G G A A G C C	A G T C T G G G T G	C C C A C G C C T T	G G A G C C A T A G			
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alignment position		1 1 0 1 . . . . .	1 1 1 1 . . . . .	1 1 2 1 . . . . .	1 1 3 1 . . . . .	1 1 4 1 . . . . .			
<b>P986561</b>	842	A G a g c c c g t c	c c c a g c g t g g	g g g t t g g - - -	- - - - -	- C G G G A C G G G			
<b>P986563</b>	852	g g c a t T G T T G	C T C T G A G C C C	A G G G T C C C A C	T G T G a T G G G G	T C G G G A C G G G			
<b>P986564</b>	819	G G c a - T G T T G	C T C T G A G C C C	A G G G T C C G A C	T G T G g T G G G G	T C G G G A C G G G			
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alignment position		1 1 5 1 . . . . .	1 1 6 1 . . . . .	1 1 7 1 . . . . .	1 1 8 1 . . . . .	1 1 9 1 . . . . .			
<b>P986561</b>	878	c t a g c t g c c g	t g g c g g g g c t	g g g g c t t t c c	C G A A T G G C G C	G C C C A G G A C G			
<b>P986563</b>	902	A G A T T G C A G -	- - - - -	- - - - -	C G A A G G G C T C	G C C C G G A G C G			
<b>P986564</b>	868	A G A T T C C T G -	- - - - -	- - - - -	C G A A G G G C T C	G C C C A G A A C G			
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alignment position		1 2 0 1 . . . . .	1 2 1 1 . . . . .	1 2 2 1 . . . . .	1 2 3 1 . . . . .	1 2 4 1 . . . . .			
<b>P986561</b>	928	G C T C T T G C G G	C T G G C T G T C C	a a a c t g g g c c	c g c G T C C T G A	A G T G A C C C C A			
<b>P986563</b>	931	A C T G C C G A A G	C C G G C T G T C C	G G A C C T G G C G	G A T a c C C T G C	A G T G A C C C C A			
<b>P986564</b>	897	A C T C C C G A A G	C C G G C T G T C T	T G A C C T G G C C	G A T G T C C T G A	A G T G A C C C C A			
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alignment position		1 2 5 1 . . . . .	1 2 6 1 . . . . .	1 2 7 1 . . . . .	1 2 8 1 . . . . .	1 2 9 1 . . . . .			
<b>P986561</b>	978	G C C T G A T C T C	G G C C A G C T G C	T T G T G A C C T T	G G C C T G T C C C	A G c - - - - -			
<b>P986563</b>	981	G C C T G A C C T C	A G C G G C T G C	A G G T G A C C T T	G G T C C G C T G C	A G T A - - - - -			
<b>P986564</b>	947	G C C T G A C C T C	A G C G G G C T G C	G G G T G A C C T T	G G T C T G C T G C	A G T A c t c t t g			
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alignment position		1 3 0 1 .							
<b>P986561</b>	1021	- - - -							
<b>P986563</b>	1025	- - - -							
<b>P986564</b>	997	g t c t t							

## Pairwise similarities:

For each pairwise alignment, the **similarity** (relative to the maximum similarity) and the **number of identical nucleic acids** (in % of shorter sequence) is given. Maximum values are underlined.

	<b>P986563</b> (1024 bp)	<b>P986564</b> (1001 bp)
<b>P986561</b> (1020 bp)	0.247 38 %	0.227 36 %
<b>P986563</b> (1024 bp)		<u>1.000</u> <u>79 %</u>

Please note that the **similarity value 1.000** marks only the two **most similar** sequences, it does not necessarily mean that these sequences are identical.

Extract alignment region	
<b>Positions in alignment</b>	from: <input type="text"/> to: <input type="text"/>
<b>Output file</b>	<input type="text" value="dialign.seq"/>
<b>Extract aligned sequences</b>	

For [comments](#), questions or bug reports, please contact [support@genomatix.de](mailto:support@genomatix.de)

**GEMS Launcher Task: *DiAlign TF*: Multiple alignment plus TF sites working on C3-HSPC051-HMR (3 seq.)**

[[Alignment](#)] [[Pairwise similarities](#)]

DiAlign professional TF Release 3.1 December 2004

Mon May 2 23:33:24 2005

### Solution parameters:

**Sequence file:** [C3-HSPC051-HMR](#) (3 seq.)  
**Type of sequences:** nucleotide sequences  
**Threshold T:** 0.00  
**'\*' signs below alignment denote:** diagonal similarity (max. similarity is represented by 10 '\*' signs)  
**Alignment output:** complete alignment is shown  
 # nucleic acids per line: 50  
**TF output:** common TF matches located in aligned regions (common to 3 (100.0 %) sequences)  
**Family matches:** yes  
**MatInspector library:** Matrix Family Library Version 5.0 (February 2005)  
 • ALL user\_defined.lib (0.75/Optimized)  
 • ALL vertebrates.lib (0.75/Optimized)  
**Selected groups** (core/matrix sim):

### Aligned Sequences:

No.	Sequence Name	Sequence Description
1	P884387	P884387 sym=HSPC051 loc=Loc29796 taxid=9606 spec=Homo sapiens chr=22 ctg=NT_011520 str=(+) start=9553427 end=9554427 len=1001 tss=501 comm=ubiquinol-cytochrome reductase complex (7.2 kD); (NM_013387/661/bronze;)
2	P884388	P884388 sym=1110020P15Rik loc=Loc66152 taxid=10090 spec=Mus musculus chr=11 ctg=NT_039515 str=(-) start=1598616 end=1599628 len=1013 tss=501,505,508,513 comm=RIK1 cDNA 1110020P15 gene; (AK003881/658/gold;AK002227/665/gold;AK012489/662/gold;NM_197979/670/bronze;)
3	rn3_dna	rn3_dna range=chr14:85372862-85373441 5'pad=0 3'pad=0 revComp=TRUE strand=? repeatMasking=none

### Alignment (DiAlign format):

Please note that only **upper-case** letters are considered to be **aligned**. For more information, please have a look at the user guide.

V\$GATA V\$XBBF V\$OCT1 V\$NRF1 V\$NRF1 V\$ZBPF V\$PAX5 V\$RORA V\$EREF V\$HNF4 V\$EREF V\$SF1F  
V\$COUP V\$SPIF

```

alignment position 1 . . . . . 11 . . . . . 21 . . . . . 31 . . . . . 41 . . . . .
P884387          1 c a c a g a g a a g g a a g t g t t c a a g t c t t c c a g t g c g g a - - - - -
P884388          1 g g t t c c c t g c c t c t g t a t t c a c t c c c c a t g c c a g a a a a g c g g a t a g c g c
rn3_dna          1 - - - - -
    
```





```
alignment position 4 0 1 . . . . . 4 1 1 . . . . . 4 2 1 . . . . . 4 3 1 . . . . . 4 4 1 . . . . .
P884387 342 - - - - - - - - - - - CTGTCC TGATATGAAC CT TTTGAGTT TTTT T c c t c a
P884388 359 AAC AT TGTAA TAAACTGTTA CCCTGTGCAC AT TATCAGTT TCTT TAA - - -
rn3_dna 210 GAC AT TGTAA TAATCTGTTA TCCTGTGCAC AT TGT CAGTT TCTT TAA - - -
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alignment position 4 5 1 . . . . . 4 6 1 . . . . . 4 7 1 . . . . . 4 8 1 . . . . . 4 9 1 . . . . .
P884387 378 t t c c c a g g a t a g g a a t a c c t c t g TG GT T CA AAAC - ACGAa g g CT GAGAT T
P884388 406 - - - - - - - - - - - - - - - - - - - - - TG GT T CA AAAt g TCGAC T - CT GAGATA
rn3_dna 257 - - - - - - - - - - - - - - - - - - - - - TG GT T CA AAAC - TCGAC T - CT GAGATA
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alignment position 5 0 1 . . . . . 5 1 1 . . . . . 5 2 1 . . . . . 5 3 1 . . . . . 5 4 1 . . . . .
P884387 427 CAGAGGAACT ACAAATCCCA TAAAGt g t t g c a c g t c t a g g g c c t t t g g g g
P884388 432 CAGAGGAACT ACAATTCCCA TAAAGCAGGG CGCGTTGAAA CTTT TGG AGc
rn3_dna 282 CCGAGGAACT ACAATTCCTA TAAAGCAGTG CGCGTTGAAA CTTT TGG AGt
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alignment position 5 5 1 . . . . . 5 6 1 . . . . . 5 7 1 . . . . . 5 8 1 . . . . . 5 9 1 . . . . .
P884387 477 a a c GA GGT CG GC CCCAGCGC AGGCGCGGT G GC GCGAGT T G GACT GTG AAG
P884388 482 a A - GAC ATT G GGTTCACGC AA GCGCAGT G GC GCGAGT T C GGCA GTG AAG
rn3_dna 332 g A - GA AGT T G GT CGCTACGC AGGCGCAGT G AC GCCAGT T C GTCAGCG AAG
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alignment position 6 0 1 . . . . . 6 1 1 . . . . . 6 2 1 . . . . . 6 3 1 . . . . . 6 4 1 . . . . .
P884387 527 AAACATGGCG GCCGC GACGT TGACT TCGAA AT TGTACTCC CTGC TGT TCC
P884388 531 CAACATGTTC TCGCC GACGA TC CCT TCGCG CC TGTACTCC TTGC TGT TCC
rn3_dna 381 CAACATGGCG TCGCC GACGG TC ACT TCGCG TT TGTACTCC TTGC TGT TCC
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alignment position 6 5 1 . . . . . 6 6 1 . . . . . 6 7 1 . . . . . 6 8 1 . . . . . 6 9 1 . . . . .
P884387 577 GCAGGACCTC CACCT TCGCC CT CAC CAT CA TC GTGGGCGt c a TGTTCTTC
P884388 581 GCAGA ACTTC CACCT TTGCC CT CAC CAT CG CAGTGGGCGC CCTGTTCTTC
rn3_dna 431 GCAGG ACTTC TACCT TCGCC CT CAC CAT CG CAGT GAGCGC CCTGTTCTTC
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alignment position 7 0 1 . . . . . 7 1 1 . . . . . 7 2 1 . . . . . 7 3 1 . . . . . 7 4 1 . . . . .  
P884387 627 GAGCGCGCCT TCGATCAAGG CGCGGACGCt ATCTACGACC ACATCAA CGA  
P884388 631 GAGCGAGCCT TCGATCAGGG CGCAGACGCG ATCTACGAGC ACATCAA CGA  
rn3\_dna 481 GAGCGCGCCT TCGATCAGGG TGCAGACGCG GTCTACGATT ACATCAA CGA  
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alignment position 7 5 1 . . . . . 7 6 1 . . . . . 7 7 1 . . . . . 7 8 1 . . . . . 7 9 1 . . . . .  
P884387 677 GGGGGTGAGG GCCTGTGCCA Tc CCTGACCT TGGACCCGCC TGAGGGGTTGA  
P884388 681 GGGGGTGAGG GCCTGGGCCA T- CCTGACCT TGGGCCCGCC TGAAAGGTTGA  
rn3\_dna 531 GGGGGTGAGG GACTGGGCCA T- CCTGACCT TGGGCCCGCC TGAAAGGTTGA  
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alignment position 8 0 1 . . . . . 8 1 1 . . . . . 8 2 1 . . . . . 8 3 1 . . . . . 8 4 1 . . . . .  
P884387 727 Ca g t g g a g t a GAGGTGGGAT GGGACTCAGT ATACTTTTAC CAGGAAGGGG  
P884388 730 Ct g g g a g g - GAGGTAGGAC GGAAC TCAAT CAAGTCTTAC CAGGTCTGGG  
rn3\_dna 580 C - - - - -  
\* \* \* \* \*  
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\* \* \* \* \*  
\* \* \* \* \*

alignment position 8 5 1 . . . . . 8 6 1 . . . . . 8 7 1 . . . . . 8 8 1 . . . . . 8 9 1 . . . . .  
P884387 777 g t a a g g g t a a a c c g t c g g c g t c t t c t g t c t c g a g t c c g c c g t c t g T C C C  
P884388 778 g t g a a c t g t g c c c g t t a a t a c a t c t a t - - - - T T C T  
rn3\_dna 581 - - - - -  
\* \* \* \* \*

alignment position 9 0 1 . . . . . 9 1 1 . . . . . 9 2 1 . . . . . 9 3 1 . . . . . 9 4 1 . . . . .  
P884387 827 CTTGGCTTGA TGTGAATTCT AAa ac g t t a a g c g a g t t a a t a t a t t t c a t  
P884388 809 CTTGACATGG TGCGAGGCCT AA t t g g t a t g t c c t g t c - - - - -  
rn3\_dna 581 - - - - -  
\* \* \* \* \*

alignment position 9 5 1 . . . . . 9 6 1 . . . . . 9 7 1 . . . . . 9 8 1 . . . . . 9 9 1 . . . . .  
P884387 877 t t t g c a g g g g t t g t a a g t a t t g c t g t g t g c c a c c c t a c a t A C C C A C T T G C  
P884388 846 -  
rn3\_dna 581 -  
\* \* \* \* \*

alignment position 1 0 0 1 . . . . . 1 0 1 1 . . . . . 1 0 2 1 . . . . . 1 0 3 1 . . . . . 1 0 4 1 . . . . .  
P884387 927 CCATTATCAG AAGCAAAAAC TAAa g c t a g t - - - - GAGAGCA AAGGAC  
P884388 856 ACATATTCAT TTGCGAAAAGC TAAc t c c t g a c t c c t g a GACATCAGAGGAC  
rn3\_dna 581 - - - - -  
\* \* \* \* \*

alignment position 1 0 5 1 . . . . . 1 0 6 1 . . . . . 1 0 7 1 . . . . . 1 0 8 1 . . . . . 1 0 9 1 . . . . .

```

P884387 971 T T A C t a g c t g c a c a g g a a g c c a g g g g c a a g t - - - - -
P884388 906 T T A C g g g t c t g a a c c a c t c c a t t a a g t c g g t g g t g a g t t g g a a c t c c g a c
rn3_dna 581 - - - - -
      * * * *

alignment position 1 1 0 1 . . . . . 1 1 1 1 . . . . . 1 1 2 1 . . . . . 1 1 3 1 . . . . . 1 1 4 1 . . . . .
P884387 1002 - - - - -
P884388 956 c c c t g c c g t c c t t g c t a g t t t c a a g g g c a g a t t t c a g c a a g g c a g t c g t t
rn3_dna 581 - - - - -

alignment position 1 1 5 1 . . . .
P884387 1002 - - - - -
P884388 1006 a a a a g t a g
rn3_dna 581 - - - - -

```

## Pairwise similarities:

For each pairwise alignment, the **similarity** (relative to the maximum similarity) and the **number of identical nucleic acids** (in % of shorter sequence) is given. Maximum values are underlined.

	<b>P884388</b> (1013 bp)	<b>rn3_dna</b> (580 bp)
<b>P884387</b> (1001 bp)	0.511 48 %	0.478 63 %
<b>P884388</b> (1013 bp)		<u>1.000</u> <u>89 %</u>

Please note that the **similarity value 1.000** marks only the two **most similar** sequences, it does not necessarily mean that these sequences are identical.

Extract alignment region	
Positions in alignment	from: <input type="text"/> to: <input type="text"/>
Output file	<input type="text" value="dialign.seq"/>
Extract aligned sequences	

For [comments](#), questions or bug reports, please contact [support@genomatix.de](mailto:support@genomatix.de)

**GEMS Launcher Task: *DiAlign TF*: Multiple alignment plus TF sites working on C3-UQCR (3 seq.)**

[\[Alignment\]](#) [\[Pairwise similarities\]](#)

DiAlign professional TF Release 3.1 December 2004

Wed Jun 8 22:07:49 2005

**Solution parameters:**

**Sequence file:** [C3-UQCR](#) (3 seq.)  
**Type of sequences:** nucleotide sequences  
**Threshold T:** 0.00  
**'\*' signs below alignment denote:** diagonal similarity (max. similarity is represented by 10 '\*' signs)  
**Alignment output:** complete alignment is shown  
 # nucleic acids per line: 50  
**TF output:** common TF matches located in aligned regions (common to 3 (100.0 %) sequences)  
**Family matches:** yes  
**MatInspector library:** Matrix Family Library Version 5.0 (February 2005)  
 • ALL user\_defined.lib (0.75/Optimized)  
 • ALL vertebrates.lib (0.75/Optimized)  
**Selected groups**  
 (core/matrix sim):

**Aligned Sequences:**

No.	Sequence Name	Sequence Description
1	P936092	P936092 sym=UQCR loc=Loc10975 taxid=9606 spec=Homo sapiens chr=19 ctg=NT_011255 str=(-) start=1544931 end=1545931 len=1001 tss=501 comm=ubiquinol-cytochrome reductase (6.4kD) subunit; (NM_006830/560/silver;)
2	P936093	P936093 sym=Uqcr loc=Loc66594 taxid=10090 spec=Mus musculus chr=10 ctg=NT_039496 str=(-) start=6269155 end=6270219 len=1065 tss=501,531,565 comm=ubiquinol-cytochrome reductase (6.4kD) subunit; (AK003443/531/gold;AK013513/565/gold;NM_025650/501/bronze;)
3	rUQCR	rUQCR sym=Uqcr spec=RATUS chr=7 str=(+) tss=343

**Alignment (DiAlign format):**

Please note that only **upper-case** letters are considered to be **aligned**. For more information, please have a look at the user guide.

**V\$ETSF** **U\$NRF2** **V\$NRF1** **U\$NRF1**

```

alignment position 1 . . . . . 1 1 . . . . . 2 1 . . . . . 3 1 . . . . . 4 1 . . . . .
P936092          1 c t g c a a a g a g a t t t c c g a c a g g g c c t c c a a g c a a c g g g c a a c g c t g a g g c
P936093          1 - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
rUQCR            1 - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
    
```

```

alignment position 5 1 . . . . . 6 1 . . . . . 7 1 . . . . . 8 1 . . . . . 9 1 . . . . .
P936092          5 1 t c a g g g a a g c a c t g c c g c t c g a c c a a a g t c c t a c a G C G A A T C A G G A A C A A
P936093          1 - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
    
```

```

rUQCR      1  -----
                                     *****
alignment position 101..... 111..... 121..... 131..... 141.....
P936092    101 CGCCTGACGC CTCCAAAAGT -----
P936093    16  CTTCAAATGT ATTCAAAAGG g t g g c c c a a c t c g a g c c t t t c c c c t t c a g g
rUQCR      1  -----
          *****
alignment position 151..... 161..... 171..... 181..... 191.....
P936092    121 -----
P936093    66 g t c t g t g c t c a a g t t c c t c t g g t t t a a a t t g a t c a a a g a t a g g g c t g t g g
rUQCR      1  -----

alignment position 201..... 211..... 221..... 231..... 241.....
P936092    121 ----- GGGCTCC AAT
P936093    116 c t c a g t g g g a c g a a c g c t c c t c t a g c g t g t c c a a g g c t c t GGGGTCC AGT
rUQCR      1  -----
                                     *****
alignment position 251..... 261..... 271..... 281..... 291.....
P936092    131 CCCAGCTCTT CCCCTCT g t g t -----
P936093    166 CCCAGCACTC CCTGTCT a c c c c A G G C T T A C A C T T T A G G A G G T G G A G G C A G
rUQCR      1  -----
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alignment position 301..... 311..... 321..... 331..... 341.....
P936092    152 GACTCTGAGC AAg a c c c t t c c c c g c t g g a c c t c a g t t t c c t t c a t t g t a a
P936093    216 GAGTCTGAGG AAt t c a c GGC CAGCCCTGAA TATAGGAGAC CCC CATATCA
rUQCR      29  GAGCGTGAGG AAa t c a a GGC CAGCCCTGGA TATACGAGAC CCC CGTC TCG
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alignment position 351..... 361..... 371..... 381..... 391.....
P936092    202 a t a a c g t t c t g g c a c a ----- - - - - T A C T A G
P936093    266 AAAACACc t a a g t ATGTGTA TTATTAAAGT TATTA Tc a g A TTA GTAC TAC
rUQCR      79  AAAACACc a - - - - ATGTGTA TTATTAAAGT TATTA T- - - A TTA GTAC TAC
          *****
          *****
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alignment position 401..... 411..... 421..... 431..... 441.....
P936092    224 GCGCACAAA TCACTGGc a g g t a g c c c c g c g g a g c c c a g a a g c a c a a t c g
P936093    316 GTGGTCAAAG TCACa -----
rUQCR      122 GTGCTCAGAG TCCCGGG-----
          *****
          *****
alignment position 451..... 461..... 471..... 481..... 491.....
P936092    274 g c c g c c a g a c c a c g t g g c c a g a a a g c a c c g c c c t a a c g c C GCC CACT CCG
P936093    331 ----- C A C A C T C T C C C
rUQCR      139 -----
                                     *****
alignment position 501..... 511..... 521..... 531..... 541.....
P936092    324 GACCACTTCT CCGCGGTc g t c c a a -----
P936093    342 CACCCATCC CCGGTGT t c c a g t GTGCATG GAGCT ACTGC TGG GATC CAC
rUQCR      139 -----
          GTGCATG GAGCT ACCGC CGG GATC CAC

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alignment position 5 5 1 . . . . . 5 6 1 . . . . . 5 7 1 . . . . . 5 8 1 . . . . . 5 9 1 . . . . .
P936092      348 - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
P936093      392 T G C A A C C - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
rUQCR        166 T G C A A C C t c a g g c a c a g a a t c t c a g a g c g c c c a g c c g g c t a g a a g t t c c g
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alignment position 6 0 1 . . . . . 6 1 1 . . . . . 6 2 1 . . . . . 6 3 1 . . . . . 6 4 1 . . . . .
P936092      348 - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - C C T C C G C C
P936093      399 - - A C A G A A C C A G G A C A G A A G C G G A T C - A G T A A C G T C T T T C T C T C C T C C G C C
rUQCR        216 c c A C T G A A G C A A G A C A G A G G C G G G T C t A G T A A G G T C T G T C T C C C T C C G C C
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alignment position 6 5 1 . . . . . 6 6 1 . . . . . 6 7 1 . . . . . 6 8 1 . . . . . 6 9 1 . . . . .
P936092      356 G G A A G T T A C T G T A A G T G G C T T C C G G T C t g c g c g c a c a g t g g c g g a t g a t
P936093      446 G G A A G T A G A T G T C A A T G T C T T C G G C G C C A C C C C G G A A A G G T G G A G C g a
rUQCR        266 G G A A G A A G A T G T C A A C G T C C T C T G T G C C A C C C G G A A G A G G T G G T G C c g
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alignment position 7 0 1 . . . . . 7 1 1 . . . . . 7 2 1 . . . . . 7 3 1 . . . . . 7 4 1 . . . . .
P936092      406 g t t t t t t t t c c t c c c c c c c c c c c g c c c t e C C C G C G C G C G T G C G C G C C G
P936093      496 t c g - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - C C T T C A C G C A T G C G C T A T A
rUQCR        316 t t g c t - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - T T C A C G C A T G C G C T G T A
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alignment position 7 5 1 . . . . . 7 6 1 . . . . . 7 7 1 . . . . . 7 8 1 . . . . . 7 9 1 . . . . .
P936092      456 C G G C C G C G C C T G C G C A G T G t a g C C G G G T C A G C T G G A C A G G G T C A T C C T G A
P936093      518 C G T C T G C A C A T G C G T A G T G C T - C C A G G G C A G C G G A A C G G G G T G A C C C T G A
rUQCR        338 C G T C T G C A C A T G C G T A G T G C T - C C A G G G C G G C G G A A C A G G G T G A C C C T G A
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alignment position 8 0 1 . . . . . 8 1 1 . . . . . 8 2 1 . . . . . 8 3 1 . . . . . 8 4 1 . . . . .
P936092      506 G g g - T G C G A C T C C G C C G C G A T G G T G A C C C G G T T C C T G G G C C C A C G C T A C C
P936093      567 G T A T T G A G A C C C T G C A G C G A T G C T G A G C A G G T T T C T A G G C C C G C G C T A C C
rUQCR        387 G T A T T G A G A C C C G C A G C G A T G C T C A G C A G A T T T C T A G G C C C G C G C T A C C
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alignment position 1 2 0 1 . . . . . 1 2 1 1 . . . . . 1 2 2 1 . . . . . 1 2 3 1 . . . . . 1 2 4 1 . . . . .
P936092 901 CCAGCCAGC Ac t c g c g g c a t c t t c g g c c t t GCC ACTA T TTT GGTT TTT
P936093 871 g CAGCCTGGC GACTT- GCA- - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
rUQCR 695 TCAGCCTAGC AACTTg GCG- - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
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alignment position 1 2 5 1 . . . . . 1 2 6 1 . . . . . 1 2 7 1 . . . . . 1 2 8 1 . . . . . 1 2 9 1 . . . . .
P936092 951 ATGATTTTTTA Ac a a g g a g c g t g a a a g c t t c a g c t g c g c c t g a g c c c a c g t
P936093 907 GCAGTCTTTC GTGTACTTc g t t t t t t c g t t t a a a c a g - T G TTT TTGT AAc
rUQCR 732 GCGGTCTTTA ATGTCCTTt a a a a a a a a a a a a a a a a c c T G TTT CTGT AAt
* * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * *
* * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * *
* * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * *

alignment position 1 3 0 1 . . . . . 1 3 1 1 . . . . . 1 3 2 1 . . . . . 1 3 3 1 . . . . . 1 3 4 1 . . . . .
P936092 1001 g - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
P936093 956 c CCAAGT TGG T CTGGAATC CCACCAATCA TCCTGCCTC a c a - - CT TCT
rUQCR 782 - CCAAGT TGG T CTGGAATC CCACCAATCA TCCTGCCTC c t c a c g CT TGT
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alignment position 1 3 5 1 . . . . . 1 3 6 1 . . . . . 1 3 7 1 . . . . . 1 3 8 1 . . . . . 1 3 9 1 . . . . .
P936092 1002 - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
P936093 1003 TGAACGCTAG AATAGCGGGC ACCCACCCTC ACCTG a a t g t t t t c t t t g c a
rUQCR 831 TGAACGGTGG AATAGCGGGC ACCCACCATC ACCTG a - - - - - - - - - - - - - - - - -
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alignment position 1 4 0 1 . . . . . 1 4 1 1
P936092 1002 - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
P936093 1053 t g c g t g t c t g t g t
rUQCR 867 - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -

```

**Pairwise similarities:**

For each pairwise alignment, the **similarity** (relative to the maximum similarity) and the **number of identical nucleic acids** (in % of shorter sequence) is given. Maximum values are underlined.

	<b>P936093</b> (1065 bp)	<b>rUQCR</b> (866 bp)
<b>P936092</b> (1001 bp)	<u>0.129</u> 29 %	<u>0.126</u> 31 %
<b>P936093</b> (1065 bp)		<u>1.000</u> <u>78 %</u>

Please note that the **similarity value 1.000** marks only the two **most similar** sequences, it does not necessarily mean that these sequences are identical.

**Extract alignment region**

<b>Positions in alignment</b>	from: <input type="text"/> to: <input type="text"/>
<b>Output file</b>	<input type="text" value="dialign.seq"/>
<b>Extract aligned sequences</b>	

For [comments](#), questions or bug reports, please contact [support@genomatix.de](mailto:support@genomatix.de)

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GEMS Launcher 4.1.1

**GEMS Launcher Task: *DiAlign TF*: Multiple alignment plus TF sites working on promoters.seq (3 seq.)**

[\[Alignment\]](#) [\[Pairwise similarities\]](#)

DiAlign professional TF Release 3.1 December 2004

Fri Apr 29 23:46:55 2005

### Solution parameters:

**Sequence file:** [promoters.seq](#) (3 seq.)  
**Type of sequences:** nucleotide sequences  
**Threshold T:** 0.00  
**'\*' signs below alignment denote:** diagonal similarity (max. similarity is represented by 10 '\*' signs)  
**Alignment output:** complete alignment is shown  
 # nucleic acids per line: 50  
**TF output:** common TF matches located in aligned regions (common to 3 (100.0 %) sequences)  
**Family matches:** yes  
**MatInspector library:** Matrix Family Library Version 5.0 (February 2005)  
 • ALL user\_defined.lib (0.75/Optimized)  
 • ALL vertebrates.lib (0.75/Optimized)  
**Selected groups**  
 (core/matrix sim):

### Aligned Sequences:

No.	Sequence Name	Sequence Description	Length
1	P879713	sym=UQCRH loc=Loc7388 taxid=9606 spec=Homo sapiens chr=1 ctg=NT_032977 str=(+) start=588249 end=588932 len=684  tss=552  comm=ubiquinol-cytochrome c reductase hinge protein; (NM_006004/552/silver;)	684 bp
2	P879718	sym=Uqcrh loc=Loc66576 taxid=10090 spec=Mus musculus chr=4 ctg=NT_039264 str=(-) start=16198124 end=16198804 len=681  tss=501,514,515,518,537  comm=ubiquinol-cytochrome c reductase hinge protein; (AK054005/514/gold;AK019085/518/gold;AK088185/515/gold;AK012552/501/gold;AK003539/537/gold;AK003266/515/gold; NM_025641/501/silver;)	681 bp
3	P879720	sym=na loc=Loc366448 taxid=10116 spec=Rattus norvegicus chr=5 ctg=NW_047718 str=(+) start=7693061 end=7693742  len=682 tss=582  comm=similar to Ubiquinol-cytochrome C reductase complex 11 kDa protein, mitochondrial precursor (Mitochondrial hinge protein) (Cytochrome C1, nonheme 11 kDa protein) (Complex III subunit VIII); (XM_345568/582/silver;)	682 bp

### Alignment (DiAlign format):

Please note that only **upper-case** letters are considered to be **aligned**. For more information, please have a look at the user guide.

V\$MAZF V\$ZBPF V\$RREB V\$NRF1 V\$NRF2 V\$NOLF V\$PLAG V\$HIF1 V\$HIF2 V\$XBBF V\$E4FF  
V\$ZF5F V\$YY1F V\$GL1F V\$AP2F V\$HOXH V\$RORA V\$CLOX V\$SETF V\$NRF2 V\$DMTF

alignment position      1 . . . . . 1 1 . . . . . 2 1 . . . . . 3 1 . . . . . 4 1 . . . . .

**P879713** 1 - - CA **GGGCGG** **GGGGA GCGTT** **GGGG** **CCC GA** G GCC GAG **CT CT** **TCG CTGGCGC**  
**P879718** 1 a ACA **GGGCGG** **GGGGA GCGCT** **GGGG** **CCC GA** G GCC GAG **CT CT** **TCG CTGGCGC**  
**P879720** 1 - ACA **GGGCGG** **GGGGA GCGCT** **GGGG** **CCC GA** G GCC GAG **CT CT** **TCG CTGGCGC**

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alignment position 5 1 . . . . . 6 1 . . . . . 7 1 . . . . . 8 1 . . . . . 9 1 . . . . .

**P879713** 49 **CGCCT** **CCCGG** **GACGTGGCCT** **CCAT** **GGT CGT** **TGc c** **GCCGCT** **ACCTCA CAGA**  
**P879718** 51 **CGCCT** **CCCGG** **GACGTGGCCT** **CCAT** **GGT CGT** **TGCT** **GCCGCT** **ACCTCA CAGA**  
**P879720** 50 **CGCCT** **CCCGG** **GACGTGGCCT** **CCAT** **GGT CGT** **TGCT** **GCCGCT** **ACCTCA CAGA**

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alignment position 1 0 1 . . . . . 1 1 1 . . . . . 1 2 1 . . . . . 1 3 1 . . . . . 1 4 1 . . . . .

**P879713** 99 ACCAGCAACT CC **GGGCGCGC** **CAGGCCT** CGG **GCGCCGCCAT** **CTT GGGGAGG**  
**P879718** 101 ACCAGCAACT CC **GGGCGCGC** **CAGGCCT** CGG **GCGCCGCCAT** **CTT GGGGAGG**  
**P879720** 100 ACCAGCAACT CC **GGGCGCGC** **CAGGCCT** CGG **GCGCCGCCAT** **CTT GGGGAGG**

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alignment position 1 5 1 . . . . . 1 6 1 . . . . . 1 7 1 . . . . . 1 8 1 . . . . . 1 9 1 . . . . .

**P879713** 149 **TGCGCGAGCC** **CGAGa g t g t c** **g CCGCGG** **GAC** **CGCCATCTTG** **AAAAGGTCAG**  
**P879718** 151 **TGCGCGAGCC** **CGAGAATG** **ACCCGCGGGC** **CGCCATCTTG** **AAGAGGTCAG**  
**P879720** 150 **TGCGCGAGCC** **CGAGAATGAC** **ACCCGCA** **GAC** **CGCCATCTTG** **AAGAGGTCAG**

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alignment position 2 0 1 . . . . . 2 1 1 . . . . . 2 2 1 . . . . . 2 3 1 . . . . . 2 4 1 . . . . .

**P879713** 199 **Ca g TTA** GGAC GGC **TCCATAA** **GCGATATGGG** GAAGAA t g t G AAT TAT TCTA  
**P879718** 201 **CTTTTA** GGAC CGC **TCCATAA** **GGGATATGGG** GAAGAA CA Ga AAC AAC ATTA  
**P879720** 200 **CTTTTA** GGGC CGC **TCCATAA** **GTGATATGGG** TAAGAA CAGG AAC TAT ATCA

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alignment position

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2 5 1 . . . . . 2 6 1 . . . . . 2 7 1 . . . . . 2 8 1 . . . . . 2 9 1 . . . . .

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P879713 249 AAGAAATTT C GAAGAAATTA GCACACTTT c CAAGTCTCTT AGGAGCTACT
P879718 251 AAAGATCGT C AAACAGAGGA GCAGATg a c t CAAGTATCTT AGGGAATACT
P879720 250 AAAGACTAT C AAACA AATTA GCAGATATT t t AAATATCTT AGGAAACACT
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* * * * *

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alignment position

```

3 0 1 . . . . . 3 1 1 . . . . . 3 2 1 . . . . . 3 3 1 . . . . . 3 4 1 . . . . .

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P879713 299 ATTTTAGATA AACTCCTAGA TCAATt a t a c t t g g g t g t g g t a t g a c t a a g
P879718 301 ACTTGGAAA A a t a CTGTAGA TCAACACAT TGGGCAAGAA GTGACCGAAA
P879720 300 ACTTGAAA A CTTCTGTAGA TCAATACGT TGGGCAAGAA GTGACCGAAA
* * * * *
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alignment position

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3 5 1 . . . . . 3 6 1 . . . . . 3 7 1 . . . . . 3 8 1 . . . . . 3 9 1 . . . . .

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P879713 349 g GGA TGT TTC TTAGCAAAGC CTCTCGGGT GCAAACATCA GCTACCCCTA
P879718 351 - GGATGT TTC TTAGCAAATT CTTTGCAGGC GTATATAGCA GCTCCCCCTA
P879720 350 a g g - TGCTTC TTAGCAAATT CTTTGCAGGC ATATATACCA GCTCCCCCTA
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alignment position

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4 0 1 . . . . . 4 1 1 . . . . . 4 2 1 . . . . . 4 3 1 . . . . . 4 4 1 . . . . .

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P879713 399 a c c t c t g c c t g c g g c t g GTA GTACATGCCA ATCTGAGCAT GTGTTTCGCGA
P879718 400 CGTCTCGTAG CTAGCGAGTA GTACAGCCCA ATTTGTGCGT GTGTTTCGGGA
P879720 399 CGTCTTG CAG CTAGCGAGTA GTACAGCCCA ATTTGTGGGT GTGTTTCGAGA
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* * * * *
* * * * *

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alignment position

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4 5 1 . . . . . 4 6 1 . . . . . 4 7 1 . . . . . 4 8 1 . . . . . 4 9 1 . . . . .

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P879713 449 CCACGA TGAG TGTGCCGCAC TTCCGGC CAG ATCGCCGGAT TTC CGc t GAG
P879718 450 CTACGA g GAG TATGCCGCAC TTCCGGC CAG ATCGCCGGAT ATC CGT CGAG
P879720 449 CTACGA TGAG TATGCCGCAC TTCCGGC CAG ATCGCCGGAT ATC CGT CGAG
* * * * *
* * * * *
* * * * *
* * * * *

```

alignment position

```

5 0 1 . . . . . 5 1 1 . . . . . 5 2 1 . . . . . 5 3 1 . . . . . 5 4 1 . . . . .

```

```

P879713 499 TGACCCTTAC AAGTTCCTTCT TGATCCTGAA CTGGg t TAGG TGC CGCTGTT
P879718 500 TGACCCTTAC TAGGTTCCTTCT TAAACCTGAA GTGGAGT a c t a - - - CTCTG
P879720 499 TGACCCTTAC AAGTTCCTTCT TAAACCTCAA GTGGAGTAGG TACCGTTGTT
* * * * *

```

Pairwise similarities:

For each pairwise alignment, the **similarity** (relative to the maximum similarity) and the **number of identical nucleic acids** (in %

of shorter sequence) is given. Maximum values are underlined.

	<b>P879718</b> (681 bp)	<b>P879720</b> (682 bp)
<b>P879713</b> (684 bp)	0.649 67 %	0.648 69 %
<b>P879718</b> (681 bp)		<u>1.000</u> <u>88 %</u>

Please note that the **similarity value 1.000** marks only the two **most similar** sequences, it does not necessarily mean that these sequences are identical.

Extract alignment region	
<b>Positions in alignment</b>	from: <input type="text"/> to: <input type="text"/>
<b>Output file</b>	<input type="text" value="dialign.seq"/>
<b>Extract aligned sequences</b>	

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GEMS Launcher 4.1.1

**GEMS Launcher Task: *DiAlign TF*: Multiple alignment plus TF sites working on van\_waveren3\_4.seq (3 seq.)**

[\[Alignment\]](#)   [\[Pairwise similarities\]](#)

DiAlign professional TF Release 3.1 December 2004

Tue May 3 00:08:58 2005

### Solution parameters:

**Sequence file:** [van\\_waveren3\\_4.seq](#) (3 seq.)  
**Type of sequences:** nucleotide sequences  
**Threshold T:** 0.00  
**'\*' signs below alignment denote:** diagonal similarity (max. similarity is represented by 10 '\*' signs)  
**Alignment output:** complete alignment is shown  
 # nucleic acids per line: 50  
**TF output:** common TF matches located in aligned regions (common to 3 (100.0 %) sequences)  
**Family matches:** yes  
**MatInspector library:** Matrix Family Library Version 5.0 (February 2005)
 

- ALL user\_defined.lib (0.75/Optimized)
- ALL vertebrates.lib (0.75/Optimized)

**Selected groups** (core/matrix sim):

### Aligned Sequences:

No.	Sequence Name	Sequence Description
1	P884800	P884800 sym=QP-C loc=Loc27089 taxid=9606 spec=Homo sapiens chr=5 ctg=NT_034772 str=(+) start=34616870 end=34617870 len=1001 tss=501 comm=low molecular ma ubiquinone-binding protein (9.5kD); (NM_014402/501/bronze;)
2	P884801	P884801 sym=1500040F11Rik loc=Loc22272 taxid=10090 spec=Mus musculus chr=11 ctg=NT_096135 str=(-) start=18541060 end=18542096 len=1037 tss=501,514,515,517,537 comm cDNA 1500040F11 gene; (AK005374/515/gold;AK007982/537/gold;AK002389/517/gold;AK003160/501/gold;NM_025352/514/bronze;)
3	rQP-C	rQP-C rn3_dna range=chr10:38898600-38899450 5'pad=0 3'pad=0 revComp=TRUE strand=? repeatMasking=none

### Alignment (DiAlign format):

Please note that only **upper-case** letters are considered to be **aligned**. For more information, please have a look at the user guide.

```

V$SPIF V$NFKB V$STAT V$SETSF V$RBPV V$IKRS V$EBOX V$HESF
alignment position 1 . . . . . 11 . . . . . 21 . . . . . 31 . . . . . 41 . . . . .
P884800      1 t a c t g g c c a a g g c c a a a t g a a a c c t c - - - - -
P884801      1 t a t g c a a a g g c c t g g t a c t g a g c g g a a a g G A C G C C T C T T G G A A C A C C C A
rQP-C        1 - - - - - - - - - - - - - - - - - - - - - - - - - - - G A C A G C C T C T T G G A A C G G C C A
                * * * * *
                * * * * *
alignment position 51 . . . . . 61 . . . . . 71 . . . . . 81 . . . . . 91 . . . . .
    
```

<b>P884800</b>	27	-	GTGCTCCTc	t g c t g t g g g g	c g g c c c g g c c	t c g g g g c t c a	g a g g c g c t c t						
<b>P884801</b>	51	GGT	GCTCCTA	AGCCaC	GC	ATCACCCTAA	TC-----						
<b>rQP-C</b>	22	GAAGCTCCTA	AGCCcC	GC	ATC	ATCCTAA	TC-----						
			*****	*****	*****	*****	*****						
			*****	*****	*****	*****	*****						
				*****	*****	*****	*****						
alignment position	101	...	111	...	121	...	131	...	141	...			
<b>P884800</b>	76	g t c t a c a g c t	g g g a a g a c t c	g	CAGGC	CCC	AAGCTCCTGGC	CAGCGCTGCC					
<b>P884801</b>	83	-----	-----	-	CGCGC	CCC	ATGCACCTATA	-GGCCCGCC					
<b>rQP-C</b>	54	-----	-----	-	CACGC	CCC	ATGCACCTATA	AGGCACCGCC					
					*****	*****	*****	*****					
					*****	*****	*****	*****					
					*****	*****	*****	*****					
alignment position	151	...	161	...	171	...	181	...	191	...			
<b>P884800</b>	126	CCGGAGg t c g	g c a g g c c c c t	t c c t c g t c a c	c t t t t t g t t c	c c t c c c c c g c							
<b>P884801</b>	111	CCGTGCACCT	CTCGACg g g G	GACCTT	ACGG	ACGTATCCAC	CTAAGATCC						
<b>rQP-C</b>	83	CCTGCGCCCT	CTAGACa a - G	GACCTT	ACGA	GC	GTATCCAA	CTAAGATCC					
			*****	*****	*****	*****	*****						
				*****	*****	*****	*****						
				*****	*****	*****	*****						
alignment position	201	...	211	...	221	...	231	...	241	...			
<b>P884800</b>	176	c t c c c g c a t t	c g g c c g c t t c	c t g a c t g g g a	t t c c a c a g a a	a a g c c g a g g g							
<b>P884801</b>	161	CAGGGt g g c t	a a TAAGCCCC	GCC	CAC	TTGC	-----						
<b>rQP-C</b>	132	TAGGGg c t - - -	TAGGCCCC	GCC	CAC	TTGC	-----						
			*****	*****	*****	*****	*****						
			*****	*****	*****	*****	*****						
			*****	*****	*****	*****	*****						
alignment position	251	...	261	...	271	...	281	...	291	...			
<b>P884800</b>	226	c t g a g g a g a a	g t g t g a g c g c	c t c c g c c t g t	c c a c t g T C C C	C C A A A G T C A G							
<b>P884801</b>	191	-----	-----	-----	-----	T t g g c a c c c c t - - -							
<b>rQP-C</b>	158	-----	-----	-----	-----	T C C C A A A A G C T C A G							
						*****	*****						
						*****	*****						
						*****	*****						
alignment position	301	...	311	...	321	...	331	...	341	...			
<b>P884800</b>	276	TTC	AATCCCC	GACg t c c t c c	g c - - - - -	- - - - -	- - - - -						
<b>P884801</b>	202	-----	CC	CACCAAGCCA	CCATTC	CTCT	TC	AAGCCC	CG	CC	CCT	Tg	GCA
<b>rQP-C</b>	172	TAC	ATT	CACCAGGCC	CCATTC	CTCT	TC	AAGCTC	CG	CC	CCT	Ta	GCA
			*****	*****	*****	*****	*****	*****	*****	*****	*****	*****	
				*****	*****	*****	*****	*****	*****	*****	*****	*****	
				*****	*****	*****	*****	*****	*****	*****	*****	*****	
alignment position	351	...	361	...	371	...	381	...	391	...			
<b>P884800</b>	298	-----	-----	-----	-----	-----	-----	-----					
<b>P884801</b>	244	ACATCAACCT	CTCCc g t g c g	t t c a c t a c t t	a c c g - T A A G C	C C A C A A G C A C							
<b>rQP-C</b>	222	ACAACACCCT	CTCCt t g a g g	t c c a c c a c g c	t c c c t T A A G C	C C A C A G G C A C							
			*****	*****	*****	*****	*****						
				*****	*****	*****	*****						
				*****	*****	*****	*****						
alignment position	401	...	411	...	421	...	431	...	441	...			
<b>P884800</b>	298	- - - - T	AGGC	TCCACC	CCAC	CGGCC	GGGC	AGGGC	CTC	CA	AGg	c a c c t c c	
<b>P884801</b>	293	CTCTAT	AAGC	CCCACC	CACG	TGT	CGC	TAGA	AGCGC	CTC	TA	AGc	t c g c c -
<b>rQP-C</b>	272	CTCTGT	AGGC	CCCACC	CACA	TGT	Ct	c t c c t	t g g g t	c a g t t	c c g	c a c c c g c	
			*****	*****	*****	*****	*****	*****	*****	*****	*****	*****	
			*****	*****	*****	*****	*****	*****	*****	*****	*****	*****	
			*****	*****	*****	*****	*****	*****	*****	*****	*****	*****	
alignment position	451	...	461	...	471	...	481	...	491	...			
<b>P884800</b>	343	c a c c t a c g g g	t c a c c c a g t C	AGC	CCA	CTT	C	TTT	CT	GGg	a c	a a a g g c g t c a	
<b>P884801</b>	342	-----	-----	C	AGC	CCT	CTT	G	GT	ACT	Gt	c c t t t c c g g c t a	
<b>rQP-C</b>	322	g - - - - -	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	



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alignment position 501 . . . . . 511 . . . . . 521 . . . . . 531 . . . . . 541 . . . . .
P884800      393 t c c c t t a g a g a c a g t - - - - - - - - - - - - - - - - - - - - - - - - -
P884801      373 c a c G A A G G T C A G G C C A C G C C C A C T C A G G T C A A C T g a c a a t T T T T T T T T T G
rQP-C        323 - - - G A A G G T C A G G C C G C G C C C A C C G A G G T C A A C T c g c a - - T T T C T T T T T G
                * * * * *
                * * * * *
alignment position 551 . . . . . 561 . . . . . 571 . . . . . 581 . . . . . 591 . . . . .
P884800      408 - - - - - - - - - - - - - - - - - - - - A G G A A A A T G G T A T C T C C C G G A A G T T A C C T C
P884801      423 A G T C T C C C C C T T G A G A T C G A A a G A A A A T G G T A G T T C C C G G A A A T G A C T T C
rQP-C        368 C A T C T C C T C C T C A A G A T A G A A G A A A A A T G G T A G C T C C C G G A A A T G A C T T C
                * * * * *
                * * * * *
alignment position 601 . . . . . 611 . . . . . 621 . . . . . 631 . . . . . 641 . . . . .
P884800      438 A C G A C C T C C A a g a g C G G C T T C C A A C C T T G C C G G A A A T G A C G a a c g a g t c a
P884801      473 A C G T T C T C T A G G c T C G G C T T C C G C T C C T C C C G G A A G T G A C G g g c g a a a g c
rQP-C        418 A C G A T C T C C A G G g T C G G C T T C C G C T C C T C C C G G A A G T G A C G t g c a a a g c c
                * * * * *
                * * * * *
alignment position 651 . . . . . 661 . . . . . 671 . . . . . 681 . . . . . 691 . . . . .
P884800      488 a c c g g a t c g g t g a C T G T G G A G G G C G A G C T G A G C c c t g t g c g t g a g t g g g g
P884801      523 c G G C T C A G A G - - - C T C T G G A G G T A G A G G T G A C C g a t c c t g g g g g t c - - -
rQP-C        468 g G G C T C A G C G - - - C T G T G G A G G T A G A G G T G A C t g g g t a c a g a g g g t c - - -
                * * * * *
                * * * * *
alignment position 701 . . . . . 711 . . . . . 721 . . . . . 731 . . . . . 741 . . . . .
P884800      538 t c t g g t t g t g c a G T G T C G T G G A C C C T G G G A - G g c t a g g g g c g c c c c g c t
P884801      566 - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
rQP-C        512 - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
                * * * * *
                * * * * *
alignment position 751 . . . . . 761 . . . . . 771 . . . . . 781 . . . . . 791 . . . . .
P884800      587 g g g c t g g g a a a g g a t a a g g a g t g c a g g g g c a g g a g t c t g g g g t t g g g g a t
P884801      588 - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
rQP-C        535 - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
                * * * * *
alignment position 801 . . . . . 811 . . . . . 821 . . . . . 831 . . . . . 841 . . . . .
P884800      637 g g a c c c c c g c g g g g a c t g c g g c g c T T C G C G A A A G C G A G C C A A G C G C C T G T
P884801      588 - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
rQP-C        535 - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
                * * * * *
                * * * * *
alignment position 851 . . . . . 861 . . . . . 871 . . . . . 881 . . . . . 891 . . . . .
P884800      687 C c a c c e t c g g t c t g C A G G G C C G C C G C C A C A A T G G G C C G C G A G T T T G G G A
P884801      614 C T T C T G T C C - - - - - C A G G G C C G C C G T C A C C A T G G G C C G C G A G T T T G G G A
rQP-C        561 C T T C T G T C C t - - - - - C A G G G C C G C C G C C A C C A T G G G C C G C G A G T T T G G G A
    
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alignment position 901 . . . . . 911 . . . . . 921 . . . . . 931 . . . . . 941 . . . . .
P884800 737 At CTGACGCG GATGCGGCAT GTGATCag CT ACAGCTTGTC ACCGTTCGAG
P884801 658 ACCTGGCGCG GATACGGCAC GTGATCTCCT ACAGCTTGTC GCCCTTTGAG
rQP-C 606 ACCTGACGCG GATACGGCAT GTGATCTCCT ACAGCTTGTC GCCCTTTGAG
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alignment position 951 . . . . . 961 . . . . . 971 . . . . . 981 . . . . . 991 . . . . .
P884800 787 CAGCGCGCCT ATCCGCACg t c t t c a c t AAA GGAATCCCCA ATGTTCTGCG
P884801 708 CAGCGCGCCT TCCCAAGCTA TTT CAGCAA GGCATCCCCA ACGTGCTGCG
rQP-C 656 CAGCGCGCCT TCCCGC ACTA TTT CAGCAA GGCATCCCCA ACGTGCTGCG
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alignment position 1001 . . . . . 1011 . . . . . 1021 . . . . . 1031 . . . . . 1041 . . . . .
P884800 837 CCGCATTCGG GAGt c t t t c t t t CGCGTGGT GCCGCGTGAG TGCct t g g g c
P884801 758 CCGCACTCGC GAGCGCA TCC TGC GCGTGGC GCCGCGTGAG TGC GG - - - -
rQP-C 706 CCGCACTCGC GAGCGCA TCC TGC GCGTGGC GCCGCGTGAG TGC GG - - - -
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alignment position 1051 . . . . . 1061 . . . . . 1071 . . . . . 1081 . . . . . 1091 . . . . .
P884800 887 c c g c g g g a g c g g g a g g c t g g a c c c a g c a g c a g c a g t c a c t g c g c c t
P884801 803 -
rQP-C 751 -

alignment position 1101 . . . . . 1111 . . . . . 1121 . . . . . 1131 . . . . . 1141 . . . . .
P884800 937 c c c c t c t g a g c g c t GGCGGC CGG Gc a g g c g c t c t g t a a c t t GCCGTACAC
P884801 803 -
rQP-C 751 -
\* \* \* \* \*
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\* \* \* \* \*

alignment position 1151 . . . . . 1161 . . . . . 1171 . . . . . 1181 . . . . . 1191 . . . . .

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P884800 987 ACCTTTCTc a t t g a a - - - - -
P884801 825 ACCTCTCCTT CCGACGCCCT CGC GGG GCA g a c g t g g a GGA GT TCT TAT CA
rQP-C 775 ACCTTTCTTA CCAACA TCTT CGACAGACA t - - - - - GGA GT TCT TAT CG
          *****
          *****
          *****
          *****

alignment position 1201 . . . . . 1211 . . . . . 1221 . . . . . 1231 . . . . . 1241 . . . . .
P884800 1002 - - - - -
P884801 875 TATCGAAATG ACTGGCCTAA GGT CAC Tt g g g t g a c t c c a a c g g c t c c c t c
rQP-C 818 TATCGAAATG ACTGGCCTAA GGT CAC Tt g g g t g a - - - - -
          *****
          *****
          *****
          *****

alignment position 1251 . . . . . 1261 . . . . . 1271 . . . . . 1281 . . . . . 1291 . . . . .
P884800 1002 - - - - -
P884801 925 t g a g g t c a t c g c t g g c c a c t a t c t g t g a t g a a a g g c t g a t g c a a t c a g t g
rQP-C 852 - - - - -

alignment position 1301 . . . . . 1311 . . . . . 1321 . . . . . 1331 . . . . . 1341 . . . . .
P884800 1002 - - - - -
P884801 975 t c t t g t g t t a g a t g t g c g g c c g a t t t t g c t g t c g g t t t c a t g g c a t t g t g
rQP-C 852 - - - - -

alignment position 1351 . . . . . 1361
P884800 1002 - - - - -
P884801 1025 a a t a t c c g t g a a g
rQP-C 852 - - - - -

```

## Pairwise similarities:

For each pairwise alignment, the **similarity** (relative to the maximum similarity) and the **number of identical nucleic acids** (in % of shorter sequence) is given. Maximum values are underlined.

	<b>P884801</b> (1037 bp)	<b>rQP-C</b> (851 bp)
<b>P884800</b> (1001 bp)	0.237 30 %	0.295 38 %
<b>P884801</b> (1037 bp)		<u>1.000</u> <u>77 %</u>

Please note that the **similarity value 1.000** marks only the two **most similar** sequences, it does not necessarily mean that these sequences are identical.

Extract alignment region	
Positions in alignment	from: <input type="text"/> to: <input type="text"/>
Output file	<input type="text" value="dialign.seq"/>
Extract aligned sequences	

For [comments](#), questions or bug reports, please contact [support@genomatix.de](mailto:support@genomatix.de)

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GEMS Launcher 4.1.1

**GEMS Launcher Task: *DiAlign TF*: Multiple alignment plus TF sites working on promoters.seq (3 seq.)**

[\[Alignment\]](#)   [\[Pairwise similarities\]](#)

DiAlign professional TF Release 3.1 December 2004

Tue May 3 03:50:06 2005

### Solution parameters:

**Sequence file:** [promoters.seq](#) (3 seq.)  
**Type of sequences:** nucleotide sequences  
**Threshold T:** 0.00  
**'\*' signs below alignment denote:** diagonal similarity (max. similarity is represented by 10 '\*' signs)  
**Alignment output:** complete alignment is shown  
 # nucleic acids per line: 50  
**TF output:** common TF matches located in aligned regions (common to 3 (100.0 %) sequences)  
**Family matches:** yes  
**MatInspector library:** Matrix Family Library Version 5.0 (February 2005)  
 • ALL user\_defined.lib (0.75/Optimized)  
 • ALL vertebrates.lib (0.75/Optimized)  
**Selected groups**  
 (core/matrix sim):

### Aligned Sequences:

No.	Sequence Name	Sequence Description	Length
1	P910348	sym=BCS1L loc=Loc617 taxid=9606 spec=Homo sapiens chr=2 ctg=NT_005403 str=(+) start=69733410 end=69734410 len=1001  tss=501 comm=BCS1-like (yeast); (AK096210/501/gold;)	1001 bp
2	P910350	sym=Bcs1l loc=Loc66821 taxid=10090 spec=Mus musculus chr=1 ctg=NT_039170 str=(+) start=52342932 end=52343944 len=1013  tss=501,505,513 comm=BCS1-like (yeast); (AK012324/513/gold;AK079385/505/gold;AK078925/501/gold; NM_025784/505/bronze;)	1013 bp
3	P910353	sym=na loc=Loc301514 taxid=10116 spec=Rattus norvegicus chr=9 ctg=NW_047816 str=(+) start=17367336 end=17368336  len=1001 comm=similar to BCS1-like; (CompGen promoter)	1001 bp

### Alignment (DiAlign format):

Please note that only **upper-case** letters are considered to be **aligned**. For more information, please have a look at the user guide.

**V\$MYTI** **V\$GABF** **V\$EKLF** **V\$SETSF** **V\$ZBPF** **V\$SPIF** **V\$PBXC**

```

alignment position 1 . . . . . 1 1 . . . . . 2 1 . . . . . 3 1 . . . . . 4 1 . . . . .
P910348           1 - - - - -
P910350           1 - - - - -
P910353           1 g g t a g g a g t g a g c c a g a a a a a g t a a c g t g c t t t c t t t g a c a c c g g a g a a
    
```

alignment	position	5 1 . . . . .	6 1 . . . . .	7 1 . . . . .	8 1 . . . . .	9 1 . . . . .
<b>P910348</b>		1 - - - - -	- - - - -	- - - - -	- - - - -	- - - - -
<b>P910350</b>		1 - - - - -	- - - - -	- - - - -	- - - - -	- - - - -
<b>P910353</b>	51	a a a a a g g a a c	a c a g a a g g c g	c c c c t g a g t a	a g c a c c t c a g	t t c c c a c g c g
alignment	position	1 0 1 . . . . .	1 1 1 . . . . .	1 2 1 . . . . .	1 3 1 . . . . .	1 4 1 . . . . .
<b>P910348</b>		1 - - - - -	- - - - -	- - - - -	- - - - -	- - - - -
<b>P910350</b>		1 - - - - -	- - - - -	- - - - -	- - - - -	- - - - -
<b>P910353</b>	101	c c t c t g g g c t	t g g a c t c a c c	g t g t g g c c t t	g a a c a g a t g c	a c t t g c c t c g
alignment	position	1 5 1 . . . . .	1 6 1 . . . . .	1 7 1 . . . . .	1 8 1 . . . . .	1 9 1 . . . . .
<b>P910348</b>		1 - - - - -	- - - - -	- - - - -	- - - - -	- - - - -
<b>P910350</b>		1 - - - - -	- - - - -	- - - - -	- - - - -	- - - - -
<b>P910353</b>	151	c t t c t c t g g g	c c t c a g c t t t	c c t a t c t g t a	a a g t g g a g g c	g g c g a c a g c c
alignment	position	2 0 1 . . . . .	2 1 1 . . . . .	2 2 1 . . . . .	2 3 1 . . . . .	2 4 1 . . . . .
<b>P910348</b>		1 - - - - -	- - - - -	- - - - -	- - - - -	- - - - -
<b>P910350</b>		1 - - - - -	- - - - -	- - - - -	- - - - -	- - - - -
<b>P910353</b>	201	a a g t c a c g a g	a t c c a g c g g a	a a a g a a a g g c	g t t t t g a a a c	c t g c a a g g c t
alignment	position	2 5 1 . . . . .	2 6 1 . . . . .	2 7 1 . . . . .	2 8 1 . . . . .	2 9 1 . . . . .
<b>P910348</b>		1 - - - - -	- - - - -	- - - - -	- - - - -	- - - - -
<b>P910350</b>		1 - - - - -	- - - - -	- - - - -	- - - - -	- - - - -
<b>P910353</b>	251	t g g g a t g a t g	c a t c g t c a c g	a t t a t g g t c c	t g a g g a g a g g	c a g c g g a t a c
alignment	position	3 0 1 . . . . .	3 1 1 . . . . .	3 2 1 . . . . .	3 3 1 . . . . .	3 4 1 . . . . .
<b>P910348</b>		1 - - - - -	- - - - -	- - - - -	- - - - -	- - - - -
<b>P910350</b>		1 - - - - -	- - - - -	- - - - -	- - - - -	- - - - -
<b>P910353</b>	301	c c g g g c g g g g	c c c g g a g c t g	t g a c g c g a c t	g a g g c g c c c a	a g t g c a g c a g
alignment	position	3 5 1 . . . . .	3 6 1 . . . . .	3 7 1 . . . . .	3 8 1 . . . . .	3 9 1 . . . . .
<b>P910348</b>		1 - - - - -	- - - - -	- - - - -	- - - - -	- - - - - CC
<b>P910350</b>		1 - - - - -	- - - - -	- - - - -	- - - - -	- - - - - CCGCAGCACCTCCTCC
<b>P910353</b>	351	a g a t g c g c c c	g a g c c c c g c t	c a t c g a c g c g	c t c c C C T C A G	C A C C T C C T C C ***** *****
alignment	position	4 0 1 . . . . .	4 1 1 . . . . .	4 2 1 . . . . .	4 3 1 . . . . .	4 4 1 . . . . .
<b>P910348</b>	3	CAGGCCACC	CTGATCCCGG	GGCTcga---	- - - - -	- - - AAAACTT
<b>P910350</b>	17	CGCGGgct-C	CACCTCCAGG	GCCCAC TCAA	GCTGGAGC T A	GAGAACTTT
<b>P910353</b>	401	CACGGCTTCC	CACCTCC AAG	GCCTAT TCAA	GCTGGGGC T A	GAGAACTTT ***** ***** ***** *****
alignment	position	4 5 1 . . . . .	4 6 1 . . . . .	4 7 1 . . . . .	4 8 1 . . . . .	4 9 1 . . . . .
<b>P910348</b>	37	TGCCTCCAGC	TCGCTCCACC	CGCATTCCCt	t c c c aGTTCC	GC CCCGCAGC
<b>P910350</b>	66	TACCTT CAGC	TCACAGC GCC	CGCACTTCCC	CT G - -GTTCC	CGCCGACAGC
<b>P910353</b>	451	TACCTC CAGC	TCGCAGC GTC	CGCACTTCCC	CT G - -GTTCC	CGCCGACAGC ***** ***** ***** ***** ***** ***** ***** *****
alignment	position	5 0 1 . . . . .	5 1 1 . . . . .	5 2 1 . . . . .	5 3 1 . . . . .	5 4 1 . . . . .

P910348 87 CGCTCACTCA CCTC C a g a CC CAGAGCCGGC GGGA GCCGCA TCTCTATGGT  
 P910350 114 CGCTCTCTCA CCTCCTACCC g t GGGCTGGC GGGA GCTGCA TCTCTATGGT  
 P910353 499 CGCTCTCTCA CCTTCTACCC CAGGGCTGGC GGGA GCTGCA TCTCTATGGT  
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alignment position 5 5 1 . . . . . 5 6 1 . . . . . 5 7 1 . . . . . 5 8 1 . . . . . 5 9 1 . . . . .

P910348 137 C- GGCCGC GG CTGGAACGGC CCCC GGGGCC CGCT Tt gTGC GACCGCCTCC  
 P910350 164 CCGACTGGGA CTGGAGTGGC TCCTCGGGGG CCTT TGATGT GGCCGCCCC  
 P910353 549 CCGACTGGA A CTGGCGTGGC TCCTCAGGGG CCTT TGATGC GACCGCCCC  
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alignment position 6 0 1 . . . . . 6 1 1 . . . . . 6 2 1 . . . . . 6 3 1 . . . . . 6 4 1 . . . . .

P910348 186 GGC TCAGCCG CCTCTAGGAt at t g g g g a TG TGGA AGCCAc t c t CTCTTCC  
 P910350 214 GGCC CAGGCG CCTCTAGGAA TCTGACG- TG TGGCAGCCA- - - CTCTGTC  
 P910353 599 GGCC CAGGCG CCTCTGGGAA TCTGACG- TG TG Gc g g t CA- - - CTCTGTC  
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alignment position 6 5 1 . . . . . 6 6 1 . . . . . 6 7 1 . . . . . 6 8 1 . . . . . 6 9 1 . . . . .

P910348 236 TCT TGCCG GC TGCCGGGGTA CTCTATGTTT Tg t c t c t g t g g t t t t c c c g  
 P910350 259 TCTCTTCAAG GCCCGTGCTA CTCTATGGTT TCCCCTCTAT GT CCTTGAGT  
 P910353 644 TCTCTTCAAG GCCCGTGCCA CTCTATGGTT TCCCCTCTGT GT CCTTGAGT  
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alignment position 7 0 1 . . . . . 7 1 1 . . . . . 7 2 1 . . . . . 7 3 1 . . . . . 7 4 1 . . . . .

P910348 286 c c c t c c a c c c c c ACTCCAGC CCTGAAGCCg g a g a a - GCA CCATCGAGAG  
 P910350 309 - - - - - - - - - - AC CCC c c t t CTGAAGCCC CAAA GCGGAA CCATCGAGAA  
 P910353 694 - - - - - - - - - - AC CCC AGC GCTGAAGCGC CAAA GCGGAA CCATCGAGAA  
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alignment position 7 5 1 . . . . . 7 6 1 . . . . . 7 7 1 . . . . . 7 8 1 . . . . . 7 9 1 . . . . .

P910348 334 CTCTGGGGTA GAGTGGCGTG GGCTTc t c t G TGGGTGTGGC GGGAAAGTAGA  
 P910350 347 TTGCAGGGAA GAGTGGCAAG GACTCCGTGG TGGGTGTGGC CGGAAGTAGA  
 P910353 732 TTT CAGGGAA GAGTGGCAAG GACCTCGTGG TGGGTGTGGC AGGAAGTAGA

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alignment position 8 0 1 . . . . . 8 1 1 . . . . . 8 2 1 . . . . . 8 3 1 . . . . . 8 4 1 . . . . .

**P910348** 384 TGAAGGACC CGGGGCGGGg ccgaacgcag ct t c c c c a a g g t g c AGGC GC  
**P910350** 397 TGACAGATC CGGGGCGGGA CTAGCGGCGC Tg c c t c t t c g t - - AGGCC C  
**P910353** 782 TTCATTC GGGGCGGGC CTAGAGGCGC Tt a t t c c g a g t a c g g a c t - -

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alignment position 8 5 1 . . . . . 8 6 1 . . . . . 8 7 1 . . . . . 8 8 1 . . . . . 8 9 1 . . . . .

**P910348** 434 GGT GAAACCA TCGAGACGGA GGGCCAGAGA GTCA CGGC GG TGAGA GGGCT  
**P910350** 444 GGC GAAACCA TCGAGTG TGA GGGCCAGAGA GTCA TGGA GG GAAGG GGGCG  
**P910353** 830 GGC GAAACCA TCGAGTC TGA GGGCCAGAGA GTCA TGaa a g t AAGG GGGCG

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alignment position 9 0 1 . . . . . 9 1 1 . . . . . 9 2 1 . . . . . 9 3 1 . . . . . 9 4 1 . . . . .

**P910348** 484 GAGTGACGGG TTACCCC AAA CCATGTGGCT GGAGGC GC GA GCTGGGGT GT  
**P910350** 494 GAGTGACAGA TTTC TCt c t c CCACGTTCCT GGAA GC GC GA GCAAGGTCT GT  
**P910353** 880 GAGTGACAGA TTTC TC CCGA CCACGTTCCT GGAA GC GC GG GCTGGGT GT

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alignment position 9 5 1 . . . . . 9 6 1 . . . . . 9 7 1 . . . . . 9 8 1 . . . . . 9 9 1 . . . . .

**P910348** 534 G - - GGC GAGG TTCAGGAGGG GGTT CCTGGG TGT C GCGG a - - - GGGGC CG  
**P910350** 544 G t a TAGGGTG TCCGGGAGTC AGCTGCTGTG TGT C AGGG T t c g GAGCC GG  
**P910353** 930 G - - TAGGGTG TCCGGGAGTC AGCCGCTGTG TGT C AGGG T c a g t - AGCC GG

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alignment position 1 0 0 1 . . . . . 1 0 1 1 . . . . . 1 0 2 1 . . . . . 1 0 3 1 . . . . . 1 0 4 1 . . . . .

**P910348** 578 GGGACGGGAG AGCTTTGTCT GTGGCc t TCC ATGC ATAGGT GTTTT GGAAT  
**P910350** 594 GGGCCAGGAG ATCTTCGTCA GCGGCt c TCC ATGC AAAGGT GCTTT GGAAT  
**P910353** 977 AGGCCAGGAG ATCTTCGTCA GTGGC - - - - - - - - - - - - - - - - -

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alignment position 1 0 5 1 . . . . . 1 0 6 1 . . . . . 1 0 7 1 . . . . . 1 0 8 1 . . . . . 1 0 9 1 . . . . .



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P910348    628 TCTGGATCCC AGtTCTGAGG CTCAGCCGAG GTCACTGCTG TCAGCTCACCC
P910350    644 TCTGGATCAC AGcTCCGAGC CTTAGCGGAG GTCACGGCTG TCAATTCACCC
P910353    1002 -----
      * * * * *
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      * * * * *

alignment position 1101 . . . . . 1111 . . . . . 1121 . . . . . 1131 . . . . . 1141 . . . . .
P910348    678 t c - - - C C T G C A T G C C A G G C G C A G G g c a a A G T G G C C G G G G T T C G G G G T G
P910350    694 a g t g g g C C G G T G T G C C A G G C A G A G G - - - - A G T G G C A G T G G A G A A G T G T T G
P910353    1002 -----
      * * * * *

alignment position 1151 . . . . . 1161 . . . . . 1171 . . . . . 1181 . . . . . 1191 . . . . .
P910348    724 g - A G G A G A G G T G T A C T A G A A A C A A C T T T G C T C T T G T C C C t c a g g a t c t t a
P910350    740 c a A G G A G A G G T G T T C T G G A A T A A T T G C C A T T T T G T C C C c t t a g g c a t t g
P910353    1002 -----
      * * * * *
      * * * * *

alignment position 1201 . . . . . 1211 . . . . . 1221 . . . . . 1231 . . . . . 1241 . . . . .
P910348    773 t t g t c t a c g a t g t g a c g a - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
P910350    790 t c t t a a g t t a g g c t t a g t c a c a t c t t a a t t g g g t t g a a t t t g a a a a g g c
P910353    1002 -----

alignment position 1251 . . . . . 1261 . . . . . 1271 . . . . . 1281 . . . . . 1291 . . . . .
P910348    791 - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - T C C G T G G A G A A A G T A G c
P910350    840 t c c a a a a a a a a a a a a a a a a g a a a a g a a a a g g c T C C G T G G A A G A A G T A G a
P910353    1002 -----
      * * * * *

alignment position 1301 . . . . . 1311 . . . . . 1321 . . . . . 1331 . . . . . 1341 . . . . .
P910348    808 a g a t g g g c a g a t t t t c a t t t g g g g a g a a t g a g g g a g a a a g a a c g g g - C A
P910350    890 c t a t a t g a t c t c a a t g a a a a g a a t g c c t a g a t a a a g g g g t g g g g g t C A
P910353    1002 -----
      * *

alignment position 1351 . . . . . 1361 . . . . . 1371 . . . . . 1381 . . . . . 1391 . . . . .
P910348    857 T T C C G A G C C A A G A G C A C T G C A T G A G C A A G G A G T t g g g a g g t t g c t t a c t t
P910350    940 T T C G G T A C C A A C A G A A C T G A G A G A G C T A G A A G T a g g t a g t g - - - - - - - -
P910353    1002 -----
      * * * * *

alignment position 1401 . . . . . 1411 . . . . . 1421 . . . . . 1431 . . . . . 1441 . . . . .
P910348    907 g t t g a a c a t a t t t g t t g c g t a t t t g c a t A T T T G C T A a a c a g g t a g t g t t a
P910350    981 - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - A T T T G C T A g t a a a g g t a c g c a t
P910353    1002 -----
      * * * * *

alignment position 1451 . . . . . 1461 . . . . . 1471 . . . . . 1481 . . . . . 1491 .
P910348    957 g g a g c t a a t c c a t g a a a g g t a g g t g g g c g c c g t a t t g t a g a g a g c
P910350    1003 t c t a a t g t a g g - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
P910353    1002 -----
  
```

**Pairwise similarities:**

For each pairwise alignment, the **similarity** (relative to the maximum similarity) and the **number of identical nucleic acids** (in % of shorter sequence) is given. Maximum values are underlined.

<b>P910350</b> (1013 bp)	<b>P910353</b> (1001 bp)
-----------------------------	-----------------------------

<b>P910348</b> (1001 bp)	0.404 50 %	0.279 32 %
<b>P910350</b> (1013 bp)		<b>1.000</b> <u>53 %</u>

Please note that the **similarity value 1.000** marks only the two **most similar** sequences, it does not necessarily mean that these sequences are identical.

Extract alignment region	
Positions in alignment	from: <input type="text"/> to: <input type="text"/>
Output file	<input type="text" value="dialign.seq"/>
Extract aligned sequences	<input type="text"/>

For [comments](#), questions or bug reports, please contact [support@genomatix.de](mailto:support@genomatix.de)

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GEMS Launcher 4.1.1

GEMS Launcher Task: DiAlign TF: Multiple alignment plus TF sites working on UQCRB.seq (3 seq.)

[Alignment] [Pairwise similarities]

DiAlign professional TF Release 3.1.2 January 2007

Fri Feb 16 20:24:21 2007

Solution parameters:

Sequence file: UQCRB.seq (3 seq.)
Type of sequences: nucleotide sequences
Threshold T: 0.00
\*\* signs below alignment denote: diagonal similarity (max. similarity is represented by 10 \*\* signs)
Alignment output: complete alignment is shown # nucleic acids per line: 50
TF output: common TF matches located in aligned regions (common to 3 (100.0 %) sequences)
Family matches: yes
MatInspector library: Matrix Family Library Version 6.2 (October 2006)
Selected groups (core/matrix sim): ALL\_user\_defined.lib (0.75/Optimized) ALL vertebrates.lib (0.75/Optimized)

Aligned Sequences:

Table with 3 columns: No., Sequence Name, and Sequence Description. Row 1: GXP\_207133. Row 2: sym=mmUQCRB|chr13:67340605-673. Row 3: GXP\_52345.

Alignment (DiAlign format):

Please note that only upper-case letters are considered to be aligned. For more information, please have a look at the user guide.

Alignment visualization showing sequence headers (VSHOME, VS...), alignment positions, and sequence alignments for GXP\_207133, sym=mmUQCRB, and GXP\_52345.

```

GXP_207133 (UQCRB)          86 caatttctcc aatattttca actcgaaata atcaatgtac caattccata
sym=mmUQCRB|chr13:67340605-673
(mmUQCRB)
GXP_52345 (Uqcrb_predicted) 130 TAGCATCCCC -----
151 TAGAATCCCC -----
*****
*****
*****

alignment position          201..... 211..... 221..... 231..... 241.....
GXP_207133 (UQCRB)        136 t a t t t t t g g g a t g g c a c a t c c a t c a g T C C T T C A A T A G A A A G T A A G A C G A T
sym=mmUQCRB|chr13:67340605-673
(mmUQCRB)
GXP_52345 (Uqcrb_predicted) 140 ----- T C C A T G C A T T T T G A G a t g c g G T T T
161 ----- T C C A T C C A T A C T G A G G A A G T G T G T
*****
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*****

alignment position          251..... 261..... 271..... 281..... 291.....
GXP_207133 (UQCRB)        186 G C C C T T A A A A C A T T T A G C T - - - - T C C T G C C T G G C A C A A A G A g c t g a a t
sym=mmUQCRB|chr13:67340605-673
(mmUQCRB)
GXP_52345 (Uqcrb_predicted) 164 G C C T G A A A A T C A T T T A C T A - - - - C A T T A C C T G T C T C C A A G A - - - - C T
185 G C C T G A A A A T C A T C T A C T A t c t a t t C A T T A C C T G T C T C C A A G c a a a g g C T
*****
*****

alignment position          301..... 311..... 321..... 331..... 341.....
GXP_207133 (UQCRB)        230 t a a t a c t g t c c a e g e t c c c a t a g c t a t t a a c a g e a a A T A A C A G A a c c c a g
sym=mmUQCRB|chr13:67340605-673
(mmUQCRB)
GXP_52345 (Uqcrb_predicted) 203 C C A T T T A T T C C G C A A A G g T T C T T T C C T - - - - - A T A A C A G A G C A T T G
235 C C A T C T A T A C C A T A A A G - T T C T T T C C T - - - - - G T A A C A G G G C A T G G
*****
*****

alignment position          351..... 361..... 371..... 381..... 391.....
GXP_207133 (UQCRB)        280 c t t t a a g c c t t g T T C T C C T A A T T c e t g a c c t g t g t T C T T C C C A T C A C A T C
sym=mmUQCRB|chr13:67340605-673
(mmUQCRB)
GXP_52345 (Uqcrb_predicted) 244 A A T A A C A C T - - G T T C T C C T A A T T T C G C A G T A C - - - T T T C C C A T T G T G T C
275 A A G A A C A C C - - G T C C C C T A A T T T C G T A C T A C - - - T T T T C C C A T T G T G T G
*****
*****

alignment position          401..... 411..... 421..... 431..... 441.....
GXP_207133 (UQCRB)        330 A C A A C C A A T A C T T C T T A G A A T G T A G C A C G C A A A A T G C C C C G C C T A C t c c a
sym=mmUQCRB|chr13:67340605-673
(mmUQCRB)
GXP_52345 (Uqcrb_predicted) 288 G C G A A G A A T G T T T T T T G T A A C A A G G C A C A C A A A A A G A T C A G C C T A A T G T G
319 A C G A A A A A T G T T T C T T - T A A C A A G G C G C A C A A A A A G A T C A G G C T A A T G T G
*****
*****

alignment position          451..... 461..... 471..... 481..... 491.....
GXP_207133 (UQCRB)        380 t t g g c c t c a c c e t g g c c g a g a g g t g c t t a c g c a g g t g e t g a a c g g c a g t c
sym=mmUQCRB|chr13:67340605-673
(mmUQCRB)
GXP_52345 (Uqcrb_predicted) 338 T G G A G T C c a T T C A G G T A G G A A A g a g t - - - A A A T G C C T T C T G C T G G C G - - -
368 T G G A G T C c g T T C A G A T A A G A A A a t t t a a a A A A C G C C T T C C A C G G G C C - - -
*****
*****

alignment position          501..... 511..... 521..... 531..... 541.....
GXP_207133 (UQCRB)        430 G T C A G A A C T G C G C C T G C G C A A G C G G C C T t t c t c t g t t e g c g a t g t g a c g t
sym=mmUQCRB|chr13:67340605-673
(mmUQCRB)
GXP_52345 (Uqcrb_predicted) 382 G T C A G A G C A G C G C C T G C c e c t c ----- C C T T
415 A T C A G A G C T G C G C C T G T G C A G G C G C C C T c a g e a c t c e e t c t t c c c t C C C T
*****
*****

alignment position          551..... 561..... 571..... 581..... 591.....
GXP_207133 (UQCRB)        480 a a c g - - - - - - - - - - - - C G C C T G C G g a c t g g G C C C A G C T T G T C C T
sym=mmUQCRB|chr13:67340605-673
(mmUQCRB)
GXP_52345 (Uqcrb_predicted) 408 C C C C T T C C T A A A G T A T C C A G G A C G C C T G C G t a g G A - G C C C G G C G T G T C C T
465 C C C C T T C C G A A A G T A T G C A G G A C G C C T G C G c g t G A - C C C C G G C G C T C C T
*****
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alignment position
GXP_207133 (UQCRB)
sym=mmUQCRB|chr13:67340605-673
(mmUQCRB)
GXP_52345 (Uqerb_predicted)

601..... 611..... 621..... 631..... 641.....
512 CTATGACTTA CCCAGAAGGC AACGCTTCTC TTCTGGTCA AAATGGCTGG
547 CTAGGACTTA CCCAGAAGGC AGCGCTTCA C TCTCAGGTCA AAATGGCGGG
514 CTAGGACTTA CCCAGAAGGC AGCTCTc t AC TCTTAGGTCA AAATGGCGGG
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alignment position
GXP_207133 (UQCRB)
sym=mmUQCRB|chr13:67340605-673
(mmUQCRB)
GXP_52345 (Uqerb_predicted)

651..... 661..... 671..... 681..... 691.....
562 TAAAGCAGGCC GGTAAGTAACT ggg g g t CTT CTGGCCGGC ATCGTCGCGC
507 CCGATCTGCT GGTGAGTAAT Tact c - - CTC CTTTGTGGGT ATCGTGGAGC
564 CCGACCTGCA GGTAAGTg a g c t c a t c - CTC TTTTGTGGGT ATCGTGGGGC
*****
*****
*****
*****
*****

alignment position
GXP_207133 (UQCRB)
sym=mmUQCRB|chr13:67340605-673
(mmUQCRB)
GXP_52345 (Uqerb_predicted)

701..... 711..... 721..... 731..... 741.....
612 t t c a c c g t t t a t - - - - - T TTTGCTGCAG CTt g c t c c g t
555 GGTGTGATTT TCTCACGAAC t TGTCTCCT TTTGCGTTAG CTAAAt a g c T
613 GGTGTGATTT TCCCACGAAa - TGCTCTCAT TTTGCTTTAG CTAAA- - - - T
*****
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*****

alignment position
GXP_207133 (UQCRB)
sym=mmUQCRB|chr13:67340605-673
(mmUQCRB)
GXP_52345 (Uqerb_predicted)

751..... 761..... 771..... 781..... 791.....
645 t t t c t c t c t t c t t t g t a a - - GTGGCCAAGT TTGTCGCGGA AGGGAAAt t g
605 AGTTTGTGAT AAGAGACGTG GCGACCCAGC - - - AGCTCA AAGGACAGGT
658 AGTTTGCAT AAGAGACGTG GTGGCCAGC CTGTAGCTCA AAGGACAGGT
*****
*****
*****
*****

alignment position
GXP_207133 (UQCRB)
sym=mmUQCRB|chr13:67340605-673
(mmUQCRB)
GXP_52345 (Uqerb_predicted)

801..... 811..... 821..... 831..... 841.....
693 g c t g c t t c a g t c c a g t g a a a g g a t g t g c t t c c c c a c t c g t t t g c t g t c c
651 TTCGCTg a g - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
708 TTCGCTt a a - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
*****
*****
*****

alignment position
GXP_207133 (UQCRB)
sym=mmUQCRB|chr13:67340605-673
(mmUQCRB)
GXP_52345 (Uqerb_predicted)

851..... 861..... 871..... 881..... 891.....
743 CCAGGGCGGG CTTGCCTGt a t a g g g t t g g g a t g t a a c c c g c t g t t g t G
660 CCAGGTGCGG CCTGCCTGAG GGTTAGAACA GGGACCTCTG CCG- - - - G
717 - - - - - CCTGCCTGAG GATTAGAACA GGGACCTCCG CCG- - - - G
*****
*****
*****
*****
*****

alignment position
GXP_207133 (UQCRB)
sym=mmUQCRB|chr13:67340605-673
(mmUQCRB)
GXP_52345 (Uqerb_predicted)

901..... 911..... 921..... 931..... 941.....
793 AAGGTGCCCG CCGTGGCTc t g a c a g c c c t g g a g t t c c a g c t g c c c g t GCT
704 AAGGAGCCCA GCGGGGCTg a c - - CG- - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
751 AAGGAGCCCG CTGTGGCa g a c a g CG- - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
*****
*****
*****
*****

alignment position
GXP_207133 (UQCRB)
sym=mmUQCRB|chr13:67340605-673
(mmUQCRB)
GXP_52345 (Uqerb_predicted)

951..... 961..... 971..... 981..... 991.....
843 TGGAAGTCCT TCCC- CTTGG CCTTAGAAAA GTTAAAGGGC Ac a a g a g g a t
730 TCGGCCTCCT TCCC- CTCCG CCTTGGGACA GCTTAGGGa g tGAGGAGGT
779 TCGGCCTCCT CCc t t CTCCG CCTTATGACA GCTTAGGAAC ATGGGGAGGT
*****
*****
*****
*****

alignment position
1001..... 1011..... 1021..... 1031..... 1041.....
```

```

GXP_207133 (UQCRB)          892 a a c t a g t g g a t g a c t t t c a a c c c g a a t g a g c t c a g t g c t t t c t a t g a c c c
sym=mmUQCRB|chr13:67340605-673 779 C A G C A G A C G A C - - - - -
(mmUQCRB)
GXP_52345 (Uqcrb_predicted) 829 C A G C A G A A G A C - - - - -
*****
*****
*****

alignment position          1 0 5 1 . . . . . 1 0 6 1 . . . . . 1 0 7 1 . . . . . 1 0 8 1 . . . . . 1 0 9 1 . . . . .
GXP_207133 (UQCRB)          942 a a g t g c t c t a t c g t g t g c a t t g g c c c t a t a a a t t t t c t T G C C A T T G C G A C
sym=mmUQCRB|chr13:67340605-673 790 - - - - -
(mmUQCRB)
GXP_52345 (Uqcrb_predicted) 840 - - - - - T G C C A C A G C G A G
*****
*****

alignment position          1 1 0 1 . . . . . 1 1 1 1 . . . . . 1 1 2 1 . . . . . 1 1 3 1 . . . . . 1 1 4 1 . . . . .
GXP_207133 (UQCRB)          992 G - - A G G G A G a t a - - - - -
sym=mmUQCRB|chr13:67340605-673 802 T a g t G G G G A G C A T T T G G A G T C A G G C G C A G G C C A C T T C A G T G A C A G T G A T C
(mmUQCRB)
GXP_52345 (Uqcrb_predicted) 852 T - - G G G G A G C A T T T A G A G T C A G A C G C A G G C C T T T T C A G T G A C A G T G A T C
* *****
* *****
* *****

alignment position          1 1 5 1 . . . . . 1 1 6 1 . . . . . 1 1 7 1 . . . . . 1 1 8 1 . . . . . 1 1 9 1 . . . . .
GXP_207133 (UQCRB)          1002 - - - - -
sym=mmUQCRB|chr13:67340605-673 852 G G A G C A A A C A G C G C C C G A G C C G C A T G A C G C T C C T a a g a c t t g t c a g a A G
(mmUQCRB)
GXP_52345 (Uqcrb_predicted) 899 T G A G C A A A T A G C T C T G G A G T C C G G A T G C C G C T C C T c g a g c t t g t c - - A G
*****
*****

alignment position          1 2 0 1 . . . . . 1 2 1 1 . . . . . 1 2 2 1 . . . . . 1 2 3 1 . . . . . 1 2 4 1 . . . . .
GXP_207133 (UQCRB)          1002 - - - - -
sym=mmUQCRB|chr13:67340605-673 902 A A T T A A A A G G A A G T A A G A T A G G t t a t A G T G A G G T T T C A G G T T A A C C T T G
(mmUQCRB)
GXP_52345 (Uqcrb_predicted) 946 A A T T A A A G G G A G G T A A G A T A G G t c a c - A G T G A G G T T T C A G G T T A A T C T T G
*****
*****

alignment position          1 2 5 1 . . .
GXP_207133 (UQCRB)          1002 - - - - -
sym=mmUQCRB|chr13:67340605-673 952 G C a - - -
(mmUQCRB)
GXP_52345 (Uqcrb_predicted) 995 G C c t a t c
**
**
**
    
```

**Pairwise similarities:**

For each pairwise alignment, the [similarity](#) (relative to the maximum similarity) and the [number of identical nucleic acids](#) (in % of shorter sequence) is given. Maximum values are underlined.

	sym=mmUQCRB chr13:67340605-673 (954 bp)	GXP_52345 (1001 bp)
GXP_207133 (1001 bp)	0.112 27 %	0.090 25 %
sym=mmUQCRB chr13:67340605-673 (954 bp)		<u>1.000</u> <u>79 %</u>

Please note that the **similarity value 1.000** marks only the two **most similar** sequences, it does not necessarily mean that these sequences are identical.

**Extract Alignment Region**

<b>Positions in alignment</b>	from: <input style="width: 150px;" type="text"/>	to: <input style="width: 150px;" type="text"/>
<b>Output file</b>	<input style="width: 100%;" type="text" value="dialign.seq"/>	

**Extract Aligned Sequences**



For [comments](#), questions, or bug reports, please contact [support@genomatix.de](mailto:support@genomatix.de).

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GEMS Launcher 4.4.0

[License Agreement](#)

**GEMS Launcher Task: *DiAlign TF*: Multiple alignment plus TF sites working on promoters\_3.seq (3 seq.)**

[\[Alignment\]](#) [\[Pairwise similarities\]](#)

DiAlign professional TF Release 3.1 December 2004

Wed Jun 8 22:14:47 2005

**Solution parameters:**

**Sequence file:** [promoters\\_3.seq](#) (3 seq.)  
**Type of sequences:** nucleotide sequences  
**Threshold T:** 0.00  
**\*' signs below alignment denote:** diagonal similarity (max. similarity is represented by 10 '\*' signs)  
**Alignment output:** complete alignment is shown  
 # nucleic acids per line: 50  
**TF output:** common TF matches located in aligned regions (common to 3 (100.0 %) sequences)  
**Family matches:** yes  
**MatInspector library:** Matrix Family Library Version 5.0 (February 2005)  
 • ALL user\_defined.lib (0.75/Optimized)  
 • ALL vertebrates.lib (0.75/Optimized)  
**Selected groups**  
 (core/matrix sim):

**Aligned Sequences:**

No.	Sequence Name	Sequence Description	Length
1	P889591	sym=UQCRC1 loc=Loc7384 taxid=9606 spec=Homo sapiens chr=3  ctg=NT_022517 str=(-) start=48586578 end=48587602 len=1025  tss=501,525  comm=ubiquinol-cytochrome c reductase core protein I; (AK129903/556/gold;NM_003365/532/silver;)	1025 bp
2	P889594	sym=Uqrcr1 loc=Loc22273 taxid=10090 spec=Mus musculus chr=9  ctg=NT_039478 str=(+) start=24319 end=25379 len=1061  tss=501,554,560,561  comm=ubiquinol-cytochrome c reductase core protein I; (AK004031/554/gold;AK013128/561/gold;AK010553/561/gold; AK002292/560/gold;NM_025407/501/bronze;)	1061 bp
3	P889596	sym=na loc=Loc301011 taxid=10116 spec=Rattus norvegicus  chr=8 ctg=NW_047802 str=(+) start=399100 end=400100  len=1001 tss=501  comm=similar to ubiquinol-cytochrome c reductase core protein I; (XM_217267/552/bronze;)	1001 bp

**Alignment (DiAlign format):**

Please note that only **upper-case** letters are considered to be **aligned**. For more information, please have a look at the user guide.

V\$EGRF
V\$NRF1
V\$NRF2
V\$EVI1
V\$YY1F
V\$NEUR
V\$MZF1
V\$RBPF
V\$IKRS
V\$RORA
V\$SPIF
V\$MAZF  
V\$CMYB
V\$VMYB

alignment position      1 . . . . . 1 1 . . . . . 2 1 . . . . . 3 1 . . . . . 4 1 . . . . .  
**P889591**                    1 g g c a g g a g a a t c g c t t g a a g c c g g g a g g c g g a g g t t g c a g t g a g c c g a g a





alignment position	4 5 1 . . . . .	4 6 1 . . . . .	4 7 1 . . . . .	4 8 1 . . . . .	4 9 1 . . . . .
<b>P889591</b>	273 - - - - T G C A	CT <b>CTGACTTC</b>	<b>CACGCGTGG</b> A	ATGGGGAGAT	GGAc t g c a c g
<b>P889594</b>	298 C A C A G T T G C A	<b>TACCGCCTCC</b>	<b>CTCAGGTGG</b> A	AGAAGGTGAT	GAATA GAACC
<b>P889596</b>	279 T G C A G T T G C A	<b>CACCGCCTCC</b>	<b>CTCAGGTGG</b> A	AGAAGGCGAC	GAATGGGACC
	* * * * *	* * * * *	* * * * *	* * * * *	* * * * *
	* * * * *	* * * * *	* * * * *	* * * * *	* * * * *
	* * * * *	* * * * *	* * * * *	* * * * *	* * * * *
alignment position	5 0 1 . . . . .	5 1 1 . . . . .	5 2 1 . . . . .	5 3 1 . . . . .	5 4 1 . . . . .
<b>P889591</b>	317 g c g g g c g g a c	c t g c t c g g g c	t g a t g g a c g -	- - - - - GCAG	GTGG- - - - -
<b>P889594</b>	348 t g t c t c a g a t	g g g a c c a g a t	g A A G G G C C C C	T C C C T C G C A G	G T T g a t a a a t
<b>P889596</b>	329 g t c t - - - - -	- - - - -	- A A G G G C C A G	C C A G T C G C A G	G T T C - - - - -
			* * * * *	* * * * *	* * * * *
alignment position	5 5 1 . . . . .	5 6 1 . . . . .	5 7 1 . . . . .	5 8 1 . . . . .	5 9 1 . . . . .
<b>P889591</b>	354 - - - - -	ACTGATGTGC	GCAGGGACt g	g c g g c a g c g c	g g t c a g a g c c
<b>P889594</b>	398 g t c c c g a a g a	T C C T A G A G G C	A C A C G G A C C A	A A T G A C T A C A	T G C G A T c A A T
<b>P889596</b>	356 - - - - -	T C T T A G A G G C	A C A A G G A C C A	A A C G A C A A C A	T G C G A T t A A T
		* * * * *	* * * * *	* * * * *	* * * * *
		* * * * *	* * * * *	* * * * *	* * * * *
alignment position	6 0 1 . . . . .	6 1 1 . . . . .	6 2 1 . . . . .	6 3 1 . . . . .	6 4 1 . . . . .
<b>P889591</b>	394 a g t c a g c c a a	a g c c a g g c c a	g c a c a a t a g a	c t g t c c c g g t	t c c c g c c a g g
<b>P889594</b>	448 T C T T G C T A A C	G T A C T T G C T G	C C C A A C A G G G	- - - - -	- - - - -
<b>P889596</b>	396 T C T T G C C A A T	G G A C T T G A T G	C C C A G C A G G G	- - - - -	- - - - -
	* * * * *	* * * * *	* * * * *	* * * * *	* * * * *
	* * * * *	* * * * *	* * * * *	* * * * *	* * * * *
alignment position	6 5 1 . . . . .	6 6 1 . . . . .	6 7 1 . . . . .	6 8 1 . . . . .	6 9 1 . . . . .
<b>P889591</b>	444 a GGC GGCCGA	GCACCAACTG	TACGGTACTG	<b>CGCCTGCGCC</b>	g c g a c c g c c a
<b>P889594</b>	478 - GGC GACTGA	GCACCAAGTC	TTCCTTACAG	<b>CGCCTGCGCC</b>	T C A G A C T - - -
<b>P889596</b>	426 - GGC GATCGA	GCACCAACTC	TTCCTTACAG	<b>CGCCTGCGCC</b>	T C A T A C T - - -
	* * * * *	* * * * *	* * * * *	* * * * *	* * * * *
	* * * * *	* * * * *	* * * * *	* * * * *	* * * * *
	* * * * *	* * * * *	* * * * *	* * * * *	* * * * *
	* * * * *	* * * * *	* * * * *	* * * * *	* * * * *
alignment position	7 0 1 . . . . .	7 1 1 . . . . .	7 2 1 . . . . .	7 3 1 . . . . .	7 4 1 . . . . .
<b>P889591</b>	494 a c g c g c C C A G	<b>TCTACGCTTG</b>	<b>CGCGGC</b>	GCa a c a g g -	GCCG AC <b>TGCAGCTG</b>
<b>P889594</b>	524 - - - - - C c g c	<b>TCTGCGCATG</b>	<b>CGCAGC</b>	GC GG	CTCTACACTG AC <b>GGAAGT TA</b>
<b>P889596</b>	472 - - - - - C C A C	<b>CCTGCGCATG</b>	<b>CGTAGC</b>	GC GG	CTTTACGCTG AC <b>GGAAGT TA</b>
	* * * * *	* * * * *	* * * * *	* * * * *	* * * * *
	* * * * *	* * * * *	* * * * *	* * * * *	* * * * *
	* * * * *	* * * * *	* * * * *	* * * * *	* * * * *
	* * * * *	* * * * *	* * * * *	* * * * *	* * * * *
	* * * * *	* * * * *	* * * * *	* * * * *	* * * * *
alignment position	7 5 1 . . . . .	7 6 1 . . . . .	7 7 1 . . . . .	7 8 1 . . . . .	7 9 1 . . . . .
<b>P889591</b>	542 <b>GAAGATGCGG</b>	<b>GCG</b> TCCGTGG	TCTGTCGGGC	CGCTACCGCC	GGGGCACAAG
<b>P889594</b>	568 <b>GAAGATGCGG</b>	<b>GCG</b> TCCGCAG	TCTGCCGAGC	GGCCTGCTCc	GGGACGCAAG
<b>P889596</b>	516 <b>GAAGATGCGG</b>	<b>GCG</b> TCCGCAG	TCTGCCGAGC	GGCCTGCTCT	GGGACGCAAG
	* * * * *	* * * * *	* * * * *	* * * * *	* * * * *
	* * * * *	* * * * *	* * * * *	* * * * *	* * * * *
	* * * * *	* * * * *	* * * * *	* * * * *	* * * * *
	* * * * *	* * * * *	* * * * *	* * * * *	* * * * *
	* * * * *	* * * * *	* * * * *	* * * * *	* * * * *
	* * * * *	* * * * *	* * * * *	* * * * *	* * * * *
	* * * * *	* * * * *	* * * * *	* * * * *	* * * * *
	* * * * *	* * * * *	* * * * *	* * * * *	* * * * *
	* * * * *	* * * * *	* * * * *	* * * * *	* * * * *



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```
alignment
position      1 1 0 1 . . . . . 1 1 1 1 . . . . . 1 1 2 1 . . . . . 1 1 3 1 . . . . . 1 1 4 1 . . . . .
P889591    868 C C C T G C T G C G G A C G C C A G C C T T G C G G A G T A C g G C A A C C T T C G C T C A G G C G
P889594    873 C C C T G C T G A G G T T A C C T G C C T T G C G G G G T A C C G C A A C C T T C G C C C A G G C C
P889596    821 C C C T G C T G A G G C T A C C T G C C T T G C G G G G T A C C G C A A C C T T C G T C C A G G C C
* * * * *
* * * * *
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* * * * *
```

```
alignment
position      1 1 5 1 . . . . . 1 1 6 1 . . . . . 1 1 7 1 . . . . . 1 1 8 1 . . . . . 1 1 9 1 . . . . .
P889591    918 C T C C A G T T C G T G C C G G A G A C g C A G G T T A G C C T G C T G G A C A A C G G C C T G C G
P889594    923 C T C C A G A G C G T G C C G G A G A C C C A G G T C A G C A T C T T G G A C A A C G G G C T G C G
P889596    871 C T C C A G A G C G T G C C G G A G A C A C A G G T C A G C G T A T T G G A C A A C G G G C T G C G
* * * * *
* * * * *
* * * * *
* * * * *
* * * * *
* * * * *
```

```
alignment
position      1 2 0 1 . . . . . 1 2 1 1 . . . . . 1 2 2 1 . . . . . 1 2 3 1 . . . . . 1 2 4 1 . . . . .
P889591    968 T G T G G C C T C c G A G C A G T C C T C T C A G C C C A C T T G C A C G G T G A G T t g g g a c
P889594    973 T G T G G C C T C G G A G C A G T C C T C G C A T G C T A C C T G C A C G G T A A G T G T g c G C C
P889596    921 T G T G G C C T C G G A G C A G T C C T C G C A T C C T A C C T G C A C G G T G A G T G T t t G C C
* * * * *
* * * * *
* * * * *
* * * * *
* * * * *
* * * * *
```

```
alignment
position      1 2 5 1 . . . . . 1 2 6 1 . . . . . 1 2 7 1 . . . . . 1 2 8 1 . . . . .
P889591    1018 g c t t t t g g - - - - -
P889594    1023 A G T C C T C T A G G T G A G G C C C G C C G T G T T G T C C c a g g t t g g
P889596    971 A G T C C T C C A G A T G A G G C G C G C C G T G T T G T C C - - - - -
* * * * *
* * * * *
```

### Pairwise similarities:

For each pairwise alignment, the similarity (relative to the maximum similarity) and the number of identical nucleic acids (in % of shorter sequence) is given. Maximum values are underlined.

	<b>P889594</b> (1061 bp)	<b>P889596</b> (1001 bp)
<b>P889591</b> (1025 bp)	<u>0.286</u> 40 %	<u>0.280</u> 41 %

<b>P889594</b> (1061 bp)		<b>1.000</b> <u>81 %</u>
-----------------------------	--	-----------------------------

Please note that the **similarity value 1.000** marks only the two **most similar** sequences, it does not necessarily mean that these sequences are identical.

**Extract alignment region****Positions in alignment**from:  to: **Output file**

dialign.seq

**Extract aligned sequences**

For [comments](#), questions or bug reports, please contact [support@genomatix.de](mailto:support@genomatix.de)

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GEMS Launcher 4.1.1

**GEMS Launcher Task: *DiAlign TF*: Multiple alignment plus TF sites working on promoters\_4.seq (3 seq.)**

[\[Alignment\]](#)   [\[Pairwise similarities\]](#)

DiAlign professional TF Release 3.1 December 2004

Mon Jun 13 19:20:05 2005

### Solution parameters:

**Sequence file:** [promoters\\_4.seq](#) (3 seq.)  
**Type of sequences:** nucleotide sequences  
**Threshold T:** 0.00  
**\*' signs below alignment denote:** diagonal similarity (max. similarity is represented by 10 '\*' signs)  
**Alignment output:** complete alignment is shown  
 # nucleic acids per line: 50  
**TF output:** common TF matches located in aligned regions (common to 3 (100.0 %) sequences)  
**Family matches:** yes  
**MatInspector library:** Matrix Family Library Version 5.0 (February 2005)  
 • ALL user\_defined.lib (0.75/Optimized)  
 • ALL vertebrates.lib (0.75/Optimized)  
**Selected groups**  
 (core/matrix sim):

### Aligned Sequences:

No.	Sequence Name	Sequence Description	Length
1	P877126	sym=UQCRC2 loc=Loc7385 taxid=9606 spec=Homo sapiens chr=16 ctg=NT_010393 str=(+) start=13276560 end=13277560 len=1001 tss=501 comm=ubiquinol-cytochrome c reductase core protein II; (AK094006/501/gold;)	1001 bp
2	P877133	sym=Uqrc2 loc=Loc67003 taxid=10090 spec=Mus musculus chr=7 ctg=NT_039433 str=(+) start=38538143 end=38539182 len=1040 tss=501,510,530,537,540 comm=ubiquinol cytochrome c reductase core protein 2; (AK088103/530/gold;AK004492/510/gold;AK075856/540/gold;AK077583/537/gold;AK003975/510/gold;NM_025899/501/bronze;)	1040 bp
3	P877136	sym=na loc=Loc293448 taxid=10116 spec=Rattus norvegicus chr=1 ctg=NW_047562 str=(+) start=22129644 end=22130644 len=1001 tss=501 comm=similar to Ubiquinol-cytochrome C reductase complex core protein 2, mitochondrial precursor (Complex III subunit II); (XM_215042/506/bronze;)	1001 bp

### Alignment (DiAlign format):

Please note that only **upper-case** letters are considered to be **aligned**. For more information, please have a look at the user guide.

**Warning: No common TF matches found.**

```

alignment position 1 . . . . . 11 . . . . . 21 . . . . . 31 . . . . . 41 . . . . .
P877126          1 t t g g g t t g a g g g c g t c c c c a g c a g g c a c a g a a a t t g g g t t g g t g c c a g g t
P877133          1 a - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
P877136          1 t g g t t c c c g a - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
    
```



**P877133** 95 g c a a g g a g a c c t a c a a G T G T G T C G A T C T G T T C G A C G A G A C A T T C G T C C T G  
**P877136** 117 a g c c c a c c t a t a g - - - G T G T G T C G A C C T G T T C G A C G A G A C A C T C G T C C T G  
\* \* \* \* \*  
\* \* \* \* \*  
\* \* \* \* \*  
\* \* \* \* \*  
\* \* \* \* \*  
\* \* \* \* \*  
\* \* \* \* \*

alignment position 551 . . . . . 561 . . . . . 571 . . . . . 581 . . . . . 591 . . . . .  
**P877126** 475 C C G G T T T C G G c t c a c a t a a c a c a c c t a c t a t c c a a a a c a t t t c t a t t t t c  
**P877133** 145 C C A G T T T C t g t g - A A C T C G G T C A -  
**P877136** 164 C C G G T C T C G G t g a A A C T C G G T C A -  
\* \* \* \* \*  
\* \* \* \* \*  
\* \* \* \* \*  
\* \* \* \* \*  
\* \* \* \* \*

alignment position 601 . . . . . 611 . . . . . 621 . . . . . 631 . . . . . 641 . . . . .  
**P877126** 525 c t a a c a c a a a a a c t a t a g c t a a g t t t t t a t a t t c t a t g t a g c c c a g c c t  
**P877133** 167 -  
**P877136** 187 -

alignment position 651 . . . . . 661 . . . . . 671 . . . . . 681 . . . . . 691 . . . . .  
**P877126** 575 a g g a c g t a a a t t c c a c g a g a c c a a a a g c c t t g t g a t g a t t c c c c g a g g t t  
**P877133** 167 -  
**P877136** 187 -

alignment position 701 . . . . . 711 . . . . . 721 . . . . . 731 . . . . . 741 . . . . .  
**P877126** 625 g c t g a c c c t c c c g g t g t g t c c c g g c c t g c t c t g g g g g a c a c a g c g g c g a  
**P877133** 167 -  
**P877136** 187 -

alignment position 751 . . . . . 761 . . . . . 771 . . . . . 781 . . . . . 791 . . . . .  
**P877126** 675 a t a c g t t g a a c g a g g c c c t g t t t c a c g g a g c t a a a g a t c c a g t a a g g a c  
**P877133** 167 -  
**P877136** 187 -

alignment position 801 . . . . . 811 . . . . . 821 . . . . . 831 . . . . . 841 . . . . .  
**P877126** 725 t t c a c c c a g c g a g a g g c a a c t a c g c c g g g c t t c g a t a c c c a a t a c c t c t g  
**P877133** 167 -  
**P877136** 187 -

alignment position 851 . . . . . 861 . . . . . 871 . . . . . 881 . . . . . 891 . . . . .  
**P877126** 775 c a g a a a g g t g g a g t g g c a g g a a t c t c c t g a a g c c t c c a a c g t C C - A G G A A  
**P877133** 167 -  
**P877136** 187 -  
\* \* \* \* \*

alignment position 901 . . . . . 911 . . . . . 921 . . . . . 931 . . . . . 941 . . . . .  
**P877126** 824 C G C G G A A A C C C A G G G C C T C C A G T G C A G G T G T C a t c c c g - - - - - - - - - -  
**P877133** 174 C G C G G T A C C G G A A G A C T A C A G T A A A A G T G G C G A G G G A C G A C T C C G A G G  
**P877136** 195 C T C G G T A C C A C T T T T A C T A C A G A A C A A G T G G C G A G G G A T G A C T C C C G G G  
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alignment position 951 . . . . . 961 . . . . . 971 . . . . . 981 . . . . . 991 . . . . .
P877126      862 - - - - - - - - - - - - - - - - - - - - GAGGGCGC ATGCCGAGTC
P877133      224 AACAGGGAGT GC CGACGAc t c c c g g - ACT T GCGAGGACTC ACGGCAGGC
P877136      245 TATAGGAAGT TCCGACGAg t c t g g g a ACT G GCGCGGACTC ACGAGCAGGT
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alignment position 1001 . . . . . 1011 . . . . . 1021 . . . . . 1031 . . . . . 1041 . . . . .
P877126      880 CCAAGAg a g g c g c g t c c c a t t g GACAATGC T GAGCGGAAG AGC CCAAGAT
P877133      273 CCAAGACg g c t g g - - - - - - - - - - GG T GACTGTGAC GGCTGCAGAC
P877136      295 CCAAGACt a g a g t t g g g c g c - - GGCTAAGG T GACCGTGAC GGCTGCAGAC
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alignment position 1051 . . . . . 1061 . . . . . 1071 . . . . . 1081 . . . . . 1091 . . . . .
P877126      930 AGCGGGGGGA GT t g t g ACAG GC- - - - - - - - - TGCTGCA GACGTA ACT TA
P877133      308 GCAGCTGGGA TT - - - - ACAG GCt g c a t g t c t t TGCAGAA AAAGA ACT CA
P877136      343 GAAGTTGGGA TT - - - - ACAG GC- - - - - - - - - TGCAGAA AAAGA ACT CA
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alignment position 1101 . . . . . 1111 . . . . . 1121 . . . . . 1131 . . . . . 1141 . . . . .
P877126      969 GAAAA Gg g g t - - - - - - - - - - - - - - - - - - - -
P877133      354 GAAAGGATAA CCTa c a a a a g c t g c a a t c t a g t c c g g g a g a c c t c t a g c c t
P877136      378 GAAAGGATAA CCTt a a c a t g c t g c g t g c t c g c a a g a c t c a t c c g - - - - -
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alignment position 1151 . . . . . 1161 . . . . . 1171 . . . . . 1181 . . . . . 1191 . . . . .
P877126      979 - - - - - - - - - - - - - - - - - - - - - - - -
P877133      404 c t c c c c a g g a g c t g g g c t c g t c c c GCCTAC C GGAGC AGTA GAGCACTGCA
P877136      422 - - - - - - - - - - - - - - - - - - - - GCCTT C C GGAGC AGTA GAGCACAGAG
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alignment position 1201 . . . . . 1211 . . . . . 1221 . . . . . 1231 . . . . . 1241 . . . . .
P877126      979 - - - - - - - - - - - - - - - - - - - - - - - -
P877133      454 TGCGT AGAGG GC CGc c g g t a CAAGGGGGCG T GGGCAAGCT CGC AGTGC AC
P877136      448 TGCGT AGAAG GC CGc t c g g c CAAGGGGGCG T GGGCAAGCT CGC AGTGC AC
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alignment position 1501 . . . . . 1511 . . . . . 1521 . . . . . 1531 . . . . . 1541 . . . . .
P877126 1002 - - - - -
P877133 754 AGCCGAGGCC TGGGAg GCTC GGCGGGTCCCT GTGAGCAGc g a g a g c t a a c
P877136 748 AGCTGAGGCC TGGGA- GCTC GGCGGGTTCT GTGAGCAGg a a g a g a a c t g a
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alignment position 1551 . . . . . 1561 . . . . . 1571 . . . . . 1581 . . . . . 1591 . . . . .
P877126 1002 - - - - -
P877133 804 g c g g - GGAAA GC GGAAGAGG AGGGTGGCCT GGAGAGTGGC GGAGAGa g CGG
P877136 797 c t c c c GGAAA GC CGGAGAGA AGGGTGGCCT TGGGAGTGGC GGAGAGt CGG
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alignment position 1601 . . . . . 1611 . . . . . 1621 . . . . . 1631 . . . . . 1641 . . . . .
P877126 1002 - - - - -
P877133 853 CTCTCGGGAG ATTCCTGAAG GTCAC TCGAG AAGCa GGTAG GGTGTAGGCC
P877136 847 GTCTCAGGAG ACTCCTGAAG GTCAC TCGAG AAGCt GGTAG GGAGAAGGCC
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alignment position 1651 . . . . . 1661 . . . . . 1671 . . . . . 1681 . . . . . 1691 . . . . .
P877126 1002 - - - - -
P877133 903 AACGCCACCC GGGCCGCCTG CT Tc c c c t a c c t a c g a c CTC TGCCCTGGG
P877136 897 AACGACACCC GAGCCTCTTA CT Tt t c c a g c a g a g a t - CTC TGCTCCTGGG
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* * * * *
* * * * *

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alignment position 1701 . . . . . 1711 . . . . . 1721 . . . . . 1731 . . . . . 1741 . . . . .
P877126 1002 - - - - -
P877133 953 TTGATCCc g a GGCGTCGGTT TCCCAATGC GTGCGAGTTT ATT Aa a t t c a
P877136 946 TTTATCCt c g GGCATCAGTT TCCCAAGTGC CTGCAAGTAT AAT At a a t a a
* * * * *
* * * * *
* * * * *
* * * * *

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alignment position 1751 . . . . . 1761 . . . . . 1771 . . . . . 1781 . . . . .
P877126 1002 - - - - -
P877133 1003 c a a a c g c g g t g c g c t g c t t a t c t c a g t g c c g g c a c c t t
P877136 996 a t g c a c - - - - -

```

**Pairwise similarities:**

For each pairwise alignment, the **similarity** (relative to the maximum similarity) and the **number of identical nucleic acids** (in % of shorter sequence) is given. Maximum values are underlined.

	<b>P877133</b> (1040 bp)	<b>P877136</b> (1001 bp)
<b>P877126</b> (1001 bp)	0.011 8 %	0.015 9 %
<b>P877133</b> (1040 bp)		<b>1.000</b> <u>71 %</u>

Please note that the **similarity value 1.000** marks only the two **most similar** sequences, it does not necessarily mean that these sequences are identical.

Extract alignment region	
<b>Positions in alignment</b>	from: <input type="text"/> to: <input type="text"/>
<b>Output file</b>	<input type="text" value="dialign.seq"/>
<b>Extract aligned sequences</b>	

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GEMS Launcher 4.1.1



					* * * * *	* * * * *	* * * * *	* * * * *	* * * * *
					***	***	***	***	***
					***	***	***	***	***
alignment position	5 1 . . . . .	6 1 . . . . .	7 1 . . . . .	8 1 . . . . .	9 1 . . . . .				
<b>P932494</b>	27 a a a a c g c a	AA ACCAAATACA	CAGT GAATAC	T TAATAAAC A	T AATCC A t a				
<b>P932495</b>	24 C - - - - -	AA ATCAAAAAGCG	T AGT AGATCA	T GAATAATCG	T AAGCC AC c g				
<b>P932496</b>	51 C - - - - -	AA ATCCAAAAGCG	T GGT GTATGA	T GAAAAATTG	T AAGCC AC g -				
	*	**	**	**	**	**	**	**	**
	*	**	**	**	**	**	**	**	**
	*	**	**	**	**	**	**	**	**
	*	**	**	**	**	**	**	**	**
alignment position	1 0 1 . . . . .	1 1 1 . . . . .	1 2 1 . . . . .	1 3 1 . . . . .	1 4 1 . . . . .				
<b>P932494</b>	77 g c - - - - -	- - - - -	- - - - -	ATT ATCGAGCTTT	GCACAGATGC				
<b>P932495</b>	67 t t t t g t t t t g	t t t t g t t t t g	t t t t g t t t t g	t t t t GTT TTT	GTCAAACCTT	GCATATAGGT			
<b>P932496</b>	93 - - - - -	- - - - -	- - - - -	- - - - - GATATT	GTCAAATTTT	GTATAAAGGT			
				**	**	**	**	**	**
				**	**	**	**	**	**
				**	**	**	**	**	**
				**	**	**	**	**	**
alignment position	1 5 1 . . . . .	1 6 1 . . . . .	1 7 1 . . . . .	1 8 1 . . . . .	1 9 1 . . . . .				
<b>P932494</b>	102 CTCTGGCCTT	TTTGTGTGt g	t t g t t g t t a g	a t g AAGATAA	TAAAAATCAT				
<b>P932495</b>	117 TTCTGGCTCT	TTTGTGTG- - - - -	- - - - -	- - - - - AAGAAGA	TCAAAAATCGT				
<b>P932496</b>	119 TTCTGGCCTT	TTTGTTTT- - - - -	- - - - -	- - - - - AAGATGA	TAAAATTTGT				
	**	**	**	**	**	**	**	**	**
	**	**	**	**	**	**	**	**	**
	**	**	**	**	**	**	**	**	**
	**	**	**	**	**	**	**	**	**
alignment position	2 0 1 . . . . .	2 1 1 . . . . .	2 2 1 . . . . .	2 3 1 . . . . .	2 4 1 . . . . .				
<b>P932494</b>	152 CATAGTAAAC	a c - - - ATAGC	GATTACTATG	T GCTGGACTT	CGTCGTAGTT				
<b>P932495</b>	152 CTTGGCAAAA	GACAAAAAGC	GGTTGGTATT	T ATTCTAGGT	GATAGGCGTT				
<b>P932496</b>	154 CATAGCAAAA	GACAGAAAGT	GGCTGGTATT	T ATTCTACAT	GATAGGCGTT				
	**	**	**	**	**	**	**	**	**
	**	**	**	**	**	**	**	**	**
	**	**	**	**	**	**	**	**	**
	**	**	**	**	**	**	**	**	**
alignment position	2 5 1 . . . . .	2 6 1 . . . . .	2 7 1 . . . . .	2 8 1 . . . . .	2 9 1 . . . . .				
<b>P932494</b>	199 GAGATATATT	ACCATC c t a a	g t t a a c t a t	a a t c g T - - - T	TATTGTTATC				
<b>P932495</b>	202 AGGAAGTAGT	AGTAGCCTGT	TGTTTt t - - - -	- - - - - T - - - T	TTTTCTCATG				
<b>P932496</b>	204 AGGAAGTAGT	AATAGCCTGT	TCTTTa a c t c	t g t a a t a a c T	TTTTCTCATG				
	**	**	**	*	**	**	**	**	**
	**	**	**	**	**	**	**	**	**
	**	**	**	**	**	**	**	**	**
	**	**	**	**	**	**	**	**	**
alignment position	3 0 1 . . . . .	3 1 1 . . . . .	3 2 1 . . . . .	3 3 1 . . . . .	3 4 1 . . . . .				
<b>P932494</b>	246 TCTAGGTCTT	CCTAGATGAA	ATT TTTa - CC	CTAAAGGAt c	g t a a a g t c g g				
<b>P932495</b>	241 CCTCGGTCTG	CCCCGATT TA	AGGT TTt GCC	CTAAATGAAG	GATCTCAATC				
<b>P932496</b>	254 CCTAGGTCTG	CCCTGATT TA	AGTT TTe GCC	GTAACGAAG	GATCTCAATC				
	**	**	**	**	**	**	**	**	**
	**	**	**	**	**	**	**	**	**
	**	**	**	**	**	**	**	**	**
	**	**	**	**	**	**	**	**	**
alignment position	3 5 1 . . . . .	3 6 1 . . . . .	3 7 1 . . . . .	3 8 1 . . . . .	3 9 1 . . . . .				
<b>P932494</b>	295 c c c a c - - - -	- - - - -	- - - - -	- - - - -	- - - - -				
<b>P932495</b>	291 ACGACCACAA	GAAa t c c c t c	c c GACTTCGG	T TTTTCCTGGG	GCAAGGCGAC				
<b>P932496</b>	304 ACGACCACAA	GAAg t t g c t a	c t GACTTCTG	T TTTTCCTGGG	GCAAAGCGAC				

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alignment position	4 0 1 . . . . .	4 1 1 . . . . .	4 2 1 . . . . .	4 3 1 . . . . .	4 4 1 . . . . .				
P932494	300 - - - - CGG AC	GTCAGTGGGG	TCCC - CTGTT	CAGCCCTCTC	GTT Ct t c t g g				
P932495	341 CGAGT CAG AC	ACCAGAGT GT	CTCC - AGGCC	CTGCCCTTTC	CTGCC - - - -				
P932496	354 CAAGT CAG AC	c c c a g c g t c a	g c g t t AGGTA	CTTCCCTTTC	CCCTCC - - - -				
	*****	*****	*****	*****	*****				
	*****	*****	*****	*****	*****				
alignment position	4 5 1 . . . . .	4 6 1 . . . . .	4 7 1 . . . . .	4 8 1 . . . . .	4 9 1 . . . . .				
P932494	344 g g a t c t c t c g	g g a c a c t g a c	g a g g t g g c a c	c g g g a c c t a c	a g g t GG GC CG				
P932495	386 - - - - -	- - - - -	- - - - -	- - - - -	- - - - GG GC CC				
P932496	400 - - - - -	- - - - -	- - - - -	- - - - -	- - - - CG CC CG				*****
									*****
alignment position	5 0 1 . . . . .	5 1 1 . . . . .	5 2 1 . . . . .	5 3 1 . . . . .	5 4 1 . . . . .				
P932494	394 CAAGC CCC GC	CCCCAGCG AC	Gg c t t g t a g c	c c c g t CCCCC	GACGCA GCG C				
P932495	392 CAACC TGC GC	CCGAAGCC AC	G - - - - -	- - - - CCCCC	AACGCG GCG T				
P932496	406 CAATT TGC GC	CCGTAGCC AC	G - - - - -	- - - - CCTCC	AACGCG GCA A				
	*****	*****	*****	*****	*****				
	*****	*****	*****	*****	*****				
alignment position	5 5 1 . . . . .	5 6 1 . . . . .	5 7 1 . . . . .	5 8 1 . . . . .	5 9 1 . . . . .				
P932494	444 CTCTC CAAGT	TTGCCCCGCC	CTGC Ag g a c t	g c a g A AT T T C	CTT T C C G G C G				
P932495	428 CCTTC CCGAT	TCGCTCAAAC	TTGC GA - - - -	- - - - A AC G C C	CTT T C C G G C G				
P932496	442 TCC TC CGGAT	TCGCTTAGCC	TT AC GA - - - -	- - - - A AT T C C	CTT T C C G G C G				
	*****	*****	*****	*****	*****				
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	*****	*****	*****	*****	*****				
	*****	*****	*****	*****	*****				
alignment position	6 0 1 . . . . .	6 1 1 . . . . .	6 2 1 . . . . .	6 3 1 . . . . .	6 4 1 . . . . .				
P932494	494 GCGCG CTGTC	GTCAC - - - -	- - - - GCGTCC	C G C G C C T C C T	C G C G C C T G C G				
P932495	470 TCGCG CTGAC	GTCACA a a c C	CTGC GCC TCC	C G C T C C T C T T	C G G G C C g t C G				
P932496	484 TCGCG CTTAC	GTCACA a g t C	CTGC GCC TCC	C G C T C C T C T T	C G G G C C T G C G				
	*****	*****	*****	*****	*****				
	*****	*****	*****	*****	*****				
	*****	*****	*****	*****	*****				
	*****	*****	*****	*****	*****				
alignment position	6 5 1 . . . . .	6 6 1 . . . . .	6 7 1 . . . . .	6 8 1 . . . . .	6 9 1 . . . . .				
P932494	535 c c g t g g t t GG	AAGGTCGT CC	CTGT	GAC CGG	C TT GGC GGT T	GGA GC G GC T G			
P932495	520 TTC GAAC - GA	AAGGTCGT CC	CTGT	GAC CGA	C GAGGT GGT T	TGAGCAGC T G			
P932496	534 TTC GAAC - GG	AAGGTCGT CC	CTGT	GAC CGA	C TAGGT a GT T	GGA GCAGC T G			
	*****	*****	*****	*****	*****	*****			
	*****	*****	*****	*****	*****	*****			
	*****	*****	*****	*****	*****	*****			
	*****	*****	*****	*****	*****	*****			
alignment position	7 0 1 . . . . .	7 1 1 . . . . .	7 2 1 . . . . .	7 3 1 . . . . .	7 4 1 . . . . .				
P932494	585 TCGCC ATGTT	GTCGGTAGCa t	CCC GCT CAG	G C C C G T T C G C	G C C C G T C C T G				

**P932495** 569 TCGCCATGTT GTCGGTCGCc GCCCGCTCGG **GCCCGTTCGC** **GCCCGTCTTA**  
**P932496** 583 TCGCCATGTT GTCGGTCGCt GCCCGCTCGG **GCCCGTTCGC** **GCCCGTCTTA**  
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alignment position 751 . . . . . 761 . . . . . 771 . . . . . 781 . . . . . 791 . . . . .

**P932494** 635 **TCG****GCCACGT** **CCCGCGGGGT** **GGCGGGCGCG** **CTGC**GGCCCT TGGTGC Ag g c  
**P932495** 619 **TCG****GCCACtT** **CCCGCGGGGT** **GGCGGGCGCG** **CTGC**GTCCCT TGC TGC AA g G  
**P932496** 633 **TCG****GCCACGT** **CCCGCGGGGT** **GGCGGAGCG** **CTGC**GGCCC TGC TGC AA a G  
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alignment position 801 . . . . . 811 . . . . . 821 . . . . . 831 . . . . . 841 . . . . .

**P932494** 685 **caCGGTGCC** **GCC**ACCCCGG AGCAGCC TGT GTTGGAC CTG **AAGCGGCCCT**  
**P932495** 669 **CGCGGTGCC** **GCC**GCCTCGG AGCCACCTGT TCTGGAT GTG **AAGCGACCCT**  
**P932496** 683 **CGCGGTGCC** **GCC**ACCTCGG AACCACTGGT TCTGGAC GTG **AAGCGACCCT**  
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alignment position 851 . . . . . 861 . . . . . 871 . . . . . 881 . . . . . 891 . . . . .

**P932494** 735 **TCCTCAGCC**G GGAGTCGCTG AGCGGCC AGG C Cg t g c g **CCG** **GCCTTTGGTC**  
**P932495** 719 **TCCTGTGCC**G CGAGTCCC TG AGTGGCC AGG C CGCAGC **CCG** **GCCTTTGGTG**  
**P932496** 733 **TCCTGTGCC**G TGAGTCGCTG AGTGGCC AGG C CGCGAC **CCG** **TCCTTTGGTG**  
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alignment position 901 . . . . . 911 . . . . . 921 . . . . . 931 . . . . . 941 . . . . .

**P932494** 785 **GCC**TCCGTGG GCCTCAATGG TGAGCCG - - - - -  
**P932495** 769 **GCC**ACGGTGG GCCTGAACGG TGAGCCGGCT TCGGAGT ACC CCGATCTCGT  
**P932496** 783 **GCC**ACAGTGG GCCTGAATGG TGAGCCGGCT TCAGGGTGC CCGATCTCGT  
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alignment position	9 5 1 . . . . .	9 6 1 . . . . .	9 7 1 . . . . .	9 8 1 . . . . .	9 9 1 . . . . .
<b>P932494</b>	812 - - - - -	- - - - -	- - - - -	GG	GCGAGGGCCG C G A G C A G G G C
<b>P932495</b>	819 T C C C t - - - -	- - - - -	- - - - -	G C G G C G G	C G G A G G G C G G T G T G C T G G G A
<b>P932496</b>	833 T T C C c t g c g g	c t c c a g g t c c	g g g	G C G G C G G	C A G A G G G C G G T G C G C T G G G A
	***			*****	*****
	***			*****	*****
	***			*****	*****
alignment position	1 0 0 1 . . . . .	1 0 1 1 . . . . .	1 0 2 1 . . . . .	1 0 3 1 . . . . .	1 0 4 1 . . . . .
<b>P932494</b>	834 T G G G G g t c t c	t c g g t g - - - -	- - - - -	- - - - -	- - - - -
<b>P932495</b>	851 T G T G G T G G g c	c G G C C G C G G C	T A C C T T G G C A	G G C C G A G C G C	t c c c c g G A G C
<b>P932496</b>	883 T G T G G T G G a c	t G G C C G C A G C	G A C C T T G G C A	G G C C A G C G C	c t c t t c G A G C
	*****	*****	*****	*****	*****
	*****	*****	*****	*****	*****
	*****	*****	*****	*****	*****
alignment position	1 0 5 1 . . . . .	1 0 6 1 . . . . .	1 0 7 1 . . . . .	1 0 8 1 . . . . .	1 0 9 1 . . . . .
<b>P932494</b>	850 - - - - -	- - - - -	- - - - -	- - - - -	C C C G C T C C T C C G G
<b>P932495</b>	901 A G G C G G G C T C	A C G G T G A C - - - -	- - - - -	G G G A T G C T C C C	G T A G C T G C A T
<b>P932496</b>	933 A G G C G G G C T C	A C G G T G A C c g	g a t g c c g c t G	G G A T G C T C C A	G G G G C C G C A T
	*****	*****		*****	*****
	*****	*****		*****	*****
				***	*****
alignment position	1 1 0 1 . . . . .	1 1 1 1 . . . . .	1 1 2 1 . . . . .	1 1 3 1 . . . . .	1 1 4 1 . . . . .
<b>P932494</b>	863 C C C C A G C A G	G G A G C G G C C G	c g g g c g c g c g	a g c g g a g c c t	g a a t C A G G T C
<b>P932495</b>	940 C C C C A G G A G	T C A G G A G C C G	g t c t g - - - -	- - - - -	- - - - C A C G T C
<b>P932496</b>	983 C C C C A G G C G	T C A G G A A C C -	- - - - -	- - - - -	- - - - -
	*****	*****			*****
	*****	*****			*****
	*****	*****			*****
alignment position	1 1 5 1 . . . . .	1 1 6 1 . . . . .	1 1 7 1 . . . . .	1 1 8 1 . . . . .	1 1 9 1 . . . . .
<b>P932494</b>	913 G G G C T G G G C G	G C C T C C G C A a	c t c t g g g c c t	g g c c c c c g g g	c t c g g g g c g t
<b>P932495</b>	971 A G T C T G G G T T	C C C T C C T C A g	g c t t c a c t t g	a c t t t c t t g a	t t a a g a t c g g
<b>P932496</b>	1002 - - - - -	- - - - -	- - - - -	- - - - -	- - - - -
	*****	*****			
alignment position	1 2 0 1 . . . . .	1 2 1 1 . . . . .	1 2 2 1 . . . . .	1 2 3 1 . . . . .	
<b>P932494</b>	963 c t t t c t g g t g	g c c g g c c t g g	a c t c g c g t c c	g c c g g c t t c	
<b>P932495</b>	1021 c c t c c c t g t a	t c a t g g c t a a	g a t a c t g t t a	g t t a c - - - -	
<b>P932496</b>	1002 - - - - -	- - - - -	- - - - -	- - - - -	

**Pairwise similarities:**

For each pairwise alignment, the **similarity** (relative to the maximum similarity) and the **number of identical nucleic acids** (in % of shorter sequence) is given. Maximum values are underlined.

	<b>P932495</b> (1055 bp)	<b>P932496</b> (1001 bp)
<b>P932494</b> (1001 bp)	0.342 49 %	0.362 43 %
<b>P932495</b> (1055 bp)		<u>1.000</u> <u>78 %</u>

Please note that the **similarity value 1.000** marks only the two **most similar** sequences, it does not necessarily mean that these sequences are identical.

Extract alignment region	
<b>Positions in alignment</b>	from: <input type="text"/> to: <input type="text"/>
<b>Output file</b>	<input type="text" value="dialign.seq"/>
<b>Extract aligned sequences</b>	

For [comments](#), questions or bug reports, please contact [support@genomatix.de](mailto:support@genomatix.de)

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