

This Supplementary Material shows the Core Promoters of Complex V 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).

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**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 May 20 21:45:09 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)  
**Selected groups**

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

(core/matrix sim):

## Aligned Sequences:

No.	Sequence Name	Sequence Description	Length
1	P924542	sym=ATP5A1 loc=Loc498 taxid=9606 spec=Homo sapiens chr=18  ctg=NT_010966 str=(-) start=25166753 end=25167864 len=1112  tss=501,502,507,512  comm=ATP synthase, H+ transporting, mitochondrial F1 complex, alpha subunit, isoform 1, cardiac muscle; (AK092735/502/gold;AK129900/501/gold;AK129739/501/gold; AK098765/512/gold;NM_004046/507/bronze;)	1112 bp
2	P924549	sym=Atp5a1 loc=Loc11946 taxid=10090 spec=Mus musculus  chr=18 ctg=NT_039675 str=(+) start=1236265 end=1237390  len=1126 tss=501,510,526  comm=ATP synthase, H+ transporting, mitochondrial F1 complex, alpha subunit, isoform 1; (AK043976/511/gold;AK098155/502/gold;AK076572/511/gold; NM_007505/527/silver;)	1126 bp
3	P924553	sym=Atp5a1 loc=Loc65262 taxid=10116 spec=Rattus norvegicus  chr=18 ctg=NW_047516 str=(+) start=9660103 end=9661203  len=1101 tss=501  comm=mitochondrial H+-ATP synthase alpha subunit; (XM_341631/526/bronze;)	1101 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.

VSEBOX VSHIFF VSHAML VSRORA VSMYTI VSSPIF VSETSF USNRF2 VSDAAT V\$YYIF VSEREF USEREF  
V\$TALE V\$PAX5

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alignment position   1 . . . . . 1 1 . . . . . 2 1 . . . . . 3 1 . . . . . 4 1 . . . . .
P924542  1 g a c t c a g a g g g t c t g a a g t g g g g - - - - -
P924549  1 t c c a c a a g c a t g CCTTGGTA CATATACATG CACACCACGC ATACa c t a c t
P924553  1 - - - - - C C T T G G C A C A T A C A C A T A C A C A G C A C A C A C A C A C t a a t a a
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alignment position   5 1 . . . . . 6 1 . . . . . 7 1 . . . . . 8 1 . . . . . 9 1 . . . . .
P924542  24 - - - - - - - - - - - - - - - - - - - - - - - - - - CT A A G A T C
P924549  51 a c t a c t a c t a a t t a t t a t t a T T T C A G T A A T T T C G G A T A G T T C C C A G G A C C
P924553  39 t a a t a a c a g - - - - - T T T C A A T A A T C T C A G A A T G T T C T C A G G A T C
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alignment position   1 0 1 . . . . . 1 1 1 . . . . . 1 2 1 . . . . . 1 3 1 . . . . . 1 4 1 . . . . .
P924542  32 T G C A G A T T A A C G G G C T C C G T G G G A G g c t c c c t g c t g g t g g c c a g t c c c g g
P924549  101 T G A G G A C T A A A A C C C T C T G G G T G G C T G C A C T G T G C A A G A G C T A C C C C G g c
P924553  79 T G A G G A C T A A A A C C C T C T G G G T G G T A C A C T G T G C A A G A G T T T C C C C G a c
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alignment position   1 5 1 . . . . . 1 6 1 . . . . . 1 7 1 . . . . . 1 8 1 . . . . . 1 9 1 . . . . .
P924542  82 g g t t t a g c t g t t c a c t g t t g c t a c t c g t g c t a a A C C A C G G T C T A A C A C T A
P924549  151 c t g c c a c a g c - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
P924553  129 c c g g a c t - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
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alignment position   2 0 1 . . . . . 2 1 1 . . . . . 2 2 1 . . . . . 2 3 1 . . . . . 2 4 1 . . . . .
P924542  132 C C G A C A C T A T T A A T C g c c c t g g t c c t c a a g a c a g c c g c g a C C C C A G A C G C
P924549  178 C C A G C A C G A T T A A C C t a G C T C T T A G T C T A G G C A G C C C G - - C C C C A G G C A C
P924553  136 - - - - - - - - - - - - - - - - - G C T C T T C A T C T A T G C A G T T C G - - C C C T A G g t g g
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alignment position   2 5 1 . . . . . 2 6 1 . . . . . 2 7 1 . . . . . 2 8 1 . . . . . 2 9 1 . . . . .
P924542  182 G- T G A g g c c c t c a t c c t c t a g c a c c a g a t g g g g c c t g g g a a c t g c t g c t t
P924549  226 G- T G A C G T T C A G - - - - G G A C G C G T C T C C T C T - - - - - - - - - - - - - - - -
P924553  167 g a T G A A G T T C A G t t c t a G G A C G C T T C C C C T C T - - - - - - - - - - - - - - - -
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alignment position   3 0 1 . . . . . 3 1 1 . . . . . 3 2 1 . . . . . 3 3 1 . . . . . 3 4 1 . . . . .
P924542  231 a g c a G A T T C A G CTACCCACG TGGTCA CCCG GGG- - CAACC ACAAGGTCGA
P924549  252 - - - G G T T C T G CTACTCAG TGGTCTCCCG - GG- - CAACC ACAAGGTCGA
    
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**P924553** 199 - - - GGT TCT G **CAACTCACG** **TGATCT** CCC G G g c a a CAACC **ACAAGGTCTGA**  
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alignment position 3 5 1 . . . . . 3 6 1 . . . . . 3 7 1 . . . . . 3 8 1 . . . . . 3 9 1 . . . . .

**P924542** 279 **CTCAA**A g a c CAAAATAAAT GTATAACGAA TGCCAGGACC AAAGCCGGA A  
**P924549** 295 **TTCAA**AAAGA CAAAAATTA AAATGTTGAG TACCAGGAG GAGGCTGGA A  
**P924553** 245 **TTCAA**AGAGA CAAAAATTA AAATGATAAG TGCCAAGGAG GAGGCTGGA A  
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alignment position 4 0 1 . . . . . 4 1 1 . . . . . 4 2 1 . . . . . 4 3 1 . . . . . 4 4 1 . . . . .

**P924542** 329 TATATCTAAT CATTCATTTT GAG**GTTTAAA** **CTTAAA**AATG TTACATAAAA A  
**P924549** 345 ACAATGTATT CGTTCATTTT TAG**TTCATAA** **CTTAAAA**AAAG AAAAAAGAAA A  
**P924553** 295 ACAATTGATT CGTTCATTTT TAG**TCCTAAA** **CTTTAA**AAAA AAAAAAAAAA A  
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alignment position 4 5 1 . . . . . 4 6 1 . . . . . 4 7 1 . . . . . 4 8 1 . . . . . 4 9 1 . . . . .

**P924542** 379 AAatagtaacctgcc - - - - - AA AAAAAATGCAG A  
**P924549** 395 Agttatag - - - - - AAAAAA AAAAAA AAG A  
**P924553** 345 Aaaaagtgttaaaaaaag aggcctatactta AAAAAA AAAAAA AAG A  
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alignment position 5 0 1 . . . . . 5 1 1 . . . . . 5 2 1 . . . . . 5 3 1 . . . . . 5 4 1 . . . . .

**P924542** 407 GTGGCGGCGG GGGCGGGGG Agaggtggtg aacgc **GAGGG** **GCAGTACTT**  
**P924549** 419 TTTGC GTCCG GAGGAGCAGG **A- - - - -** **- - - -** **GAGGG** **GCGGTA CTTC**  
**P924553** 395 TTTGC ATCCG GAGGAGCTGG **A- - - - -** **- - - -** **GAAGG** **GCGGTA CTTC**  
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alignment
position      5 5 1 . . . . . 5 6 1 . . . . . 5 7 1 . . . . . 5 8 1 . . . . . 5 9 1 . . . . .
P924542 457 CGGGTCA GGT GGGCCG GCTG TCTTGACCTT CTTTGC GGCT CGGCCATTTT
P924549 455 CGGGTCA GGC GGGCTG GCTG CCTTGACCTT CCTTT GCGCT CGGCCATTTT
P924553 431 CGGGTCA GGT GGGCCG GCTG CCTTGACCTT CCTTC GCGCT CGGCCATTTT
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alignment
position      6 0 1 . . . . . 6 1 1 . . . . . 6 2 1 . . . . . 6 3 1 . . . . . 6 4 1 . . . . .
P924542 507 GTCCAGTCa GTCCGGAGGC TGCGGCTGCA GAAGt accgc ctgcggagt a
P924549 505 GTGCCAGTC- GTCCGGAGGC TGCGGCTGCA GACGGTCTCT CCgAGAAG- -
P924553 481 GTGCCAGTC- GTCCGGAGGC TGCGGCTGCA GAAGATCTCT CCaAGAAG- -
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alignment
position      6 5 1 . . . . . 6 6 1 . . . . . 6 7 1 . . . . . 6 8 1 . . . . . 6 9 1 . . . . .
P924542 557 a CTGCAAAGA TGCTGTCCGT GCGCGTTGCT GCGGCCGTGG t CCGCGCCCTI
P924549 552 - CTGCAAAGA TGCTGTCTGT GCGCGTCGCC GCGGCCGTGG CCGGTGCCCTI
P924553 528 - CTGCAAAGA TGCTGTCCGT GCGCATCGCC GCGGCCGTGG CCGGTGCCCTI
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alignment
position      7 0 1 . . . . . 7 1 1 . . . . . 7 2 1 . . . . . 7 3 1 . . . . . 7 4 1 . . . . .
P924542 607 TCCT CGGCGG GCCGGACTGG TGAGCACCGa aggcaggc at gatgcaaggc g
P924549 601 CCCT CGACGG GCGGGACTGG TGAGCACCGG GGCCTAG- - - - -
P924553 577 CCCT CGACGG GCGGGACTGG TGAGCGCCGG GGCCTAG- - - - -
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alignment position		7 5 1 . . . . .	7 6 1 . . . . .	7 7 1 . . . . .	7 8 1 . . . . .	7 9 1 . . . . .			
<b>P924542</b>	657	g c c g g g t g g g	g c t G C A G G G T	G G T G G T G C G C	C G G - - - C T C	G G G c g c t c t c			
<b>P924549</b>	638	- - - - -	- - - G C A G G C T	G G C G C G G G A G	C G G a g a t C T C	A G G T C T C T G C			
<b>P924553</b>	614	- - - - -	- - - G C A G G C T	G G C G T G G G A G	C G G - - - C T C	A G G T C T C T G C			
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alignment position		8 0 1 . . . . .	8 1 1 . . . . .	8 2 1 . . . . .	8 3 1 . . . . .	8 4 1 . . . . .			
<b>P924542</b>	703	t g c a g g a g g - - - - -	- - - - - G C G A G G G G	C T G T G G C G A A	<b>T G C C G C C A T C</b>				
<b>P924549</b>	675	G G A G C G G A G C	c g g a G C G G T G	C A G C G C G G G G	C A G G G G C G G A	<b>C G G C G C C A T C</b>			
<b>P924553</b>	647	G G A T C G G A G C	- - - G C G G T G	C A G T G C A G G A	C T G G G G C G G A	<b>C G G C G C C A T C</b>			
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alignment position		8 5 1 . . . . .	8 6 1 . . . . .	8 7 1 . . . . .	8 8 1 . . . . .	8 9 1 . . . . .			
<b>P924542</b>	740	<b>T T G C A C C c g t</b>	g g c t t c t c	C G G C T G G A C A G A	G C A G G C G A C A	C A G G T G C C C T			
<b>P924549</b>	725	<b>T T G C A C C G T G</b>	G - - - - - C T	G C G G A G C A G C	G C G G A C G G C C	G A G G G G C T T T			
<b>P924553</b>	693	<b>T T G C A C C G T G</b>	G - - - - - C T	G C C A G G C A G C	G C G G A C G G C A	A A G G G G C T C T			
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alignment position		9 0 1 . . . . .	9 1 1 . . . . .	9 2 1 . . . . .	9 3 1 . . . . .	9 4 1 . . . . .			
<b>P924542</b>	790	T T T G C t c g t c	a c c t g c g c a g	a g g c a g a a t g	g t a c a g g g c a	g a c a g t t a a c			
<b>P924549</b>	768	G C T G C G G G C C	T T C G G g g c g c	G C G C G G C G G G	G C G G G G T C T	G G G A C C T C G C			
<b>P924553</b>	736	T T T G C A G G C C	T T C G G t - - - -	G C G C T G T G G G	G C G T G G A T C C	G T G A C C T C G C			
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alignment position		9 5 1 . . . . .	9 6 1 . . . . .	9 7 1 . . . . .	9 8 1 . . . . .	9 9 1 . . . . .			
<b>P924542</b>	840	t c g a t g g t g t	c c a g a g a c a g	g g c c t c A A G A	T T C C T G T C T T	C G G C T G A C A C			
<b>P924549</b>	818	C G T G G C t g a g	c a a g G G G G C T	C T A G G - A G G G	A T C T G G G C T T	G G G G T G A G A C			
<b>P924553</b>	782	C G T T G C g g g c	a a a - G G G G C T	T T A G G - A A G G	T T T C G A T C T T	G G G G T G A G G C			
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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 . . . . .			
<b>P924542</b>	890	C G G C C C T A G A	a g g g g g a t c t	t G G G T G A A G G	T C A G G G C T T G	G G C G C T a g c t			

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P924549 867 CGGGCCTGGA - - - - - - - - - - GGTGAAGG TCAGGGTGTG TGCCCTGCTC
P924553 830 CGGGGCTAa - - - - - - - - - - GGGTGAATG TCAGGGTTTG TGCACTGCTT
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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 . . . . .
P924542 940 c t c c g a g g c c t g t t c t g a a t c g g t g a g g t t c c t c t c t t t c g a T T C T T A G C
P924549 905 G T C T G G C C T G C C c g g a a g c t t g - - - - - - - - - - - - - - - - - - - T C C T G G C
P924553 868 G T C T G G C C T G C C c t g t g g c t t g - - - - - - - - - - - - - - - - - - - T T C C T G G C
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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 . . . . .
P924542 990 G T C G C G T CCC GCTGAAGGTC AGAa a a c t GC TGTCAGCt c t t g t t g a a g c t
P924549 934 G T C C G G C TCT GCTGAAGGTC AGAGGA- - GC TGTCAGCc g t c t t g t g c c g g
P924553 898 G T C T G G C TCC GCTGAAGGTC AAAGGA- - GC TGTCAGCa g c c t t c t g 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 . . . . .
P924542 1040 a g t c a g t g - - - - - G A G T C T G A C A TTGT GTGAAGGTCA GCAGGCCc - A
P924549 982 a g g a g g a g g A G G A G G C G A G C C T G A C A TTGT GTGAAGGTCA ACAGGCCGGA
P924553 943 - - - - - - - - A G G A G G A G A G T C T G A C A TTGT ATGAAGGTCA ACAGGCCGGA
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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 . . . . .
P924542 1081 GCATTTACCC TCTGCCTGGA GC T C A G t t t a g a - - - - - - - - - - - - - - - -
P924549 1032 GCAGTTACCC TCTGCTCCGA GG T C A A T C C A A G G G A A A G G A A T A A A T G A A A
P924553 984 GCATTTACCC TCTGCTCGGA GG T C G T T T C A A G G G A A A G G A A T A A A T G A A 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 . . . . .
P924542 1113 - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
P924549 1082 G T G A C T C T T G C A T T G T G G G A T G G T t t A C C C A T T T G G A G C T G a c c c - - - -
P924553 1034 G T G A C C C T T C A A T T G T T G G A T G G T c - A C T C A C T T G G T G C T G t a t a c g g a
  
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alignment      1 3 0 1 . . . . . 1 3 1 1 . . . . .
position
P924542 1113 - - - - -
P924549 1127 - - - - -
P924553 1083 a a g g t c g c g a a a a c a t c g 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>P924549</b> (1126 bp)	<b>P924553</b> (1101 bp)
<b>P924542</b> (1112 bp)	0.341 43 %	0.337 43 %
<b>P924549</b> (1126 bp)		<u>1.000</u> <u>76 %</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 style="width: 50px;" type="text"/> to: <input style="width: 50px;" type="text"/>
Output file	<input style="width: 100%; border: none;" type="text" value="dialign.seq"/>
<b>Extract aligned sequences</b>	

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**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 May 20 23:47:21 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)  
**Selected groups** (core/matrix sim):

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

## Aligned Sequences:

No.	Sequence Name	Sequence Description	Length
1	P978027	sym=ATP5B loc=Loc506 taxid=9606 spec=Homo sapiens chr=12  ctg=NT_029419 str=(-) start=19182563 end=19183563 len=1001  tss=501  comm=ATP synthase, H+ transporting, mitochondrial F1 complex, beta polypeptide; (NM_001686/523/bronze;)	1001 bp
2	P978029	sym=Atp5b loc=Loc11947 taxid=10090 spec=Mus musculus chr=10  ctg=NT_081856 str=(+) start=5829087 end=5830098 len=1012  tss=501,502,512  comm=ATP synthase, H+ transporting mitochondrial F1 complex, beta subunit; (AK083276/541/gold;AK084009/552/gold;AK011035/541/gold; AK010314/542/gold;NM_016774/542/bronze;)	1012 bp
3	P978031	sym=Atp5b loc=Loc171374 taxid=10116 spec=Rattus norvegicus  chr=7 ctg=NW_047773 str=(+) start=1376032 end=1377032  len=1001 tss=501  comm=ATP synthase, H+ transporting, mitochondrial F1 complex, beta polypeptide; (XM_343136/501/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\$EREF USEREF V\$E4FF V\$ECAT V\$SHOXF V\$SNKXH V\$HOMF V\$DPAI V\$SETSF V\$DMTF V\$RORA  
 V\$RARF V\$SFIF

alignment position 1 . . . . . 1 1 . . . . . 2 1 . . . . . 3 1 . . . . . 4 1 . . . . .  
**P978027** 1 c a c t a c t t c g a g a - - - - -  
**P978029** 1 - - - - - C T T T C G T T G C A C G G A T T T A T A T G A T A A A G A g C C T C  
**P978031** 1 c g t c t a t c g a c g t t t C T T T C G T T G C A C A G A T T T A A A T G A T A A A G A c C C T C  
 \* \* \* \* \*  
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alignment position 5 1 . . . . . 6 1 . . . . . 7 1 . . . . . 8 1 . . . . . 9 1 . . . . .  
**P978027** 14 - - - - -  
**P978029** 36 C A G G T T T C G G A C C T G C T G G G C C G C C t G G A A A C T T C C A C C C T C A C T A C T G T  
**P978031** 51 C A G G T T T C C G A C C T G C T G G G C C G C C c G G A A G C T T C C A C C C T C A C T A C T G T  
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alignment position 1 0 1 . . . . . 1 1 1 . . . . . 1 2 1 . . . . . 1 3 1 . . . . . 1 4 1 . . . . .  
**P978027** 14 - - - G A A A A A C C T T A T T T T G - - - - - G C T C T A A A G A G G G C T C C T G A C T  
**P978029** 86 C G A G G A A A C C C C A C G T T T T G - - - - - G A G C C A C A G A A G G T T C C T G A C T  
**P978031** 101 G G A G G A A A C t t c a t g a c t c c g c c a t g t t G A G C C A C A G A A A G C T C C T G C C T  
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alignment position 1 5 1 . . . . . 1 6 1 . . . . . 1 7 1 . . . . . 1 8 1 . . . . . 1 9 1 . . . . .  
**P978027** 52 T c g c c a c g c t c a c c t t c a g t g g t g c t t c a c c g c a c t a c c a c t t c c c t a a c  
**P978029** 128 T T C A G G A C G C C G C C A C T C a a c c t t a G C - - - - -  
**P978031** 151 T T C G G G A C G C C A G G A C T C c a t a t c t G C - - - - -  
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alignment position 2 0 1 . . . . . 2 1 1 . . . . . 2 2 1 . . . . . 2 3 1 . . . . . 2 4 1 . . . . .  
**P978027** 102 c a c c g c c c c t a t G G C T G T C A C C T A g a t c a a g g a c c t a t c t a a g g a g **AAAG**  
**P978029** 155 - - - - - G G C T G T C A C C T A A C T C - - - - - **AAAG**  
**P978031** 178 - - - - - G G C T G T C A C C C A A C T C - - - - - **AAAG**  
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alignment position 2 5 1 . . . . . 2 6 1 . . . . . 2 7 1 . . . . . 2 8 1 . . . . . 2 9 1 . . . . .

**P978027**152 **CCCAA**GGACA **GGCAA**AGAC a g g c c a c g c a c t t t c a a c a - - GGA ACT CG GC  
**P978029**175 **TCCAA**GGACA **GTCAA**AGAC g GCCTAGTGCA CAGGTTC AAC GGA ACC CCG C  
**P978031**198 **TCCAA**GGACA **GTCAA**AGAC c GCCTAGTGCA TAGGTTC AAC GGA ACC CCG C  
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alignment position 3 0 1 . . . . . 3 1 1 . . . . . 3 2 1 . . . . . 3 3 1 . . . . . 3 4 1 . . . . .

**P978027**200 CCCTTTCCTA - AACGTAGTT Cc t c t g a t t a c c c t g t c c a a **c g GACGTCGC**  
**P978029**225 CCCTTTATTT c AACGTAGTT CCGCCAAAAA Cc t - CTCCTA **CTGACGTTCC**  
**P978031**248 CCCTTTATTT - AACGTAGTT CCGCCAAAAA Cc c a CTCCTA **CTGACGTTCC**  
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alignment position 3 5 1 . . . . . 3 6 1 . . . . . 3 7 1 . . . . . 3 8 1 . . . . . 3 9 1 . . . . .

**P978027**249 **TATGA**TCCAA **TTAAGTTT**T G AGGCTCAGAG t g a c g c c c t c t a a c c t c a c a  
**P978029**274 **CATGG**GCCAA **TTAGGTTT**C G AGGCTTAGAG G G C G G C T C C T C C A A T T A - -  
**P978031**297 **TATGG**CCCAA **TTAGGTTT**C G AGGCTTAGAG G G C G G T T C C T T C A A T T A - -  
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alignment position 4 0 1 . . . . . 4 1 1 . . . . . 4 2 1 . . . . . 4 3 1 . . . . . 4 4 1 . . . . .

**P978027**299 c t g t c c a a t A A A A A A A G G A G T T T C A G A T T A G C A C C A G T T T T G A C C A A T G G  
**P978029**321 - - - - - A A A A A G A G A A T T T T C A G A T T G G C A C C A G T T T A G A C C A A T A G  
**P978031**344 - - - - - A A A A A A G G T A T C T T C A G A T T G G C A C C A G T T T T G A C T A A T A G  
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alignment position 4 5 1 . . . . . 4 6 1 . . . . . 4 7 1 . . . . . 4 8 1 . . . . . 4 9 1 . . . . .

**P978027**349 ATGAGAAGa t c a g c g t g - T A T T A A C C T G T A G A A G C A G C A c a G A G A A T G A T  
**P978029**362 CTGATAAGCT CCGAGT t t T T T T A C C C T A T A G A A G C G T T A G T G G T G A T G A C  
**P978031**385 CTGATGAGCT CCGAGT - - T T T T A C C C T A T A G G A G C G T C A G T G A A G A T A A C

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alignment position

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P978027398 GAGCAGCCAG T TCACCCAAT GGACCT GCCT ACTGCAGCGT AGGCCTCGCC
P978029412 GAACAGCAA A TCACCCAAT TACTGT GCCT ACGGCGGAGG TTGCCCGGCC
P978031433 TAACATCAAG A TCATCCAAT GACTGT GCCT ATGGCGGAAG CTGCCCGGCC
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alignment position

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

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P978027448 TCAACGGCAG G A g a g c a g g c g g c t g c g g t t GCTGCAGCCT TCAGTCTCCA
P978029462 CCAGCTGCAG G ACCGGCGGA GAGGACC- - - GCTTCGGCGC TCAGTCTCCA
P978031483 TCGGCTGCAG G GCTGGCGCC CCGGACC- - - GCTGGAGCGC TCAGTCTCCA
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alignment position

6 0 1 . . . . . 6 1 1 . . . . . 6 2 1 . . . . . 6 3 1 . . . . . 6 4 1 . . . . .

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P978027498 CCCGGACTAC GCCATGTTGG GGT TTGTGGG TCGGGTGCC GCTGCT CCGG
P978029509 CCCGGATTCC GCCATGTTGA GTCTTGTGGG GCGTGTGGC TCGGCC TCGG
P978031530 CCCGGACTCC GCCATGTTGA GTCTTGTGGG GCGTGTGGC TCGGCC TCGG
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alignment position

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

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P978027548 CCTCCGGGGC CTTGCGGAGA CTCACCCCTT CAGCGTCGCT GCCCCAGCT
P978029559 CCTCCGGGGC CTTGCGGGGA CTCAGCCCTT CGGC GGCTCT GCCACAGGCG
P978031580 CCTCCGGGGC CTTACGGGGA CTC AACCCCTT TGGCGGCCTT GCCACAGGCG
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alignment position 701 . . . . . 711 . . . . . 721 . . . . . 731 . . . . . 741 . . . . .

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P978027598 CAGCTCTTAC T GCGGGCCGC TCCGACG GCG GTCCATCCTG GTAAGTGCTT
P978029609 CAGCTTCTAC T GCGAGCTGC TCCCGCC GGG GTTCATCCTG GTAAGCGCCT
P978031630 CAGCTTCTAC T ACGAACCGC TCCCGCC GGG GTCCATCCTG GTAAGCGCCT

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alignment position 751 . . . . . 761 . . . . . 771 . . . . . 781 . . . . . 791 . . . . .

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P978027648 TTCTC TAGGA GCTAacgttc cattttgc CG CCCATGACC TTGAGCCGGG
P978029659 TCCTG GAGGA GCTAgttcgg tt c TT - - CT CCCGTGACC TTGAGCTTGG
P978031680 TCCTG GAGga ggggat t c g g t t - TT - - CT CCCGTGACC TTGAGCCTGG

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alignment position 801 . . . . . 811 . . . . . 821 . . . . . 831 . . . . . 841 . . . . .

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P978027698 Gaacgatggt agctcgggCC TAAGGGATCC GTggtgttaa aaggatgCCT
P978029706 G - - - - - - - - - - - - - - - - CC TATCGGATCC GTtCTCCATA AGGAT- - TCC
P978031726 G - - - - - - - - - - - - - - - - CC TAGCAGATCT GTgCTCCATT AGGAT- - CCT

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alignment position 851 . . . . . 861 . . . . . 871 . . . . . 881 . . . . . 891 . . . . .

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P978027748 GGAGCCGCGT CTTGCTCTCT AATGGCTGga gaacaagaaat gggacaccca
P978029737 CGGCGAGCGG ACTACTGTCC AGCCGagGAG TGCAAGGACA GTCGCCCGTG
P978031757 GGCAGCAGCA ACTACTGTCC AGCCGCAGAG TGCAAGGACA GTCGCCGGTG

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alignment position 901 . . . . . 911 . . . . . 921 . . . . . 931 . . . . . 941 . . . . .

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P978027798 taGGAGGTTT CTCGACCCA GCTCTGTCCC ATTTTGTata aagtccttg
P978029787 - - GGAGCGTT GATATAACCA GCAGCGTCCC ATTTTGTG- - - - -

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P978031807 - - G G A G C G T T G A T C G A A C C A G C T G T G T C C C A T T T T G T T - - - - -
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```

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

```

P978027848 t g t g A C G G A A A A G G T G C G G G C A G G T G C G T T G A C C T T C C G G T T g a - A T A G G
P978029823 - - - A G G C T A G A G T G G C C G G C A G C T G C C T C G A C C T T G A G G T T T T G A G G G G
P978031843 - - - A C G T T A A A G T G G A G G G C A G C T G C C T T G A C C T T G A G G T T C C T A T G G G
      * * * * *
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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 . . . . .

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P978027897 G G T A C T G A A C T C T C G A A A A A T G G - G G T C T T G T G C A T G C G G A T G G G A A G G C
P978029869 G A T A C C A A A C T C G A G A A T A A T G G C G G T T C T G T G C A C G A G G T C G G G A A A A C
P978031889 G G T A C T A A A C T C A A G A A T A A T G G C G G T T T T G T G C A C G A G G T T G G G A A A G C
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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 . . . . .

```

P978027946 T G T G C A G G C G C T T T A T C G A T C G C T G C G C G G C C T T C C C t c t t g g a c a c g c g
P978029919 A G T G C G G G T G G G T T C C C G A T T G C A G C G T G C C C T T C T C C A t g c c t c c t C C T
P978031939 A G C G C G G G C G G G T T C C C G A T T G C A G C G T G G C C T T C T C C A c a c g g c t c C C T
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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

```

P978027996 t t c c g t - - - - -
P978029969 A T C T T G C A G G A G A c t t a g t c t g g g c t c a g c t a a c c t t c c c t c g g
P978031989 A T T T T G C A G G A G A - - - - -
      * * * * *
  
```

**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>P978029</b> (1012 bp)	<b>P978031</b> (1001 bp)
--	-----------------------------	-----------------------------

<b>P978027</b> (1001 bp)	0.291 49 %	0.309 50 %
<b>P978029</b> (1012 bp)		<u>1.000</u> <u>83 %</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

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**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

Sat May 21 01:24:15 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)  
**Selected groups** (core/matrix sim):

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

## Aligned Sequences:

No.	Sequence Name	Sequence Description	Length
1	P978102	sym=ATP5D loc=Loc513 taxid=9606 spec=Homo sapiens chr=19  ctg=NT_011255 str=(+) start=1181249 end=1182249 len=1001  tss=501  comm=ATP synthase, H+ transporting, mitochondrial F1 complex, delta subunit; (NM_001687/530/silver;)	1001 bp
2	P978103	sym=Atp5d loc=Loc66043 taxid=10090 spec=Mus musculus chr=10  ctg=NT_039496 str=(+) start=5994807 end=5995837 len=1031  tss=501,507,527,531  comm=ATP synthase, H+ transporting, mitochondrial F1 complex, delta subunit; (AK018011/508/gold;AK011374/532/gold;AK076064/528/gold; NM_025313/502/bronze;)	1031 bp
3	P978104	sym=Atp5d loc=Loc245965 taxid=10116 spec=Rattus norvegicus  chr=7 ctg=NW_047773 str=(-) start=11075406 end=11076406  len=1001 tss=501  comm=ATP synthase, H+ transporting, mitochondrial F1 complex, delta subunit; (NM_139106/563/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\$NRF1	USNRF1	V\$SWHZF	V\$AP4R	V\$NEUR	V\$SRP58	V\$EGRF															
alignment position	1	1	1	1	2	3	4	4															
P978102	1	g g g t c a a g t g a t t c t - - -	CC	TG	CC	TT	GG	CC	TCT	CAAGg	TG	CT	GGG	ATT	TAC								
P978103	1	c t c a a a c t c a g a a a g c c g	CC	TG	CC	TCT	GCC	TCCC	CAAG-	TG	CT	GGG	AATA	TAA									
P978104	1	t t t a c c t a t t t c c a g a a t g c	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -								
					*	*	*	*	*	*	*	*	*	*	*								
alignment position	5	6	7	8	9	10	11	12															
P978102	48	AG	GTT	GG	AGC	CAC	CAc	a c c t	g g c c c a g a g c	c g g a a a c t t g	a t g t t t t c t t												
P978103	50	AG	GCAC	GC	GC	CAC	CAc	t g c c	c a t c t a t a t t	t g a t g c a c t t	t t g g a a a t a g												
P978104	21	-	-	-	-	-	-	-	-	-	-	-	-	-	-								
		*	*	*	*	*	*	*	*	*	*	*	*	*	*								
alignment position	10	11	12	13	14	15	16	17															
P978102	98	g a t g t c t a t c	c a g g g c c c t g	c a t c c a a t g a	g c g c c c c a a a	a a t c t t t t t t																	
P978103	100	g t t g t t c c g	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -															
P978104	21	-	-	-	-	-	-	-															
alignment position	15	16	17	18	19	20	21	22															
P978102	148	t t t t t t t t g	t a c a g a c g g g	t c g g g g g t g g	g g g c g a t c t a	c a c t a t t g c c																	
P978103	109	-	-	-	-	-	-	-															
P978104	21	-	-	-	-	-	-	-															
alignment position	20	21	22	23	24	25	26	27															
P978102	198	c a g g c t g g t t	t c c a g c t c c t	g g c c t c a a g t	g a t c c t c t g g	c c t c a g c c t c																	
P978103	109	-	-	-	-	-	-	-															
P978104	21	-	-	-	-	-	-	-															
alignment position	25	26	27	28	29	30	31	32															
P978102	248	c t a a A	GC	GCT	GGT	ATT	AC	AG	TC	GT	GAG	CCA	CC	AC	GC	a g c c	g a a t c t t g a a						
P978103	109	- - -	AG	TGC	G	GG	ATT	GC	AA	GAG	TGT	GTC	CA	CC	GC	AC	- - - - -	TCT					
P978104	21	- - - - -	-	GG	ATT	GC	AA	AA	AG	TGC	GTC	CA	CC	AC	AC	c t g a	c t g g t a a TCT						
		*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*					
		*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*					
alignment position	30	31	32	33	34	35	36	37															
P978102	298	t t t c a c t g a a	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -															
P978103	144	AC	ATT	TT	AAT	TCT	TCT	GT	t C	CA	AC	AC	GTT	A	CAG	GTT	TG	CT	TCT	TCT	GG	GC	
P978104	60	AC	ATT	TT	AAT	TCT	TCT	GT	c C	CA	AC	AC	GTT	A	CAG	GTT	TG	CT	TCT	TT	TG	GG	GC
		*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*
		*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*
alignment position	35	36	37	38	39	40	41	42															

<b>P978102</b>	308	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	
<b>P978103</b>	194	CTcgaatgc	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	TTGGCACC	TGATATCAAG	
<b>P978104</b>	110	CTgaaatgcgc	gctaaagtgcc	tctctccaat	ggTTGGGACC	TGACATCAAA	*	*	*	*	
		**					**	**	**	**	
		**					**	**	**	**	
		**					**	**	**	**	
		**					**	**	**	**	
alignment position		401	...	411	...	421	...	431	...	441	...
<b>P978102</b>	308	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	
<b>P978103</b>	221	CCCATATCAT	TTC CGCGCAA	ACat tcc cCT	CCTGAGGGAA	TATGTTCGTT					
<b>P978104</b>	160	CCGGCATCTT	TTCAGCTCAA	ACgt a c t - CT	CCGGAGGGAA	GGTGTCCGTT	*	*	*	*	
		**	**	**	**	**	**	**	**	**	
		**	**	**	**	**	**	**	**	**	
alignment position		451	...	461	...	471	...	481	...	491	...
<b>P978102</b>	315	Tt a c t c c a c c	t c c c a g g a c g	g t t t c a c c g c	c c t t a t c t g a	c c a c c c c t g					
<b>P978103</b>	271	TGCAGAAa g a	a c c g c a TC	CC AA GA ACC CAG	AGt - - CGTTT	GCTGT TAGAA					
<b>P978104</b>	209	TGCAGAAc a c	g g - - - TCCT	ATGGACC CAG	GGc a c CGTTT	GCTGT TAGAA	*	*	*	*	
		**	**	**	**	**	**	**	**	**	
		**	**	**	**	**	**	**	**	**	
		**	**	**	**	**	**	**	**	**	
		**	**	**	**	**	**	**	**	**	
alignment position		501	...	511	...	521	...	531	...	541	...
<b>P978102</b>	365	g t t c t g c c g c	a g c c c g g g c c	g GAACAAAAC	TGC AACC	CCC	AGAATACCTC				
<b>P978103</b>	319	GGC- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	GAAGAAAAC	TAC AATT	CCC	AGAATGACCC	
<b>P978104</b>	255	GGC- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	GAAGAAAAC	TAC AAGT	TCC	AGAATGATTC	
		**	**	**	**	**	**	**	**	**	
		**	**	**	**	**	**	**	**	**	
		**	**	**	**	**	**	**	**	**	
		**	**	**	**	**	**	**	**	**	
		**	**	**	**	**	**	**	**	**	
alignment position		551	...	561	...	571	...	581	...	591	...
<b>P978102</b>	415	ACGACGg	gggc a c t g c g t c g t	c a a c g t c g c g	t g c g c - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	
<b>P978103</b>	351	ACCCGGC	ATA GGAGGATCC	ACTTCTAGGC	At CACTGCAA	GGGGTGGGGC					
<b>P978104</b>	287	ACGAGGC	ATA GGAGGGTCC	ACTTCTAGGC	AgCACTGCAA	GGGGTGTGGC	*	*	*	*	
		**	**	**	**	**	**	**	**	**	
		**	**	**	**	**	**	**	**	**	
		**	**	**	**	**	**	**	**	**	
		**	**	**	**	**	**	**	**	**	
alignment position		601	...	611	...	621	...	631	...	641	...
<b>P978102</b>	450	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	
<b>P978103</b>	401	CAAGGGAAAG	TATACCTCCC	AGa ATGCTCA	GCGCGTACTG	CATCGCGCAG					
<b>P978104</b>	337	TAAGGCAAAG	TATACCTCCC	AGt ATGCTCA	GCGCGTTCTG	CACCGCGCAG	*	*	*	*	
		**	**	**	**	**	**	**	**	**	
		**	**	**	**	**	**	**	**	**	
		**	**	**	**	**	**	**	**	**	
		**	**	**	**	**	**	**	**	**	

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

**P978102** 450 CCTGCGGGGA GTCGTA**GTTC** **GCGCTTGCGC** **TCT**CGCGGg ACTCC**TCCTC**  
**P978103** 451 CCTTCGGAGA ATC**ctgt---** **GCGCGTGCGT** **TCT**TGTGGGA ACTGC**GCCTC**  
**P978104** 387 CCTTCGGAGC ATCG**CAGTGC** **GCGCGTGCGT** **TCT**TGTGGGA ACTGC**GCCTC**

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alignment  
position 7 0 1 . . . . . 7 1 1 . . . . . 7 2 1 . . . . . 7 3 1 . . . . . 7 4 1 . . . . .

**P978102** 500 **CCAGACGTCC** **CTGCGCGT****CGT** CCTCCTCGC CCTCCa - - - - -  
**P978103** 498 **CCAGAAGGCA** **CCGCGCGT****CGT** CCTTCTC- - CCTCCTGAA GGCCGCCCTCG  
**P978104** 437 **CCAGAAGACA** **CCGCGCGT****CGT** CCTCCTCGC CCTCCTGAA GGCCGCCCTCG

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

**P978102** 536 - - - - - GGCCG CCGCGCg c g c GCCGGAGTCC GCTGT Cc g c c  
**P978103** 546 CTtg CCCAGT GTGTGCGCCG CCGCGAA- - GCTAGAGTCC ACTGACt TTT  
**P978104** 487 CTat CCCTGT GTGTCTGCTG TCCGCTAA- - GCTAAAGTCC ACTGACg TTT

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

**P978102** 571 a g c t a c c c g c t t c c t g c c g c c c g CCGCTGC CATGCTGCC GC CGCGCTGC  
**P978103** 594 - - - - - CCGCAC CATGTTGCC GCCTCAC TGC  
**P978104** 535 - - - - - CCGCAC CATGCTGCC GC CGCAT TGC

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

**P978102** 621 TCCGCGCCC GGGaCTTGGC CGCCTCGTCC GCCACGCCCG TGCCTATGCC  
**P978103** 621 TTCGTCACCC GGGCCTGC GC CGCCTGATGC TTCAGGCGCG TACATACGCC

**P978104** 562 TT CGT CACCC AGGTCTGCGC CGTCTGGTGC TCCAGGCGCG TACGTACGCC  
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alignment position 901 . . . . . 911 . . . . . 921 . . . . . 931 . . . . . 941 . . . . .

**P978102** 671 GAGGCCGCCG CCGCCCGGC TGCCGCTCT GGCC **CCaacC** **AGATGTCCTT**  
**P978103** 671 GAGGCCGCCG CTGCACCTGC CCGCGCCGCC GGGC **CCGGAC** **AGATGTCCTT**  
**P978104** 612 cAGGCCGCCG CCTCACCTGC CCGCGCCGCT GGGC **CtGGAC** **AGATGTCCTT**

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alignment position 951 . . . . . 961 . . . . . 971 . . . . . 981 . . . . . 991 . . . . .

**P978102** 721 **CACCT** **TCGCC** **TCTCCCACGC** **AGGT** TCGg g c g c t g c g g g t c g g g a c c c t c c  
**P978103** 721 **CACCT** TT **GCC** **TCCCCGACGC** **AGGT** ACGa AC TCACA- - - - -  
**P978104** 662 **CACCT** TC **GCC** **TCCCCGACGC** **AGGT** ACG- AC TCACA- - - - -

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

**P978102** 771 g t g g c c g c c G CCCCCGAGT Cc a g g t c c c c a c c - - - - -  
**P978103** 756 - - - - - T CCCCCAGACT CGTC AAGCCC CTGA t c t g AC CC GTGGAAGA  
**P978104** 696 - - - - - G CCCCCAGAGT CGTC AAGCCC CTGA c t t t AC CC GTGGGAGA

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alignment position 1051 . . . . . 1061 . . . . . 1071 . . . . . 1081 . . . . . 1091 . . . . .

**P978102** 805 - - - - -  
**P978103** 797 GGTTCCTTG TATTAGGT Ca t t t GTTT CAT CCCCATGGGG CCCTGTGAAC  
**P978104** 737 GGGTCACTTG TATTGGGT Ct c a g GTTT CAC CCCCATGGGG CC GCGTGAAC

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P978102 1002 - - - -  
 P978103 1032 - - - -  
 P978104 998 t a g g

## 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.

	P978103 (1031 bp)	P978104 (1001 bp)
P978102 (1001 bp)	0.162 30 %	0.185 33 %
P978103 (1031 bp)		<u>1.000</u> <u>75 %</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"/>
<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

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**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

Sat May 21 00:40:19 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)  
**Selected groups** (core/matrix sim):

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

## Aligned Sequences:

No.	Sequence Name	Sequence Description	Length
1	P925014	sym=ATP5C1 loc=Loc509 taxid=9606 spec=Homo sapiens chr=10 ctg=NT_077569 str=(+) start=2192536 end=2193536 len=1001  tss=501  comm=ATP synthase, H+ transporting, mitochondrial F1 complex, gamma polypeptide 1; (NM_005174/589/silver;)	1001 bp
2	P925017	sym=Atp5c1 loc=Loc11949 taxid=10090 spec=Mus musculus chr=2 ctg=NT_039202 str=(-) start=7031016 end=7032041 len=1026  tss=501,508,526  comm=ATP synthase, H+ transporting, mitochondrial F1 complex, gamma polypeptide 1; (AK007063/547/gold;AK088164/572/gold;NM_020615/554/silver;)	1026 bp
3	P925020	sym=Atp5c1 loc=Loc116550 taxid=10116 spec=Rattus norvegicus chr=17 ctg=NW_047492 str=(+) start=33088545 end=33089545  len=1001 tss=501  comm=ATP synthase, H+ transporting, mitochondrial F1 complex, gamma polypeptide 1; (XM_341555/501/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\$NKH	V\$SRP58	V\$AP4R	V\$SF1F	V\$SETSF	V\$SP1F	V\$MAZE	V\$NRF1	V\$NRF1	V\$RORA	V\$GREF	V\$HAND			
alignment position	1 . . . . .			1 1 . . . . .			2 1 . . . . .			3 1 . . . . .			4 1 . . . . .		
<b>P925014</b>	1 g a c t c g c c c a c t g - - - - -														
<b>P925017</b>	1 g a c c g a c c g A C C C C A C C A G G G A A G T C T A A A T G T A A A A C C T C A G T G C T c - -														
<b>P925020</b>	1 c - - - - - A C C C C A C C A G G G A A G T C T A A A T G T A A A A C G T C A A T G C T g t a														
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alignment position	5 1 . . . . .			6 1 . . . . .			7 1 . . . . .			8 1 . . . . .			9 1 . . . . .		
<b>P925014</b>	14 - - - - -														
<b>P925017</b>	49 - - - A G C C T A G C G A T T G T A A G C G a t c a g t g a G T G C T T G T C T G C G A C C A C T T														
<b>P925020</b>	43 c g g A G C C T A G C A A G T G G A C G T G t c a g t g c - G T G C T T G T C T G G G A T C A C T T														
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alignment position	1 0 1 . . . . .			1 1 1 . . . . .			1 2 1 . . . . .			1 3 1 . . . . .			1 4 1 . . . . .		
<b>P925014</b>	14 - - - - - C A G A C C T C A C														
<b>P925017</b>	96 C T C G T G G A G C T G G A G G G C t t c - - - - -														
<b>P925020</b>	92 C T C G G G G A G C T G G A G G G C g g c g c t a a g g g c t g t g a g g a a a C A G A C C T C A C														
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alignment position	1 5 1 . . . . .			1 6 1 . . . . .			1 7 1 . . . . .			1 8 1 . . . . .			1 9 1 . . . . .		
<b>P925014</b>	24 A A G C C t c a c g a c c c g g a c c c c g g g a g e c c c a g e c c c g e g c c c t c a g c c c c														
<b>P925017</b>	117 G C G C C G A G C T G - - - - -														
<b>P925020</b>	142 G C G C C G A G C T G - - - - -														
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alignment position	2 0 1 . . . . .			2 1 1 . . . . .			2 2 1 . . . . .			2 3 1 . . . . .			2 4 1 . . . . .		
<b>P925014</b>	74 g c g t c c a g g a c c t g a t c c t g g a t t g c c a g g g g c c c t c c t G G G A A G A C G G C														
<b>P925017</b>	128 - - - - - G G G A A G A C T G C														
<b>P925020</b>	153 - - - - - A G G A A G A C T G A														
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alignment position	2 5 1 . . . . .			2 6 1 . . . . .			2 7 1 . . . . .			2 8 1 . . . . .			2 9 1 . . . . .		
<b>P925014</b>	124 G C C a c t c c g g g c c - - - - -														
<b>P925017</b>	139 G C C G G A G A G G G C T C c a A G C C G A G G G a - - - - -														
<b>P925020</b>	164 G C C G G A G A G C G C T C a g A G C C G A G G G t a c c a g g g t c g c c g t c a g g c c c t c														



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alignment position		3 0 1 . . . . .	3 1 1 . . . . .	3 2 1 . . . . .	3 3 1 . . . . .	3 4 1 . . . . .
<b>P925014</b>	137	- - - - -	- - - - -	- CACTCACCT	CGTCCCGGCA	CTGCTTCTGC
<b>P925017</b>	165	GGGGT CGCGG	CCAGCCT GAG	TCACTTACCT	CGT CGCGGCA	T TGC T T T T G C
<b>P925020</b>	214	GGGGT CGCGG	CCACCCT GAG	CCACTTACCT	CGT CGCGGCA	T TGT T T T T G C
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alignment position		3 5 1 . . . . .	3 6 1 . . . . .	3 7 1 . . . . .	3 8 1 . . . . .	3 9 1 . . . . .
<b>P925014</b>	166	CACATCTGGC	AATACC	AGCG TAGCTTCTGC	AGCCCTTGG	ACTTGATCCT
<b>P925017</b>	215	CACATCTGGC	AGTACC	AGCG AAGCTTCTGg	AGCCCTTGG	ACTTAATTCT
<b>P925020</b>	264	CACATCTGGC	AGTACC	AGCG AAGCTTCTGC	AGCCCTTAG	ACTTAATTCT
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		* * * * *	* * * * *	* * * * *	* * * * *	* * * * *
alignment position		4 0 1 . . . . .	4 1 1 . . . . .	4 2 1 . . . . .	4 3 1 . . . . .	4 4 1 . . . . .
<b>P925014</b>	216	GTTGGCGATA	GCCTTGGGAG	TAAGAAAATC	CGACTTCCCC	ATGGCGACC a
<b>P925017</b>	265	ATTGGCGATG	GCCTTGGGGC	TCAGAAAATC	CGACTTGCCC	ATGGCGACC C
<b>P925020</b>	314	ATTCGCGATG	GCCTTGGGGC	TCAGAAAATC	TGACTTGCCC	ATGGCGACC C
		* * * * *	* * * * *	* * * * *	* * * * *	* * * * *
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		* * * * *	* * * * *	* * * * *	* * * * *	* * * * *
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			* * * * *	* * * * *	* * * * *	* * * * *
			* * * * *	* * * * *	* * * * *	* * * * *
alignment position		4 5 1 . . . . .	4 6 1 . . . . .	4 7 1 . . . . .	4 8 1 . . . . .	4 9 1 . . . . .
<b>P925014</b>	266	c g g c a g c g a t	c a c t t t c t g g	a c c c a g t a c	t c a g e CAGCC	GGAAACGGAA
<b>P925017</b>	315	TGAGc g c TAC	AACTACAAAG	- - - - -	- - - - - CGGTC	GGAAACGGAA
<b>P925020</b>	364	TGAGa g - TAC	AACAGCGAAG	- - - - -	- - - - - CCGTC	GGAAACGGAA

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alignment
position    5 0 1 . . . . . 5 1 1 . . . . . 5 2 1 . . . . . 5 3 1 . . . . . 5 4 1 . . . . .
P925014 316 C C G G G C T G G C G g c g g t g - - G G C G G G A C A A A t c c c a g C T G A G A G G C G G A A C
P925017 350 C T G G c t c a G C G C G G G G A C A G G C G G G A C C G A A A - - - T T G A C A G C A G G A A a
P925020 398 C T G G A C C C G C G C G C G G A T A G G C G G G A C C A A A A - - - C T G A C A G C A G G A A C
** ** *      ** ** *      *      *      *      *      *      *      *      *      *      *      *      *
** ** *      ** ** *      *      *      *      *      *      *      *      *      *      *      *      *
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alignment
position    5 5 1 . . . . . 5 6 1 . . . . . 5 7 1 . . . . . 5 8 1 . . . . . 5 9 1 . . . . .
P925014 364 G A G G T G G G G C C T G G G A A G A C T G G G T T G C A A C G G T C G C G A G A C T c c c c t c g
P925017 396 T G G G T G G G G C C A G G G A A C T C G C G G C T T C G G C G C T C A C G A G A T T T - - - - -
P925020 444 T G G G T G G G G C C A G G G A C C T C G C G G C T T C C G C G C T C A C G A G A T T T - - - - -
** ** *      ** ** *      *      *      *      *      *      *      *      *      *      *      *      *
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alignment
position    6 0 1 . . . . . 6 1 1 . . . . . 6 2 1 . . . . . 6 3 1 . . . . . 6 4 1 . . . . .
P925014 414 c c g t a g c g c g a a g a A A C G A G A C T G A A G A A G A G A G C A A G G T G G G A G G G G c g
P925017 440 - - - - - - - - - - - - - - - - A G C G A G A C C G A G G A C G C A G G C G G A G C G G G C C G G G g c
P925020 488 - - - - - - - - - - - - - - - - A G C G A G A C T G A G G G C G C T A G C G G A G C A G G C C G c t g c
** ** *      ** ** *      *      *      *      *      *      *      *      *      *      *      *      *
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** ** *      ** ** *      *      *      *      *      *      *      *      *      *      *      *      *

alignment
position    6 5 1 . . . . . 6 6 1 . . . . . 6 7 1 . . . . . 6 8 1 . . . . . 6 9 1 . . . . .
P925014 464 c g c t g g g G A G C T T C G G C G C A T G C G C G C T G A G G C C T G C C T G A C C G A C C T T C
P925017 476 g - C C T - - G A G C T C C C G C G C A C G C G C A C T G A G T C C C G T C T G C C C G A C C T T C
P925020 524 t c C C C - - G A G C T C C C G C G C A C G C G C A G T G A G C C T C G T C T G C C C G A C C T T C
** ** *      ** ** *      *      *      *      *      *      *      *      *      *      *      *      *
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alignment
position    7 0 1 . . . . . 7 1 1 . . . . . 7 2 1 . . . . . 7 3 1 . . . . . 7 4 1 . . . . .
P925014 514 A g c a g g g c t g t g g C T A C C A T G T T C T C T C G C G C G G T G T C G c t G G G C T G T C
P925017 523 A A G G C T - - - - - - - C C A C C A T G T T C T C G C G G G C G A G C G T T G T C G G G C T G T C
P925020 572 A A G G T T - - - - - - - C T A C C A T G T T C T C G C G G G C G A G T A T T G T C G G G C T G T C
** ** *      ** ** *      *      *      *      *      *      *      *      *      *      *      *      *
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alignment
position    7 5 1 . . . . . 7 6 1 . . . . . 7 7 1 . . . . . 7 8 1 . . . . . 7 9 1 . . . . .
P925014 564 GGCCTGGACC TTGCAGCCGC AATGGTATGg c a g c t t g c g g g a a g a t c g g c
P925017 566 GGCCTGC GCC GTGCAGCCGC AATGGTA g GA CCAC- - - - -
P925020 615 GGCCTGCTCC TTGCAGCCGC AATGGTATGA CTAC- - - - -
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alignment
position    8 0 1 . . . . . 8 1 1 . . . . . 8 2 1 . . . . . 8 3 1 . . . . . 8 4 1 . . . . .
P925014 614 a g g A C C G C A A G G G A T G G A A G A G C T T G G G C A C G G G C A G G G a g g a g g a g a t
P925017 600 - - - A T C G G G A G G G A T G C G G G G G C T C G G G C T T G C T G C G A G G C A G G A G G G A T
P925020 649 - - - G C C G G G A G G C A T G C C G G G G C T T G G G C T T G C T G C A A G A C A G G A G G G A T
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alignment
position    8 5 1 . . . . . 8 6 1 . . . . . 8 7 1 . . . . . 8 8 1 . . . . . 8 9 1 . . . . .
P925014 664 g g g c g c g g g g g c a g a t g t g g g g t c g c a g g g c c t a g c t g g g c c c c t g g c c c
P925017 647 - - - - -
P925020 696 - - - - -

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alignment
position    9 0 1 . . . . . 9 1 1 . . . . . 9 2 1 . . . . . 9 3 1 . . . . . 9 4 1 . . . . .
P925014 714 g t c g g a g g c g c c g g g t a g c g G G G C T G C A g g a a g c g g c t c t g a g g t c g - -
P925017 647 - - - - - G G a G C T G C A T G C T C A C T C C T G G C G G A A G A A
P925020 696 - - - - - G G G G C T G C A T G C T C G C T C C T G G C G G A G G A A
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alignment
position    9 5 1 . . . . . 9 6 1 . . . . . 9 7 1 . . . . . 9 8 1 . . . . . 9 9 1 . . . . .
P925014 762 - - - - - G G C A A G G T G T G C g
P925017 677 G G C C C A G C T C a - - - - - G G C C G C G G G G A T G T C T G C A
P925020 726 G A C C C A G C T C t t g c a c g g c c c g g c c a c t c g G G C C G C G G C A A G G T C T G C A

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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 . . . . .
<b>P925014</b>	775	c a - - - - -		- - - - -		- - - - -		GGG CCGGGCTCCG GC		<b>GGAGCAAC</b>
<b>P925017</b>	708	GAGCTGGAAGGTTGCGTGCC		g g a c c c c t		GG TAGGGGTCAA AG		<b>AGAAACAAC</b>		
<b>P925020</b>	776	GAGCTGGAAGGTCGCGTGCC		a g t c c c g		GGG CTGGGGTCAA AG		<b>GGAAACAAC</b>		
		* * * * *		* * * * *		* * * * *		* * * * *		* * * * *
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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>P925014</b>	800	<b>GTCCCGCCCG</b> G		TTCCCTgaggt		<b>cggag - - G</b>		GCCACCTGGG		ACCTCGGGAC
<b>P925017</b>	758	<b>GTACGGTCT</b> G		ATCCCCTGA		GA		<b>GGAACG</b> GCCATCCGGG		ACCTCGGGAC
<b>P925020</b>	826	<b>GTACGGCCT</b> G		ATCCgCTGG		GA		<b>GGAACG</b> GCCACCTGGG		ACCTCAGGAC
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		* * * * *		* * * * *		* * * * *		* * * * *		* * * * *
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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>P925014</b>	848	t g c g g c c t		GA GTCCAAATTG		ACGTCTGGGC		GGTCTTGAGT		TCCCTCAGCT
<b>P925017</b>	808	CCGgACGGGA		TTCGGGTTGA		GCTTTGGAGC		CATCTGGGTT		TCGATCAACT
<b>P925020</b>	876	CCGtACGAGA		GTCGGATTGA		GC GTTTGGAGC		CATCTGGGTT		TCGATCAACT
		* * * * *		* * * * *		* * * * *		* * * * *		* * * * *
		* * * * *		* * * * *		* * * * *		* * * * *		* * * * *
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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>P925014</b>	898	a a t c a g c a c t		t c c t g a g c t t		<b>cc ACTTCCAC</b>		<b>TGCA</b> AGCCAG		G c c c c c a g t c
<b>P925017</b>	858	<b>CCGT - - - - -</b>		- - - - -		<b>- - ACTTCCGC</b>		<b>TCCGT</b> ACCCG		GGAGCACAg C
<b>P925020</b>	926	<b>CCGT - - - - -</b>		- - - - -		<b>- - ACTTCCGC</b>		<b>TCCGT</b> ACTAG		GGAGCACAt 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 . . . . .
<b>P925014</b>	948	t c - - - - -		- - - - -		AGGG CCTGCAAGGT		GACGGGagcc		t g a g c a a t a g
<b>P925017</b>	890	TTGCAAAGTC		T TTAGAAAGG		CCCTGAAGGT		GAAGGGGcga		- - - - -
<b>P925020</b>	958	TTGCAAAGTC		T TTAGAAAGG		GCCTCAAGGT		GAAGGGGgaga		t c c g - - - - -
		* * * * *		* * * * *		* * * * *		* * * * *		* * * * *
		* * * * *		* * * * *		* * * * *		* * * * *		* * * * *
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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 . . . . .

```

P925014 984 c c CAGGGGAA GGT TAA GT - - - - -
P925017 930 - - CCGGGGAA CGT TTGGT t g t a a c t t t t g g c t t t g a a g c c c t g t g a a a c a
P925020 1002 - - - - -
          * * * * *
alignment
position 1 3 0 1 . . . . . 1 3 1 1 . . . . . 1 3 2 1 . . . . . 1 3 3 1 . . . . . 1 3 4 1 . . . . .
P925014 1002 - - - - -
P925017 978 c t g c a c g g g g g a g c a g c g t g a c c c t t t a a g g t g t g a t g g c t t g c t t g a g
P925020 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.

	P925017 (1026 bp)	P925020 (1001 bp)
P925014 (1001 bp)	0.228 37 %	0.242 42 %
P925017 (1026 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	
Positions in alignment	from: <input type="text"/> to: <input type="text"/>
Output file	<input type="text" value="dialign.seq"/>
<input type="button" value="Extract aligned sequences"/>	

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

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[Frequently asked questions](#) [Your Results](#) [Your Sequences](#) [Your Protocol](#) [Help](#)

**GEMS Launcher Task: *DiAlign TF*: Multiple alignment plus TF sites  
 working on C5-ATP5E-HM.seq (2 seq.)**

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

DiAlign professional TF Release 3.1 December 2004

Tue May 24 16:38:33 2005

### Solution parameters:

**Sequence file:** [C5-ATP5E-HM.seq](#) (2 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 2 (100.0 %) sequences)  
**Family matches:** yes  
**MatInspector library:** Matrix Family Library Version 5.0 (February 2005)  
**Selected groups** (core/matrix sim):
 

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

### Aligned Sequences:

No.	Sequence Name	Sequence Description	Len
1	P927229	P927229 sym=ATP5E loc=Loc514 taxid=9606 spec=Homo sapiens chr=20 ctg=NT_011362 str=(-) start=22659786 end=22660796 len=1011 tss=501,511 comm=ATP synthase, H+ transporting, mitochondrial F1 complex, epsilon subunit; (AK026556/511/gold;NM_006886/501/bronze;)	1011
2	mATP5E	mATP5E m6_dna range=chr2:173888263-173889536 5'pad=0 3'pad=0 revComp=TRUE strand=? repeatMasking=none	1274

### 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\$ECAT
V\$PCAT
V\$PBXC
V\$SP1F
V\$SETF
V\$NRF2
V\$AREB
V\$YY1F

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

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P927229 1 g g g g g t c c t c c a c t g - - - - -
mATP5E 1 t c a a g t t c t t a g c t t c c t a c t t t a a a g g a t t a c t c a g t t t a a t a a t t c t t

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

P927229 16 - - - - -
mATP5E 51 t g g a c a t t t g t a a a a g a t t t t t a a a a g t a a a g g a a a a t c g t t t g a c a a

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

P927229 16 - - - - -
mATP5E 101 g t g g a a t g a a t g t t c c a g c t a a a c a g a g c a c t a c t t a a c a t t g t t g g a c a

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

P927229 16 - - - - - G G T T T C C A G G G T T T A g - - - - -
mATP5E 151 a a g t g t c a g g t a c G G T T T C T A G G A G T T A c a c c t g t t c t g g a a g g g t c t g a
      *****

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

P927229 32 - - - - -
mATP5E 201 t g c c c t g a t g a t g t t t t t t t a a g t a t a t a c a t t t c c a c t t t g c a a t g t g g

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

P927229 32 - - - - -
mATP5E 251 t t c c a t c g t g a a t t c t g c c t g a g t a c a a a t g g a a t c c t g g g c a t g g g t a c

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

P927229 32 - - - - - T G T C A C T C C G A G a a a g g g g g t g c c c t a a g a
mATP5E 301 a t g c a g a c a g g a a c a t t a g c T G T C A C T C A G A G c g g g - - - - -
      *****

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

P927229 62 g c c t t t c t a a a t c t c a g c t c t c a g g a c a c g c t t g t c t g t c c a c a g a t t t a
mATP5E 337 - - - - -

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

P927229 112 a a a a a g c c g g c g c c g t t t c c c t g a a g c g g g c g c a a a g c c a g g c c C T C G G G
mATP5E 337 - - - - - C T C G A G
      *****

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

P927229 162 G C G G C C G T G C C C G C g c c g c c t c - - - - - G C G
mATP5E 343 G A G G C C C C G C C C C t g c c c g c a g c a c c t g g a a g g t g a c c g g c a t g c a G C G
      *****
    
```

alignment position	501 . . . . .	511 . . . . .	521 . . . . .	531 . . . . .	541 . . . . .
<b>P927229</b>	187 T C C T C G C T T C	CC g a a a g c a c	g c g g c t c a g t	g g t c c t t a g c	g a g c g g g g a c
<b>mATP5E</b>	393 G C C T C G C T T T	CC c a g g t g t c	t c t a c g g c c a	c a g c t t - - -	- - - - -
		*****			
alignment position	551 . . . . .	561 . . . . .	571 . . . . .	581 . . . . .	591 . . . . .
<b>P927229</b>	237 a c c c c g g c c t	t c t t g c c c c c	g t c g t c c c c g	c c g g g g t a a t	a c g g a a g g t c
<b>mATP5E</b>	429 - - - - -	- - - - -	- - - - -	- - - - -	- - - - -
alignment position	601 . . . . .	611 . . . . .	621 . . . . .	631 . . . . .	641 . . . . .
<b>P927229</b>	287 g g g g a c a c a	c g c c C C G G A	G C T C T T <b>GGAG</b>	<b>CCAATAGGTG</b>	<b>GGC</b> G C G G C C G
<b>mATP5E</b>	429 - - - - -	- - - C C G G T A	G C C G C T <b>TCGGC</b>	<b>CAATGGGCAA</b>	G G C G C G A C C G
		*****	*****	*****	*****
alignment position	651 . . . . .	661 . . . . .	671 . . . . .	681 . . . . .	691 . . . . .
<b>P927229</b>	337 g c c g g c c c g c	c c c g g g a t t g	g c a c c c g c a g	t c c a g a c c g c	<b>GCGCGC</b> <b>CCAT</b>
<b>mATP5E</b>	465 - - - - -	- - - - -	- - - - -	- - - - -	<b>GCGCTC</b> <b>CTAT</b>
					*****
					*****
alignment position	701 . . . . .	711 . . . . .	721 . . . . .	731 . . . . .	741 . . . . .
<b>P927229</b>	387 <b>TGGCTCC</b> C G G	c g c c g g g g g g	c t t c c g c g g c	a g g g c a g c a g	g g g c c g t g c t
<b>mATP5E</b>	475 <b>TGGCTCC</b> T G G	t t g g c a a g g g	c - - - - -	- - - - -	- - - - -
	*****				
	*****				
alignment position	751 . . . . .	761 . . . . .	771 . . . . .	781 . . . . .	791 . . . . .
<b>P927229</b>	437 c a g g g g c g g g	g c c g G G T A G G	A G <b>GCGGTGAT</b>	<b>TGGCAGGTC</b> C	G C a c g C C C C G
<b>mATP5E</b>	496 - - - - -	- - - G G G A T G	A G <b>GCGCTGAC</b>	<b>TGGCAGGTC</b> C	G C g t a C C C C A
		*****	*****	*****	*****
		*****	*****	*****	*****
		*****	*****	*****	*****
		*****	*****	*****	*****
alignment position	801 . . . . .	811 . . . . .	821 . . . . .	831 . . . . .	841 . . . . .
<b>P927229</b>	487 <b>CCTCTTCCGC</b>	<b>TTCTGTGGTC</b>	<b>TGATCTTCCT</b>	<b>GC</b> <b>GGC</b> t g a a c	c g c c c g g c t g
<b>mATP5E</b>	532 <b>CCCCTTCCGC</b>	<b>TACTCAGGCC</b>	<b>TGACCTTCCT</b>	<b>GCTGC</b> c g g g c	c g g t t t g a g g
	*****	*****	*****	*****	
	*****	*****	*****	*****	
	*****	*****	*****	*****	
	*****	*****	*****	*****	
	*****	*****	*****	*****	
alignment position	851 . . . . .	861 . . . . .	871 . . . . .	881 . . . . .	891 . . . . .
<b>P927229</b>	537 a g c c g a c a t t	g c c g G C G T C T	T G G C G A T T C G	G C C C G A C G A G	C t c c g c t t t c
<b>mATP5E</b>	582 c t a c t c t g a a	- - - G C G A C C	C A G C G G T T C T	G C C C G A C G C G	C c c g c t c g a g
		*****	*****	*****	
		*****	*****	*****	



alignment position	9 0 1 . . . . .	9 1 1 . . . . .	9 2 1 . . . . .	9 3 1 . . . . .	9 4 1 . . . . .	
<b>P927229</b>	587 g c t ACAGCAT	GGTGGCCTAC	TGG	AGACAAGG	CTGGACTCAG	GTA g g c c a g
<b>mATP5E</b>	628 - - - ACACCAT	GGTGGCGTAC	TGG	CGACAAGG	CTGGACTCAG	GTA c g c c a g
	* * * * *	* * * * *	* * * * *	* * * * *	* * * * *	* * * * *
	* * * * *	* * * * *	* * * * *	* * * * *	* * * * *	* * * * *
	* * * * *	* * * * *	* * * * *	* * * * *	* * * * *	* * * * *
	* * * * *	* * * * *	* * * * *	* * * * *	* * * * *	* * * * *
	* * * * *	* * * * *	* * * * *	* * * * *	* * * * *	* * * * *
	* * * * *	* * * * *	* * * * *	* * * * *	* * * * *	* * * * *
	* * * * *	* * * * *	* * * * *	* * * * *	* * * * *	* * * * *
	* * * * *	* * * * *	* * * * *	* * * * *	* * * * *	* * * * *
	* * * * *	* * * * *	* * * * *	* * * * *	* * * * *	* * * * *
	* * * * *	* * * * *	* * * * *	* * * * *	* * * * *	* * * * *
alignment position	9 5 1 . . . . .	9 6 1 . . . . .	9 7 1 . . . . .	9 8 1 . . . . .	9 9 1 . . . . .	
<b>P927229</b>	637 g c c t c c a g a g	GG AAGGCTT	C G C G A G C C G G	C C C G C G C G C A	T C C c g g t g c c	
<b>mATP5E</b>	675 a a a g c g t t - -	GG GAAGGCCT	G G C C G G C C G T	C A C C A G G C C G	T A C g a g a c - -	
		* * * * *	* * * * *	* * * * *	* * * * *	
alignment position	1 0 0 1 . . . . .	1 0 1 1 . . . . .	1 0 2 1 . . . . .	1 0 3 1 . . . . .	1 0 4 1 . . . . .	
<b>P927229</b>	687 c a g a g g t c a t	g c a g g a c a c a	g a g c a g c g g c	c c c a c g c g t g	a c c g g g t t g	
<b>mATP5E</b>	721 - - - - -	- - - - -	- - - - -	- - - - -	- - - - -	
alignment position	1 0 5 1 . . . . .	1 0 6 1 . . . . .	1 0 7 1 . . . . .	1 0 8 1 . . . . .	1 0 9 1 . . . . .	
<b>P927229</b>	737 G G C C A A G C C T	C G g g c g t	c g C	C G C C A A G A T G	G C G T C G C T G T	G G G C A A A G C G
<b>mATP5E</b>	721 G G C C A A G C C A	C G c g g c c	a e C	C T C C A A G A T G	G C G T C G C C G T	G G A C A A G G C T
	* * * * *	* * * * *	* * * * *	* * * * *	* * * * *	* * * * *
			* * * * *	* * * * *	* * * * *	* * * * *
			* * * * *	* * * * *	* * * * *	* * * * *
			* * * * *	* * * * *	* * * * *	* * * * *
			* * * * *	* * * * *	* * * * *	* * * * *
			* * * * *	* * * * *	* * * * *	* * * * *
alignment position	1 1 0 1 . . . . .	1 1 1 1 . . . . .	1 1 2 1 . . . . .	1 1 3 1 . . . . .	1 1 4 1 . . . . .	
<b>P927229</b>	787 C T c a g g c g g g	c g c g g c c t c g	a c c t c g c g t g	g g a g c g c g t c	t g t g t c c t g c	
<b>mATP5E</b>	771 C T t c g c g g g g	t c a t g g g g t c	a g g g a c c c t a	a a c a g a g g t g	g c t g c t c c t c	
	* *					
	* *					
	* *					
	* *					
	* *					
alignment position	1 1 5 1 . . . . .	1 1 6 1 . . . . .	1 1 7 1 . . . . .	1 1 8 1 . . . . .	1 1 9 1 . . . . .	
<b>P927229</b>	837 c t c g c t t c c c	g a c g g t g c g -	- - - - -	- - - - -	- - - - - G C C	
<b>mATP5E</b>	821 g g g a g a g g t a	g c c t a c a g t a	c c t g c a t g a t	c g c t g t g a c g	g c c a a g t G C A	
					* * *	
alignment position	1 2 0 1 . . . . .	1 2 1 1 . . . . .	1 2 2 1 . . . . .	1 2 3 1 . . . . .	1 2 4 1 . . . . .	
<b>P927229</b>	859 C A G C A C C C a c	a g a g t g c c c c	t - - - - -	- - - - -	- - - - -	
<b>mATP5E</b>	871 C A G C A C C C t t	g a c c t g g c c a	c g c t g a c a c t	g a c c t t g c t c	a c c t g c g c a g	
	* * * * *					

alignment position	1 2 5 1 . . . . .	1 2 6 1 . . . . .	1 2 7 1 . . . . .	1 2 8 1 . . . . .	1 2 9 1 . . . . .
<b>P927229</b>	880	- - - - -	- - - - -	- - - - -	- - - - -
<b>mATP5E</b>	921	a g g g a g g g g c	g c a c a a g t t c	a t t t t c a a g t	g t g a c c t t a g t g a c c t t t t c
alignment position	1 3 0 1 . . . . .	1 3 1 1 . . . . .	1 3 2 1 . . . . .	1 3 3 1 . . . . .	1 3 4 1 . . . . .
<b>P927229</b>	880	- - - - -	- - - - -	- - - - -	- - - - -
<b>mATP5E</b>	971	c c a g t a g t g a	a a a a a g g t g a	a a g c c c t c t a	a c c t g t g g a g c g c c c t g c a g
alignment position	1 3 5 1 . . . . .	1 3 6 1 . . . . .	1 3 7 1 . . . . .	1 3 8 1 . . . . .	1 3 9 1 . . . . .
<b>P927229</b>	880	- - - - -	- - - - -	- - - - -	- - - - -
<b>mATP5E</b>	1021	g g g c c c c g t g	a t g g g t g c g a	g c t g t g g g c c	t a g g a g t g g t g g t g c a t g g t
alignment position	1 4 0 1 . . . . .	1 4 1 1 . . . . .	1 4 2 1 . . . . .	1 4 3 1 . . . . .	1 4 4 1 . . . . .
<b>P927229</b>	880	- - - - -	- - - - -	- - - - -	- - - - GGACAC
<b>mATP5E</b>	1071	t t c c t t g c t c	c a g g a g t g c	a t c t t g t t a g	t g t g c t g g g t g g a g GAACAC *****
alignment position	1 4 5 1 . . . . .	1 4 6 1 . . . . .	1 4 7 1 . . . . .	1 4 8 1 . . . . .	1 4 9 1 . . . . .
<b>P927229</b>	886	CTTTGTGAAT	GGCAGGTTt c	t c g a g a g a g a	g g c c a g - - - - -
<b>mATP5E</b>	1121	CTTTCTGGGT	ATCAGGCTg a	a g g c c c a g t g	c c c c g a c a g a g t t c a a g c a a *****
alignment position	1 5 0 1 . . . . .	1 5 1 1 . . . . .	1 5 2 1 . . . . .	1 5 3 1 . . . . .	1 5 4 1 . . . . .
<b>P927229</b>	922	- - - - -	- - - - -	- - - - -	- - - - CTCTTATTT
<b>mATP5E</b>	1171	a g t t g t g t a g	a a c a a a g g a	c g g t a g g c t c	a c a g t t g a t g c CTCTTATTa *****
alignment position	1 5 5 1 . . . . .	1 5 6 1 . . . . .	1 5 7 1 . . . . .	1 5 8 1 . . . . .	1 5 9 1 . . . . .
<b>P927229</b>	931	a g c a a a c c t t	t t t c t t c t a g	a a t g g t g c t g	g a g c c a g g t g g t g a a a g t a g
<b>mATP5E</b>	1221	a a c t a t c t c c	c a t g g c g t c c	a t c a c c t t a t	t t t c c t g c g c c c a g c c g c t t
alignment position	1 6 0 1 . . . . .	1 6 1 1 . . . . .	1 6 2 1 . . . . .	1 6 3 1	
<b>P927229</b>	981	t a c a g t c a c a	t c c a c c t c g g	g a a a c a g g a g a	
<b>mATP5E</b>	1271	g a a g - - - - -	- - - - -	- - - - -	

**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>mATP5E</b>
	<b>(1274 bp)</b>

<b>P927229</b> (1011 bp)	<u>1.000</u> <u>26 %</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	dialign.seq <input type="text"/>

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

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**GEMS Launcher Task: *DiAlign* TF: Multiple alignment plus TF sites  
working on C5-ATP5E.seq (3 seq.)**

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

DiAlign professional TF Release 3.1 December 2004

Tue May 24 16:14:29 2005

## Solution parameters:

**Sequence file:** [C5-ATP5E.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)  
**Selected groups** (core/matrix sim):

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

## Aligned Sequences:

No.	Sequence Name	Sequence Description	Len
1	P927229	P927229 sym=ATP5E loc=Loc514 taxid=9606 spec=Homo sapiens chr=20 ctg=NT_011362 str=(-) start=22659786 end=22660796 len=1011 tss=501,511 comm=ATP synthase, H+ transporting, mitochondrial F1 complex, epsilon subunit; (AK026556/511/gold;NM_006886/501/bronze;)	1011
2	mATP5E	mATP5E m6_dna range=chr2:173888263-173889536 5'pad=0 3'pad=0 revComp=TRUE strand=? repeatMasking=none	1274
3	rATP5E	rATP5E n3_dna range=chr14:83622419-83623508 5'pad=0 3'pad=0 revComp=FALSE strand=? repeatMasking=none	1090

## 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\\$SETSF](#) [V\\$SP1F](#)

```

alignment position 1 . . . . . 11 . . . . . 21 . . . . . 31 . . . . . 41 . . . . .
P927229      1 g g g g g t c c t c c a c t g - - - - -
mATP5E      1 t c a a g t t c t t a g c t t c c t a c t t t a a a g g a t t a c t c a g t t t a a t a a t t c t t
rATP5E      1 c c g c - - - - -

alignment position 51 . . . . . 61 . . . . . 71 . . . . . 81 . . . . . 91 . . . . .
P927229     16 - - - - -
mATP5E     51 t g g a c a T T T G T A A A A G A T T T T T A A A A A g t a a a g g a a a a a t c g t t t g a c a a
rATP5E     5 - - - - - T T T G C A A G A G A A A T T T G A A A A t a g a g c c a c a g c c a a g a c c t t c g
                * * * * *
alignment position 101 . . . . . 111 . . . . . 121 . . . . . 131 . . . . . 141 . . . . .
P927229     16 - - - - -
mATP5E    101 g t g g a a t g a a t g t t c c a g c t a a a - - - - -
rATP5E     49 t t t c a g a g a g t g a t t t c a t a a c a g g a g a a g c t t g a g a g a g t c g a c t c t t a

alignment position 151 . . . . . 161 . . . . . 171 . . . . . 181 . . . . . 191 . . . . .
P927229     16 - - - - -
mATP5E    124 - - - - -
rATP5E     99 a t c t g g c c g a g c t g t t t c c a t g t g t t t g a c g a a g t t a t t a a c t c a g c c t g

alignment position 201 . . . . . 211 . . . . . 221 . . . . . 231 . . . . . 241 . . . . .
P927229     16 - - - - -
mATP5E    124 - - - - -
rATP5E    149 g t c c a g a g g g c t a a a a g t g t g t t g t t g g c t c a t c c t c c t a a t c c a g g t t

alignment position 251 . . . . . 261 . . . . . 271 . . . . . 281 . . . . . 291 . . . . .
P927229     16 - - - - -
mATP5E    124 - - - - - C A G A G C A C T A C T T A A C A T T G T T G G A C A A A G T G T
rATP5E    199 c t c t g g a g a c a a g a g t g C T G A A C A T T C C C T A G A G T T C T T G G A C T A T G T A A
                * * * * *
alignment position 301 . . . . . 311 . . . . . 321 . . . . . 331 . . . . . 341 . . . . .
P927229     16 - - - - - G G T T T C C A G G G T T T A G T G T C A C T C C G A G a a a g g g g g t g c c c t a
mATP5E    157 C A G G T A c G G T T T C T A G G A G T T A c a c c t g t t c t g g a a g g g t c t g a t g c c c t
rATP5E    249 C A A G A A a a c - - - - - G G G G T G T G T G T A A C T C G G A G c g a a t t g c t a a c t t a
                * * * * *
alignment position 351 . . . . . 361 . . . . . 371 . . . . . 381 . . . . . 391 . . . . .
P927229     59 a g a g c c t t t c t - - - - -
mATP5E    207 g a t g a t g t t t t T T A A G T A T A t a c a t t t c c a c t t t g c a a t g t g g t t c c a t
rATP5E    293 c t g t a a a c t g - - T T A A G T A T A a t t a a g a a a t a c a a g t t a a t g - - - - -
                * * * * *
alignment position 401 . . . . . 411 . . . . . 421 . . . . . 431 . . . . . 441 . . . . .
P927229     70 - - - - -
mATP5E    257 c g t g a a t t c t g c C T G A G T A C A A A T G G A A T c c t g g g c a t g g g t a c a t g c a g
rATP5E    333 - - - - - C T A A G T A C A A A T G T A A T G T A C A A A G A C A A G C T T G a a a g
                * * * * *
alignment position 451 . . . . . 461 . . . . . 471 . . . . . 481 . . . . . 491 . . . . .
P927229    100 t c c a c a g a t t - - - - -

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<b>mATP5E</b>	307	a c a g g a a c a t	t a g c t g t c a c	t c a g a g c g g g	- - - - -	- - - - -
<b>rATP5E</b>	371	g a g a g a c c a a	t t t a t a t t t c	c c a t t a t a t a	c t c t t t g t t	g t c a a a g t t a
alignment position		5 0 1 . . . . .	5 1 1 . . . . .	5 2 1 . . . . .	5 3 1 . . . . .	5 4 1 . . . . .
<b>P927229</b>	110	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -
<b>mATP5E</b>	337	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -
<b>rATP5E</b>	421	a a c c t a a g g t	a c a t a a c t c a	a a a c a a g t t t	a g a t t a a a c t	t a a a t c t g t
alignment position		5 5 1 . . . . .	5 6 1 . . . . .	5 7 1 . . . . .	5 8 1 . . . . .	5 9 1 . . . . .
<b>P927229</b>	110	- - - T A A A A A	A G C c g g c g c c	g t t t c c c t g a	a g c g g g c g c a	a a g c c a g g c c
<b>mATP5E</b>	337	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -
<b>rATP5E</b>	471	t t g a T A A A A A	A G C a <b>a t a t c c</b>	<b>g</b> - - - - -	- - - - -	- - - - -
			*****	***		
alignment position		6 0 1 . . . . .	6 1 1 . . . . .	6 2 1 . . . . .	6 3 1 . . . . .	6 4 1 . . . . .
<b>P927229</b>	156	C T C G G G G C G G	C C G T G C C C G C	g c c g c c t c - -	- - - - -	- - - - -
<b>mATP5E</b>	337	C T C G A G G A G G	C C C C G C C C C C	t g c c c g c a g c	a c c t g g a a g g	t g a c c g g c a t
<b>rATP5E</b>	492	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -
		*****	*****			
alignment position		6 5 1 . . . . .	6 6 1 . . . . .	6 7 1 . . . . .	6 8 1 . . . . .	6 9 1 . . . . .
<b>P927229</b>	184	- - - G C G T C C T	C G C T T C C C g a	a a g c a c g c g g	c t c a g t g g t c	c t t a g c g a g c
<b>mATP5E</b>	387	g c a G C G G C C T	C G C T T C C C a	g g t g t c t c t a	c g g c c a c a g c	t t - - - - -
<b>rATP5E</b>	492	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -
		*****	*****			
alignment position		7 0 1 . . . . .	7 1 1 . . . . .	7 2 1 . . . . .	7 3 1 . . . . .	7 4 1 . . . . .
<b>P927229</b>	231	g g g g a c a c c c	c g g c c t t c t t	g c c c c c g t c g	t c c c c g c c g g	g g t a a t a c g g
<b>mATP5E</b>	429	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -
<b>rATP5E</b>	492	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -
alignment position		7 5 1 . . . . .	7 6 1 . . . . .	7 7 1 . . . . .	7 8 1 . . . . .	7 9 1 . . . . .
<b>P927229</b>	281	a a g g t c g g g g	g a c a c a c g c c	C C G G G A G C T C	T T G G A G C C A A	T A G G T G G G C G
<b>mATP5E</b>	429	- - - - -	- - - - -	C C G G T A G C C G	C T C G G C C A A T	G G G C A A G G C G
<b>rATP5E</b>	492	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -
				*****	*****	*****
alignment position		8 0 1 . . . . .	8 1 1 . . . . .	8 2 1 . . . . .	8 3 1 . . . . .	8 4 1 . . . . .
<b>P927229</b>	331	C G G C C G g c c g	g c c c g c c c c g	g g a t t g g c a c	c c g c a g t c c a	g a c c g c G C G C
<b>mATP5E</b>	459	C G A C C G - - - -	- - - - -	- - - - -	- - - - -	- - - - - G C G C
<b>rATP5E</b>	492	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -
		*****				***
alignment position		8 5 1 . . . . .	8 6 1 . . . . .	8 7 1 . . . . .	8 8 1 . . . . .	8 9 1 . . . . .
<b>P927229</b>	381	G C C C A T T G G C	T C C C G G c g c c	g g g g g g c t t c	c g c g g c a g g g	c a g c a g g g g c
<b>mATP5E</b>	469	T C C T A T T G G C	T C C T G G t t g g	c a a g g g c - - -	- - - - -	- - - - -
<b>rATP5E</b>	492	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -
		*****	*****			
alignment position		9 0 1 . . . . .	9 1 1 . . . . .	9 2 1 . . . . .	9 3 1 . . . . .	9 4 1 . . . . .
<b>P927229</b>	431	c g t g c t c a g g	g g c g g g g c c g	G G T A G G A G G C	G G T G A T T G G C	A G G T C C G C a c
<b>mATP5E</b>	496	- - - - -	- - - - -	G G G A T G A G G C	G C T G A C T G G C	A G G T C C G C g t
<b>rATP5E</b>	492	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -

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alignment position 951..... 961..... 971..... 981..... 991.....
P927229 481 g CCCC GCCTC TT CCGCT TCT GTGGTCTGAT CTTCTGCGG CTGAACCGc c
mATP5E 526 a CCCC ACCCC TT CCGCT ACT CAGGCCTGAC CTTCTGCTG CCGGCCGGt
rATP5E 492 ----- ----- ----- -TTCTGCTG CCGGCCGGg
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alignment position 1001..... 1011..... 1021..... 1031..... 1041.....
P927229 531 c g g c t g a g c c g a c a t t g c c g GCGTCTTGCC GATTCGGCC GACGAGCTCC
mATP5E 576 t t g AGGCTAC TCTGAA- - - GCGACCCAGC GGT TCT GC CC GACGC GC- CC
rATP5E 511 c t c AGGCTAC TCTGAA- - - GCGACCCAGC AGT TCT GC CT GACACGCCCC
*****
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*****

alignment position 1051..... 1061..... 1071..... 1081..... 1091.....
P927229 581 GCTt t c g c t A CAGCATGGTG GCCTACTGGA GACAGGCTGG ACTCAGGTAg
mATP5E 621 GCTCGAG- - A CACCATGGTG GCGTACTGGC GACAGGCTGG ACTCAGGTAC
rATP5E 557 GCTCGAG- - A CACCATGGTG GCTTACTGGC AACAGGCTGG ACTCAGCTAC
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*****

alignment position 1101..... 1111..... 1121..... 1131..... 1141.....
P927229 631 g c c c a g g c c t c c a g a g G G A A G G C T T C G C G A G C C G G C C G C G C G C A T C C c
mATP5E 669 GCCCAGa a a g c g t t - - G G G A A G G C C T G G C C G G C C G T C A C C A G G C C G T A C g
rATP5E 605 ATCCGGt t c t c c c a g a t c t g t g c a a a a g c a g t g a g g g a t - - - - -
*****

alignment position 1151..... 1161..... 1171..... 1181..... 1191.....
P927229 681 g g t g c c c a g a g g t c a t g c a g g a c a g a g c a g c g g c c c a c g c g t g a c c g
mATP5E 717 a g a c - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
rATP5E 644 - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -

alignment position 1201..... 1211..... 1221..... 1231..... 1241.....
P927229 731 g g g t t g G G C C A A G C C T C G g g c g t c g C C G C C A A G A T G G C G T C G C T G T G G G C
mATP5E 721 - - - - - G G C C A A G C C A C G c g g c c a c C C T C C A A G A T G G C G T C G C C G T G G A C
rATP5E 644 - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
*****
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alignment position 1251..... 1261..... 1271..... 1281..... 1291.....
P927229 781 AAAGCGCTc a g g c g g g c g c g g c c t c g a c c t c g c g t g g g a g c g c g t c t g t g

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mATP5E 765 AAGGCTCTt c g c g g g g t c a t g g g g t c a g g g a c c c t a a a c a g a g g t g g c t g
rATP5E 644 -----
      *****
      *****

alignment position 1301 . . . . . 1311 . . . . . 1321 . . . . . 1331 . . . . . 1341 . . . . .
P927229 831 t c c t g c c t c g c t t c c c g a c g g t g c g -----
mATP5E 815 c t c c t c g g g a g a g g t a g c c t a c a g t a c c t g c a t g a t c G C T G T G A C G G C C A
rATP5E 644 ----- G C C C T G A A G A C C G
      *****

alignment position 1351 . . . . . 1361 . . . . . 1371 . . . . . 1381 . . . . . 1391 . . . . .
P927229 856 --- G C C C A G C A C C C a c -----
mATP5E 865 A G T G C A C A G C A C C C t t g a c c t g g c c a c g c t g a c a c t g a c c t t g c t c a c c t
rATP5E 657 A G T T C A A A G C g a a c g c t g a g a a g a c t t c g g g c a g c a g c a t -----
      *****

alignment position 1401 . . . . . 1411 . . . . . 1421 . . . . . 1431 . . . . . 1441 . . . . .
P927229 869 ----- A G A G T G C C C C T G G A C A C
mATP5E 915 g c g c a g a g g g a g g g g c g c a c a a g t t c a t t t t c a A G T G T G A C C T T A G T G A C
rATP5E 697 -----
      *****

alignment position 1451 . . . . . 1461 . . . . . 1471 . . . . . 1481 . . . . . 1491 . . . . .
P927229 886 C T T T g t g a a t g g c a g g t -----
mATP5E 965 C T T T t c c c a g t a g t g A A A A A A G G T G A A A G c c c t c t a a c c t -----
rATP5E 697 ----- A A A A A C A G T G A A A G t g a a g a a g c c t g a c t g a a g c c
      *****

alignment position 1501 . . . . . 1511 . . . . . 1521 . . . . . 1531 . . . . . 1541 . . . . .
P927229 903 -----
mATP5E 1005 --- G T G G A G C G C C C T G C A G G G C C C G T G A T G G g t g c g a g c t g t g g g c c
rATP5E 732 t g a a G T G C T G A G T C T T C A G G T G A A C C A T G T G G G c a c c t g t t c c g g c a g a
      *****

alignment position 1551 . . . . . 1561 . . . . . 1571 . . . . . 1581 . . . . . 1591 . . . . .
P927229 903 ----- T T C T C G A G A G A G A G C C A G C T C T T A T T T A
mATP5E 1051 t a g g a g t g g t g g t g c a t g g t t T C C T T G C T C C A G G G A G T G C A T C T T G T T A G
rATP5E 782 t g g a g a t c a g c c g t a c c --- T C C T G G A G A C A G A C G A C C C A T C T T G T T G A
      *****

alignment position 1601 . . . . . 1611 . . . . . 1621 . . . . . 1631 . . . . . 1641 . . . . .
P927229 932 G C A A a c c t t t t t c t t c t a g a a t g g t g c t g g a G C C A G G T G G T G A A A G T A G T
mATP5E 1101 T G T G C T G --- G g t g g a g g a a c a c c t t t c t
rATP5E 828 T G A A T T G --- G C C A T G T C A A T A A A T T A A C
      *****

alignment position 1651 . . . . . 1661 . . . . . 1671 . . . . . 1681 . . . . . 1691 . . . . .
P927229 982 A C A G T c a c a t c c a c c t c g g g a a a c a g g a g a -----
mATP5E 1127 g g g t a t c a -----
rATP5E 854 A C A G T t c a c t c t c g g c t g g a a a a a a c a a a c a a a a t t c a a a a c a t t g a a
      *****

alignment position 1701 . . . . . 1711 . . . . . 1721 . . . . . 1731 . . . . . 1741 . . . . .
P927229 1012 -----
mATP5E 1135 ----- G G C T G A A G G C
rATP5E 904 t g c c t g a g t a a a t g g g t t a a a t c t a t a a t a g g c t t c c a t G G C A G A A G G C

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alignment position 1751..... 1761..... 1771..... 1781..... 1791.....
P927229 1012 -----
mATP5E 1145 CCAGTgcccc gac-----
rATP5E 954 CCAGTagt t t c c t t a g a g g g a g c a t a a a t c a t c c a a c c a g a g t a a g t t g c
      *****

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alignment position 1801..... 1811..... 1821..... 1831..... 1841.....
P927229 1012 -----
mATP5E 1158 ----- AGAGTTCA AGCAAAGTTG t g t a g a a c a a
rATP5E 1004 a t g t t a g c c t c a t t a c a g a a t a A G G G T T C A T G G G A A G T A G g a c c t g c t a g
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alignment position 1851..... 1861..... 1871..... 1881..... 1891.....
P927229 1012 -----
mATP5E 1186 a a g g a c g g t a g g c t c a c a g t t g a t g c c t c t t a t t a a a c t a t c t c c c a t g g
rATP5E 1054 a g g c c t g -----

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alignment position 1901..... 1911..... 1921..... 1931..... 1941...
P927229 1012 -----
mATP5E 1236 c g t c c a t c a c c t t a t t t T C C T G C G C C C A g c c g c t t g a a g -----
rATP5E 1061 ----- T C C T G C T C C C A c t a t g t a g g c c a a a a c a a t
      ***

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## 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.

	mATP5E (1274 bp)	rATP5E (1090 bp)
P927229 (1011 bp)	0.958 <u>26 %</u>	0.343 16 %
mATP5E (1274 bp)		<u>1.000</u> 22 %

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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[Logout](#)      [Personal](#)      [Messages](#)      [GEMS-Logo](#)

[Genomatix](#) [Main](#) [GEMSEI](#) [Dorado](#) [Gene2Promoter](#) [BiblioSphere](#)  
[Frequently asked questions](#) [Your Results](#) [Your Sequences](#) [Your Protocol](#) [Help](#)

**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 24 16:57:02 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)  
**Selected groups**

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

(core/matrix sim):

## Aligned Sequences:

No.	Sequence Name	Sequence Description	Length
1	P978188	sym=ATP5F1 loc=Loc515 taxid=9606 spec=Homo sapiens chr=1  ctg=NT_019273 str=(+) start=8077683 end=8078683 len=1001  tss=501  comm=ATP synthase, H+ transporting, mitochondrial F0 complex, subunit b, isoform 1; (NM_001688/501/silver;)	1001 bp
2	P978189	sym=Atp5f1 loc=Loc11950 taxid=10090 spec=Mus musculus chr=3  ctg=NT_039239 str=(-) start=7786845 end=7787863 len=1019  tss=501,507,509,518,519  comm=ATP synthase, H+ transporting, mitochondrial F0 complex, subunit b, isoform 1; (AK011312/524/gold;AK002960/535/gold;AK019459/518/gold; AK081249/536/gold;NM_009725/526/bronze;)	1019 bp
3	P978190	sym=Atp5f1 loc=Loc171375 taxid=10116 spec=Rattus norvegicus  chr=2 ctg=NW_047627 str=(-) start=9451549 end=9452549  len=1001 tss=501  comm=ATP synthase, H+ transporting, mitochondrial F0 complex, subunit b, isoform 1; (NM_134365/536/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\$NFKB V\$RREB V\$AP2F V\$PLAG V\$SETSF V\$EBOX V\$SHIF V\$CHRE V\$ZBPF V\$MAZF V\$E2F V\$HAND  
V\$YYIF V\$GLIF

alignment position 1 . . . . . 1 1 . . . . . 2 1 . . . . . 3 1 . . . . . 4 1 . . . . .  
P978188 1 c a g g g t c a g g a t a a c a t g c a g g g c g g g g a t g g g c t g g g a g g g t c a g t c t c  
P978189 1 a g c a c C G - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -  
P978190 1 g a a g - C G - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -  
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alignment position 5 1 . . . . . 6 1 . . . . . 7 1 . . . . . 8 1 . . . . . 9 1 . . . . .  
P978188 51 c G G G G A G G G G C G C C C T G G G C C G G G G T A A G G G A G C T C C C A G G - C C C G G G A T  
P978189 8 - G G A G A G G G C A C C C G A G A C T G G G G G T A A A G G G G C T T C C A G G c C C C G G G A T  
P978190 7 - G G A G A G G G T A C C C G T C A C T G G G T A A A G G G G G A C T T C C A G G - C C C G G G A T  
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alignment position 1 0 1 . . . . . 1 1 1 . . . . . 1 2 1 . . . . . 1 3 1 . . . . . 1 4 1 . . . . .  
P978188 100 C T C G G C T C A C C G G A C C G G T A C C G C G C A G C C T C C A A C T G C C G T T C C A T G C A  
P978189 57 C T C G G C T C A C C A G A C C G G T A C C G T G C A G C C T C C A A T T G A C G T T C C A T G C A  
P978190 55 C T C G G C T C A C C A G A G C G G T A C C G T G C A G C T T C C A A C T G C C G T T C C A T G C A  
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alignment position 1 5 1 . . . . . 1 6 1 . . . . . 1 7 1 . . . . . 1 8 1 . . . . . 1 9 1 . . . . .  
P978188 150 G G C G G G C G C A T T T G G G G G A A G A T T C C A C T C C C G G G C C G C C G G G G G C A C T A  
P978189 107 T G C G G G C G C A T T G G G G G G C A G G T T C C A C T C G C G G G C C G C C G G G G G C A C G A  
P978190 105 G G C G G G C G C A T T G G G G G G C A G G T T C C A C T C G C G G G C C G C C G G G G G C A C G A  
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alignment position	2 0 1 . . . . .	2 1 1 . . . . .	2 2 1 . . . . .	2 3 1 . . . . .	2 4 1 . . . . .	
P978188	200	GGGGGGGTGG	GGTTTCCTTC	CGCATCT	CCA CGGTTCCAAC	TCCAACCTAC
P978189	157	GCGGAGGAGG	Ggt g TCCTTC	CGCATCT	CCA CGATTCCAAA	TCTAACCTAC
P978190	155	GCGGAGGTGG	GCTTTCCTTC	CGCATCT	CCA CGATTCCAAA	TCTAACCTAC
		*****	*****	*****	*****	*****
		*****	*****	*****	*****	*****
		*****	*****	*****	*****	*****
		*****	*****	*****	*****	*****
		*****	*****	*****	*****	*****
		*****	*****	*****	*****	*****
		*****	*****	*****	*****	*****
		*****	*****	*****	*****	*****
alignment position	2 5 1 . . . . .	2 6 1 . . . . .	2 7 1 . . . . .	2 8 1 . . . . .	2 9 1 . . . . .	
P978188	250	ACTCAAAGT	GACGCCGGCC	GGAGACTCCG	CTCCGGc a g c a	a ACCCCACC
P978189	207	ACCCAGACTC	GACGAGAGAC	CCTGACTCGG	CGCCGGAGGG	A Cc g CA CACC
P978190	205	ACCCAAACTA	GACGAGAt c c	t g a c t - - -	G CGCTGGAGGA	A CACCA CACC
		*****	*****	*****	*****	*****
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		*****				*****
alignment position	3 0 1 . . . . .	3 1 1 . . . . .	3 2 1 . . . . .	3 3 1 . . . . .	3 4 1 . . . . .	
P978188	300	TGGTGCACT	CTGAGCCTCC	GCCCCTCTCC	c g a g g g a a c c	g c a a CTCTAC
P978189	257	TGGTGTACT	CTGCGCAACC	GCCCCTCTCC	g a g GGAATTC	G - - - CTCTAC
P978190	251	TGGTGCACT	CTGCGCATCC	GCCCCTCTCC	a - - GGGATTC	G - - - CTCTAC
		*****	*****	*****	*****	*****
		*****	*****	*****	*****	*****
		*****	*****	*****	*****	*****
		*****	*****	*****	*****	*****
		*****	*****	*****	*****	*****
		*****	*****	*****	*****	*****
		*****	*****	*****	*****	*****
		*****	*****	*****	*****	*****
		*****	*****	*****	*****	*****
alignment position	3 5 1 . . . . .	3 6 1 . . . . .	3 7 1 . . . . .	3 8 1 . . . . .	3 9 1 . . . . .	
P978188	350	TTCTCGCGAG	AATTGCTTCT	ATGGCTCCAT	CCTGc - TTTC	CGGCTGt c g c
P978189	304	TTCTCGCGAG	AATTGTGTCT	ACCCTTCCAG	CCTGCTTTTC	CGTCTCCTGT
P978190	296	ATCTCGCGAG	AGTTGTGTCT	ACaCTTCCAG	CTCGCTTTTC	CGTCTGCTAI
		*****	*****	*****	*****	*****
		*****	*****	*****	*****	*****
		*****	*****	*****	*****	*****
		*****	*****	*****	*****	*****
		*****	*****	*****	*****	*****
		*****	*****	*****	*****	*****
		*****	*****	*****	*****	*****
		*****	*****	*****	*****	*****
		*****	*****	*****	*****	*****
		*****	*****	*****	*****	*****

```

alignment
position      4 0 1 . . . . . 4 1 1 . . . . . 4 2 1 . . . . . 4 3 1 . . . . . 4 4 1 . . . . .
P978188 399 c c t c a t g c g a t a g g c t c t c a g c g t t a c t t g a - - - - - - - - - - - - - - - - - - -
P978189 354 C C C C G C A G C G G G A - - - - - - - - - T T T T G T T T G T T T C C C T C C C t c a g c c
P978190 346 A C C C G C A A C G G G A t c t t c g g a c t t t T T T T T T T T T T T T C C C G C C C c - - - - -
      * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * *
      * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * *

```

```

alignment
position      4 5 1 . . . . . 4 6 1 . . . . . 4 7 1 . . . . . 4 8 1 . . . . . 4 9 1 . . . . .
P978188 430 - - - - - - - - - - - - - - - C T C T T C T C G C G A T A a t t t t t t t t a a a a t c t c c c
P978189 392 c c a c c c a t t t t T T C T C C T C T T C T C G C G A T A G T G G G g a g g g g g c G G G G A A A
P978190 391 - - - - - - - - - - - T T T T C C T C T T C T C G C G A T A G G G G a g - - - - - G G G G A A A
      * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * *
      * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * *
      * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * *

```

```

alignment
position      5 0 1 . . . . . 5 1 1 . . . . . 5 2 1 . . . . . 5 3 1 . . . . . 5 4 1 . . . . .
P978188 464 a a g g a a a g t t g a a g g a a g a g t a c a a a a t t t t c a - - - T C T C G C G A G A C T T
P978189 442 A A G C C G A G A A C T T C C G A G A A A A G C G A G C t G A T C T C T T C T C G C G A G A T G T
P978190 424 A A A A T C A G C A C T T C C G A G A G A A A G T G T G C a G A T C T C T T C T C G C G A G A T A T
      * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * *
      * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * *
      * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * *
      * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * *
      * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * *
      * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * *
      * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * *

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```

alignment
position      5 5 1 . . . . . 5 6 1 . . . . . 5 7 1 . . . . . 5 8 1 . . . . . 5 9 1 . . . . .
P978188 510 G T G A G C G G C C A T C T T G G T C C T G C C C t g a c a g a t t c t c c t a T C G G G G T C A C
P978189 492 G C G A G C G G C C A T C T T G C T C C T G C C C T G A C A G G C T C G G G - T C G G G G T C A C
P978190 474 G T G A G C G G C C A T C T T G T T C C T G C C C T G A G T G T C T C G G G - T C G G G G T C A C
      * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * *
      * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * *
      * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * *
      * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * *
      * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * *
      * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * *
      * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * *

```

```

alignment
position      6 0 1 . . . . . 6 1 1 . . . . . 6 2 1 . . . . . 6 3 1 . . . . . 6 4 1 . . . . .
P978188 560 A G G G A C g c t a a g a t t G C T A C C T G G A C T T T C G T T G A C C A T G C T G T C C C G G C
P978189 541 A G G G A C A c g g a g c C C G C T G T C C C G C T C T T C G C A G A C A A T G C T G T C C C G G C
P978190 523 A G G G A C A t c g g t a C C G C T G T C T G G A T C T T C G C A G A C A A T G C T G T C C C G G C
      * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * *
      * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * *
      * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * *
      * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * *
      * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * *
      * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * *
      * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * *

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```
alignment
position      6 5 1 . . . . . 6 6 1 . . . . . 6 7 1 . . . . . 6 8 1 . . . . . 6 9 1 . . . . .
P978188 610 TGGTACTTTC CGC CGC CGCC ACAGCGGGT A AGg g g t a TAG ACCCTGCTCT
P978189 591 TGGTGCTTTC T GCT G C C G C C ACAGCGGGT G AGAGACGTAG AGCCTAGGTT
P978190 573 TGGTACTTTC T G C C G C C G C C ACAGCGGGT A AGAGATGTAA ACCCGAAGCT
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```
alignment
position      7 0 1 . . . . . 7 1 1 . . . . . 7 2 1 . . . . . 7 3 1 . . . . . 7 4 1 . . . . .
P978188 660 G G A C T A T C A G A G T G A T T G G A A A G A A G C g a a t c t a g g g g t g a c a g g g a g g g
P978189 641 A G C G T A G C A G G G T G A C T A G G A A G A A G C - - - - -
P978190 623 G G C A T A T C A G G A T G A C T G G G A A G A A G C - - - - -
*****
*****
*****
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```
alignment
position      7 5 1 . . . . . 7 6 1 . . . . . 7 7 1 . . . . . 7 8 1 . . . . . 7 9 1 . . . . .
P978188 710 g a g a a g g g c g c a g c g a c a C G G G C C T G A G A G G C G A G T G G T C A G T G C A G T T C
P978189 668 - - - - - C A G G C C G G G G A G G C G G A A G C G G G T A G A G G A C
P978190 650 - - - - - T A G G T C A G G a g G C G G A A A G T G C G T A A A G A A
*****
*****
```

```
alignment
position      8 0 1 . . . . . 8 1 1 . . . . . 8 2 1 . . . . . 8 3 1 . . . . . 8 4 1 . . . . .
P978188 760 G G A a g g - - - - -
P978189 700 G G A C T G C G G C G T T T G G G C C c g a g c t c a c c c a c g g g a g c G A T C T G G A G A G C
P978190 682 G G A C T G C A G T G T T T G G G C C t - - - - - G A T C C G A A G A G T
*****
*****
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```
alignment
position      8 5 1 . . . . . 8 6 1 . . . . . 8 7 1 . . . . . 8 8 1 . . . . . 8 9 1 . . . . .
P978188 767 - - - - - A G C G T G G G G T C T T G A G G G A C G G G A A A G A G G G G T A C A T A G G C t
P978189 750 T C C C G G G C C G C C C A G C A T C T C A G G G C G C G G C A G A G A C G G A T G C C A G G G C C
P978190 714 T C C C T G A C A G T G T A G G A T T C G G A G G A C C T C T G A G A A G G A T G C A G G G G C C
*****
*****
```

```
alignment
position      9 0 1 . . . . . 9 1 1 . . . . . 9 2 1 . . . . . 9 3 1 . . . . . 9 4 1 . . . . .
P978188 809 - T A G T G A T A G A G C C T g g c g g g g g t a - A G G A A A G G G C A A A C C A G A T T T C a t
P978189 800 G a c a c c c g - - - - - - - - - - - - - - - - G G A A G G T A G A A A C G C G A T T T C T C
P978190 764 G T A G T G A T C G C G A C T c a c c g a g a c c g A G G A A G G T A G A A A A T G G A T T T C T C
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alignment
position  9 5 1 . . . . . 9 6 1 . . . . . 9 7 1 . . . . . 9 8 1 . . . . . 9 9 1 . . . . .
P978188 857 - TTGACTTTG CTGACCTTCG CCTTGTCTAT CTGCAGCCCC c t c TCTGAAC
P978189 831 CTGACTTTG CTAACCTTCG TCTTGTGTAT TTCAGCCCC GTGTCTGAAC
P978190 814 CTGACTTTG CTAACCTACG TCTTGTGTGT TTGCAGCCCC GTGTCTGAAC
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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 . . . . .
P978188 906 AATGCAGCCT TCCTAGGTCC AGGGTAAGTG T g a g g a t a a t g c t c c c t t t c
P978189 881 AACGC GGCCG CCCTAGGTCC AGGGTGAGTG T - - - - - - - - - - - - - - -
P978190 864 AACGC GGCCG TCCTGGGTCC AGGGTAAGTG T - - - - - - - - - - - - - - -
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* * * * *

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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 . . . . .
P978188 956 g t c t t t g t t t t CACTACCTT TTATTtccc g a t t c c t g c c c c a c c c - - - -
P978189 912 - - - - - - - - - CACCACGTC TTATTCTCTT t c CATTTCCT AGCGTCAAGC
P978190 895 - - - - - - - - - CACCACATT TTATTCTCTT a a CATTTCCT ACCGTTAAGC
* * * * *
* * * * *
* * * * *

```

```

alignment
position  1 1 0 1 . . . . . 1 1 1 1 . . . . . 1 1 2 1 . . . . . 1 1 3 1 . . . . . 1 1 4 1 . . . . .
P978188 1002 - - - - - - - - - - - - - - - - - - - - - - - - -
P978189 951 CAAAATTGC TGT TTT CCTT CA c g TTAGCC AGCTTGCATA CTCATT CGG A
P978190 934 CAGAAATTAC TGT TTT CCTT CA c t TTAGCA AGCTTACATC CCCATT CAG A
* * * * *
* * * * *
* * * * *

```

```

alignment
position  1 1 5 1 . . . . . 1 1 6 1 . . . . .
P978188 1002 - - - - - - - - - - - - - - - -
P978189 1001 CGTTT GTTCT TCT Aa t t g c
P978190 984 CATTC GTTCT TCT Ac t t g -
* * * * *
* * * * *

```

## 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>P978189</b> (1019 bp)	<b>P978190</b> (1001 bp)
<b>P978188</b> (1001 bp)	0.500 50 %	0.557 53 %
<b>P978189</b> (1019 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	
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



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**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 24 17:43:43 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)  
**Selected groups** (core/matrix sim):

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

## Aligned Sequences:

No.	Sequence Name	Sequence Description	Length
1	P879005	sym=ATP5G1 loc=Loc516 taxid=9606 spec=Homo sapiens chr=17 ctg=NT_010783 str=(+) start=5622841 end=5623941 len=1101 tss=601 comm=ATP synthase, H+ transporting, mitochondrial F0 complex, subunit c (subunit 9), isoform 1; (NM_005175/501/bronze;)	1101 bp
2	P879006	sym=Atp5g1 loc=Loc11951 taxid=10090 spec=Mus musculus chr=11 ctg=NT_039521 str=(-) start=7475581 end=7476681 len=1101 tss=601 comm=ATP synthase, H+ transporting, mitochondrial F0 complex, subunit c (subunit 9), isoform 1; (NM_007506/562/bronze;)	1101 bp
3	P879007	sym=Atp5g1 loc=Loc29754 taxid=10116 spec=Rattus norvegicus chr=10 ctg=NW_047338 str=(-) start=167149 end=168249 len=1101 tss=601 comm=ATP synthase, H+ transporting, mitochondrial F0 complex, subunit c, isoform 1; (NM_017311/565/bronze;)	1101 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\$SOCT1 V\$SAPIR V\$SEGRF V\$SSF1F V\$YY1F V\$SECAT V\$PAX6 V\$NFKB V\$SETSF V\$PCAT  
V\$EBOX V\$H1FF V\$OAZF V\$INSM V\$ZF5F V\$HNF4 V\$BARB V\$RXRF V\$EREF V\$MYOD V\$AREB V\$RREB  
V\$CLOX V\$GATA V\$ATBF V\$CART V\$PDX1 V\$FAST V\$LHXF V\$HOME V\$RBIT V\$HNF1 V\$NKXH V\$IKRS  
V\$IRFF V\$TEAF V\$CEBP V\$RORA V\$HOXF

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

**P879005** 1 t c c a t g a c t g c t g a a c a c c g g c t g a g g t c c a c a a a a c t g c g c t c a c c g c t

**P879006** 1 - - - - -

**P879007** 1 - - - - -

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

**P879005** 51 t g g g a c t t t c CAGCCGGCC TT t a c t c t c c a t - - GGAAAG CGGTCTTTCC

**P879006** 1 - - - - - CAGCCTGCC TT AACTATTG GACGAAAATG GGGg - TTTTT

**P879007** 1 - - - - - CTGCC TT AATTCTTG GTCAGAAACG GGGATTTTTT

\* \* \* \* \*

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

**P879005** 99 AC AAACCTCC ACGGTGGGAA TT ACTGCAAA GGCATCGGCT CTCCCGGCC T

**P879006** 39 AC AAATCACG ATGGTGGGAA GT ACTGTAAA GGC GTCGGCT CTCTTGCC A

**P879007** 36 AC AAATCACT ATGGTGGGAA GT ACTGTAAA GGC GTCGGCT CTCCCTGCC A

\* \* \* \* \*

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

**P879005** 149 AGAA t - - - A TCTCGCGGGA TCTCAGCTGT CCTTGGGCC c c c c c c t c a g

**P879006** 89 GGAAGCAACA TCTCGCGGGA TGTCGGTGGT CCTTGAGTCC TTGGACAGG-

**P879007** 86 AGAAGCAACG TCTCGCGGGA TGTCGGTGGT CCTTAAGTCC TCGGACGGG-

\* \* \* \* \*

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

**P879005** 195 c g c a ACTAC **C AATCCCAACA** **TGCAACGCGC** **CC**GTGGGCC AAGCGCCGA

**P879006** 138 - - - ACTAC **A AGCCCAACA** **TGCAATGCGC** **CC**CAAGGTCC AAGCGCCGA

**P879007** 135 - - - ACTAC **A AAGCCCAATA** **TGCAATGCGC** **TC**CAAGGTCC AAGCGCCGA

\* \* \* \* \*

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* * * * *
alignment
position 2 5 1 . . . . . 2 6 1 . . . . . 2 7 1 . . . . . 2 8 1 . . . . . 2 9 1 . . . . .
P879005 245 ATGAAGGCTC GGGGCCAAAG TCATGTGTCT GACTGCGTCA CACGTCCGT
P879006 184 ATGAAGGCCT GGAGCCCTTA TCACGTGTCA GCTTGCCTCA AGCGGCCGT
P879007 181 ATGAAGACTC GGAGCCACG TTACGTGTCC GCCTGCGTCA AGCGGGCGG
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alignment
position 3 0 1 . . . . . 3 1 1 . . . . . 3 2 1 . . . . . 3 3 1 . . . . . 3 4 1 . . . . .
P879005 295 CATCTCTCCC ACGCCTTT TTCTTCAGCGTA CACCTTGGTC GCCATCTTGT
P879006 234 TGCACTCCC ACGCTTTT TTCTTCGCTTG CACCTTGGTC GCCATTTTGT
P879007 231 aGCACTCCC ACGCTTTT TTCTTCGCTTG CACCTTGGTC GCCATTTTGT
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```

alignment
position 3 5 1 . . . . . 3 6 1 . . . . . 3 7 1 . . . . . 3 8 1 . . . . . 3 9 1 . . . . .
P879005 345 Gcgcg AGGTT ATGGAACCTC TGAGTCCCGC CAACTCTATG GTCGAGCGT
P879006 284 GTTGA AGGTT GTAGAACCTC TGAGTCTCGT CCACTCTATG GTCAAGCAT
P879007 281 GTTGA AGGCT GTAGAACCTC TGAGTCTCGT CCACTCTATG GTCAAGCAT
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alignment
position 4 0 1 . . . . . 4 1 1 . . . . . 4 2 1 . . . . . 4 3 1 . . . . . 4 4 1 . . . . .
P879005 395 TCAGGGA TCG GCCAATCGTA ATCCAGATCT CGTAGGAAAG CCCC GCCTCT
P879006 334 TCGGAT TCG ACCAATCGTA ACCCGAACT CGGAAAAGA ACCCGCCTT
P879007 331 TCGGAT TCG ACCAATCGTA ATCACGATCT CGGAAAAGA CCCC GCCTT
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```

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

```

**P879005** 445 AT **CCGCATGG** **AGGCGGGAAT** **TGCCACG**AAG CTCCTGTGGA **GGGAGA**GGAA  
**P879006** 384 AT **CCGCAAGG** **AGGCGGGAAT** **TGCCACG**AAG CTCCTGTGGA **GAGAGA**GGAA  
**P879007** 381 AT **CCGCAAGG** **AGGCGGGAAT** **TGCCACG**AAG CTCCTGTGGA **GAGAGA**GGAA

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alignment position 5 0 1 . . . . . 5 1 1 . . . . . 5 2 1 . . . . . 5 3 1 . . . . . 5 4 1 . . . . .

**P879005** 495 **GCAGCTG**CGG **AAAGCCAATA** **AGAg t g g g a** **a t c - GATGAC** **GTCAACCAAT**  
**P879006** 434 **GAAGCTG**AAG **AAGACCAATA** **AGAA G**GATGG **AGTTGATGAC** **GCCAGCCAAT**  
**P879007** 431 **GAACCTG**AAA **AAGACCAATA** **AGAAA**GATGA **AGTTGATGAC** **GCCAGCCAAT**

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

**P879005** 544 **GGGGA**CGCGG GGATATT **ACG** **GCCAATGAGA** **AT**GGAGa a g g t c **c a g g**ACA  
**P879006** 484 **TGGAA**CGTGG AGAGATA **ACG** **ACCAATGGGA** **GT**Ga AGGGAC T **CCGA-**ACA  
**P879007** 481 **TGGAA**CGTGA GGAGATA **ACG** **GCCAATGGGA** **GT**GGAGGGAC C **CCGA-**ACA

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alignment position 6 0 1 . . . . . 6 1 1 . . . . . 6 2 1 . . . . . 6 3 1 . . . . . 6 4 1 . . . . .

**P879005** 594 **GTGGGTGGGG** **GAa** **GCTGAGC** **GCTGA**GACCA **AGGGCTAAAG** **CTGGGAGGT**  
**P879006** 533 **GTGGGTGGGG** **GA-** **GCTGAGC** **GCTCA**GACCA **AGGGCTAAAG** **CTGGGAGGT**  
**P879007** 530 **GTGGGTGGGG** **GA-** **GCTGAGC** **GCTGA**GACCA **AGGGCTAAAG** **CTGCGAGGT**

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

**P879005** 644 **AGTc t** **GT CAC** **CTTGAGCC**GG GCGAGCGCTG TGGG **CCAAGC** **AGGGGt** TGCA  
**P879006** 582 **AGTCA** **GT CAC** **CTTGAGCA**GG GAGTGTGCTG TGGG **CCGAGC** **AGGGGCT** TGCA

**P879007** 579 **AGTCA** **GT CAC** **CTT GAG CA GG** GAGTGTGCTG TGGG **CCGAGC** **AGGGGCTGCA**  
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alignment position 701 . . . . . 711 . . . . . 721 . . . . . 731 . . . . . 741 . . . . .

**P879005** 694 **GGGTAGT** AGG **AGTGCAGGTG** **ACTTGGGG** CC GGGAGc c a g c a a t a g g c a g C  
**P879006** 632 **GGGGAGT** GGG **AGTGCAGGTG** **ACTTGGGG** CT GGGAGACAGG Gg TCCGCAAC  
**P879007** 629 **GGGGAGT** GGG **AGTGCAGGTG** **ACTTGGGG** CC CGGAGACAGG G- TCCGCTAC  
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alignment position 751 . . . . . 761 . . . . . 771 . . . . . 781 . . . . . 791 . . . . .

**P879005** 744 GT TGT GGGCT GGGCAGTGTG GAGGGGT ATT TCCCC CAGt g c t g g g a g a g  
**P879006** 682 GC CGT GGGTT GTGCCACGTG GAGC ACC ATT TGCCTCCAGG GATAGGGAA C  
**P879007** 678 GC CGT GGGCT GTGCCATGTG GAGC AGC ATT TGCCTCCAGG GATAGGGAA C  
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alignment position 801 . . . . . 811 . . . . . 821 . . . . . 831 . . . . . 841 . . . . .

**P879005** 794 g c t a t g g c a a t c t a g a t a t g **GCCTTATCAA** **TGAATGTTAA** **TTACCAACGC**  
**P879006** 732 GAGGACT Ag A GTCTTTA **A - -** **GCCTTATCAA** **TTAATGTTAA** **TTACCAACGC**  
**P879007** 728 GAGGACT Aa A GTCTTTA **A - -** **GCCTTATCAA** **TTAATGTTAA** **TTACCAACGC**  
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alignment position 851 . . . . . 861 . . . . . 871 . . . . . 881 . . . . . 891 . . . . .

**P879005** 844 **TAATGAA CGA** t t g a c t g c c t CGGCTGGGGC GGGTc GGG **GA** **CTGCTGTGTA**  
**P879006** 780 **TAATGAG CGA** TAAACGG- - - CCGCTGGGGA GAGTAGGG **GA** **CAGCAGTGTA**

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P879007 776 TAATGAGCGA TAAACGG- - - CCGCTGGGGA GAGTAGGGGA CAGCTATGTA
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alignment position 9 0 1 . . . . . 9 1 1 . . . . . 9 2 1 . . . . . 9 3 1 . . . . . 9 4 1 . . . . .

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P879005 894 AGATGGGCAG GATCCTGCGC GACa c c t g c C CAGTATCCGC CTCC AGTCTT
P879006 827 ACTTGGGCAG GATCCTGCAC GACGTCTG- C CAGTTTCTGC CTCC GGTCTT
P879007 823 ACATGGGCAG GATCCTGCAC GACGTCTG- C CAGTTTCTGC CTCC AGTCTT
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alignment position 9 5 1 . . . . . 9 6 1 . . . . . 9 7 1 . . . . . 9 8 1 . . . . . 9 9 1 . . . . .

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P879005 944 CCCGAGAGAC CATTCCCTTT CGCAACATTT CCTTCCTGGG GCTTGGGCa c
P879006 876 CCCGGGAGAC CATTCCCTTT CGCAACATTT CCCTCTTGGG GCCTGAGCC A
P879007 872 CCCGGGAGAT CATTCCCTTT CGCAACGTTT CCCTCTTGGG GCCTGAGCC A
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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 . . . . .

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P879005 994 a t TTCCTTGA CTTCCGATCT CCATGACTTT GCTTt g a a g a c c c a - - - - -
P879006 926 CCTCCTTTTA TTTCCGATCT CGGTTGCTGT CCTTCTGCAG ACCCGCTGCC
P879007 922 CCTCCTTTTA CTTCCGTTCT TGATTGCTGT CCTTCTGCAG ACCCGCTGCC
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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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P879005 1038 - - - - - CTGCTCT GTCCCTCTGA CCTCTAATGC
P879006 976 CAGAg AGTGG TTGACCCCGG AATCTGCTCT GTCCTTCTGA CCTCTAATGC
P879007 972 CAGAa AGTGG TTGACCCCGG AATCTGCTCT GTCCTTCTGA CCTCTAATGC
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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 . . . . .
P879005 1065 CCTCC TC AGC T GG g g c a c g g t g c a AGGAA G AGCGT g g - - - - -
P879006 1026 CCTCC TT AGC T GG GGT AT - - - - - AGGAA G AGGGT T GGGG G - GA AC GAT T
P879007 1022 CCTCC TT AGT T GG AGT AT - - - - - AGGAA G AGGGT T GGGG G a GA AC GAT T
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alignment
position    1 1 5 1 . . . . . 1 1 6 1 . . . . . 1 1 7 1 . . . . . 1 1 8 1 . .
P879005 1102 - - - - -
P879006 1069 GGAGGTGGAT GGGGACAA CA GGAGGTTGCC AGt - - -
P879007 1066 GGAGGTGGAT GGGAACGACA GGAGGTTGCC AGt a t c
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## 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>P879006</b> (1101 bp)	<b>P879007</b> (1101 bp)
<b>P879005</b> (1101 bp)	0.443 64 %	<u>0.442</u> <u>62 %</u>
<b>P879006</b> (1101 bp)		<u>1.000</u> <u>92 %</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"/>
<input type="button" value="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



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**GEMS Launcher Task: *DiAlign TF*: Multiple alignment plus TF sites  
working on C5-ATP5G1-HMRC (4 seq.)**

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

DiAlign professional TF Release 3.1 December 2004

Mon May 30 23:24:49 2005

## Solution parameters:

**Sequence file:** [C5-ATP5G1-HMRC](#) (4 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 4 (100.0 %) sequences)  
**Family matches:** yes  
**MatInspector library:** Matrix Family Library Version 5.0 (February 2005)  
**Selected groups**

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

(core/matrix sim):

## Aligned Sequences:

No.	Sequence Name	Sequence Description	Length
1	P879005	P879005 sym=ATP5G1 loc=Loc516 taxid=9606 spec=Homo sapiens chr=17 ctg=NT_010783 str=(+) start=5622641 end=5623941 len=1301 tss=801 comm=ATP synthase, H+ transporting, mitochondrial F0 complex, subunit c (subunit 9), isoform 1; (NM_005175/501/bronze;)	1301 bp
2	P879006	P879006 sym=Atp5g1 loc=Loc11951 taxid=10090 spec=Mus musculus chr=11 ctg=NT_039521 str=(-) start=7475581 end=7476881 len=1301 tss=801 comm=ATP synthase, H+ transporting, mitochondrial F0 complex, subunit c (subunit 9), isoform 1; (NM_007506/562/bronze;)	1301 bp
3	P879007	P879007 sym=Atp5g1 loc=Loc29754 taxid=10116 spec=Rattus norvegicus chr=10 ctg=NW_047338 str=(-) start=167149 end=168449 len=1301 tss=801 comm=ATP synthase, H+ transporting, mitochondrial F0 complex, subunit c, isoform 1; (NM_017311/565/bronze;)	1301 bp
4	cATP5G1	cATP5G1 canFam1_dna range=chr9:17785192-17786691 5'pad=0 3'pad=0 revComp=FALSE strand=? repeatMasking=none	1500 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\$SEGRF	V\$SFI1	V\$YYIF	V\$FCAT	V\$PAX6	V\$NFKB	V\$SETSF	V\$PCAT	V\$EBOX	V\$SHIF	V\$OAZF
	V\$EKL1	V\$BARB	V\$RXRF	V\$USERF	V\$MYOD	V\$AREB	V\$RREB	V\$CLOX	V\$ATBF	V\$CART	V\$FAST	V\$LHXF
	V\$HOMF	V\$RBIT	V\$HNF1	V\$NKXH	V\$PDX1	V\$IKRS	V\$TEAF	V\$RORA	V\$HOXF			

  

alignment position	1	1	2	3	4
<b>P879005</b>	1	t t a c a g g c a c	g c g c c a c c a -	- - - - -	- - - - - C C A T G C C C G G C
<b>P879006</b>	1	a - - - - -	- - - - -	- - - - -	- - - - - G A A G C - - -
<b>P879007</b>	1	a c a a t t g t c t	g g a c c t a c g t	t g g c t t t t t g	a c c t a a a c t c a t G A A A C - - -
<b>cATP5G1</b>	1	t t c t t t a a t t	t c t a t t t t t c	t t t a g c g g a c	t g c c t a t t c C T A T C C T T T G C
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alignment position	5	6	7	8	9
<b>P879005</b>	31	T A A T T T T T G T	A T t c t t a g t a	g a g a c g g g g t	t t c a c c a t g c t g g T C A G G C T
<b>P879006</b>	7	- - - - -	- - - - -	- - - - -	- - - - - T T A G T C T
<b>P879007</b>	48	- - - - -	- - - - -	- - - - -	- - - - - T T A G T C T
<b>cATP5G1</b>	51	T C G T T T T T C T	A T a g g a g t - -	- - - - -	- - - - -
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alignment position	10	11	12	13	14
<b>P879005</b>	81	G A T C T C G A A C	T C C T G A C C T C	A G G T G A T C - -	- - - C G C C C G C c t c g g c c t c c
<b>P879006</b>	14	G G C C T T G A A C	T C C T G A C T T T	C C T G T C T C c t	a a g C A C C T G C C - - - - -
<b>P879007</b>	55	G G C T T T G A A C	T C C T G A C C T T	C C G G T C T C - -	- - - C A C C T G C C - - - - -
<b>cATP5G1</b>	69	- - - - -	- - - - -	- - - - -	- - - - -
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alignment position	15	16	17	18	19
<b>P879005</b>	126	c a A A G T G C T G	G G A T T A C A G G	C G T G A G C C A C	T G C A C C C G G C c c a a c a a a t g
<b>P879006</b>	55	- - A A G T G C T A	A A A T T T C G G G	T A C G A A a T A G	C A A G C C T G G T T T T A A T T G T A
<b>P879007</b>	91	- - A A G T A C T A	A G A T T T C A G G	T A T G A A C T A G	C A A G C C T G G C T T T A A T T G T g
<b>cATP5G1</b>	69	- - - - -	- - - - -	- - - - -	- - - - - A T T A T T
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alignment position	20	21	22	23	24
<b>P879005</b>	176	t t t t a g a a a g	c c - - - - -	- - - - -	- - - - - A T C T G G A T G A
<b>P879006</b>	103	T T T T G T T G A G	T T T T T T T T T T	C C A C C A T T C A	A C T - - - - - T G T
<b>P879007</b>	139	- - - - -	- - T T G T T G T T	T C A A C A T T C A	A T T - - - - - T G T
<b>cATP5G1</b>	75	T T A C C C T T A G	T T G G T T T T T T	T T A C A A T A A A	A a a a a a a a a A T C T G G C T G C
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alignment position	25	26	27	28	29
<b>P879005</b>	198	T A G T C C A T G A	C T G C T G A A C A	C C G G C T G A G G	t c c a c a a a a c t g C G C T C A C C
<b>P879006</b>	139	G A G T C C A T G T	T G A C T G A C T A	C T G A C A G A c c	c a C A A G A G C A - - C G C T C A C T
<b>P879007</b>	163	G A G T - - - - -	- - - - -	- - - - -	- - C A A G A G C A - - C G C T C A C T

<b>cATP5G1</b>	125	TAGTCCAGGG	CTGCTGAGCT	CTGCCCGAGG	c c a a c a a g g c	g c t c g t c c a c
		*****	*****	*****	*****	*****
alignment position		3 0 1 . . . . .	3 1 1 . . . . .	3 2 1 . . . . .	3 3 1 . . . . .	3 4 1 . . . . .
<b>P879005</b>	248	- - - - - GCTT	GGGGACTTTC	CAGCCGGCCT	TTACTCTCCA	t - - GGAAAGC
<b>P879006</b>	187	- - - - - ACTT	AGAAGTTTTC	CAGCCTGCCT	TAATACTTGG	ACGAAAATGC
<b>P879007</b>	183	- - - - - ACTT	AGAAAATTTTC	CAACCTGCCT	TAATTCTTGG	TCAGAAACGC
<b>cATP5G1</b>	175	t a g c g a	ACTT TCCAGGCCAG	CAGCCGGCCT	TTATTCTCCA	a g g c g g a a g c
		*****	*****	*****	*****	*****
alignment position		3 5 1 . . . . .	3 6 1 . . . . .	3 7 1 . . . . .	3 8 1 . . . . .	3 9 1 . . . . .
<b>P879005</b>	290	G- GTCTTTCC	ACAAACCTCC	ACGGTGGGAA	TTACTGC AAA	GGCATCGGCT
<b>P879006</b>	231	G- GG- TTTT	ACAAATCACG	ATGGTGGAAAG	GTACTGT AAA	GGCGTCGGCT
<b>P879007</b>	227	G- GATTTT	ACAAATCACT	ATGGTGGAAAT	GTACTGT AAA	GGCGTCGGCT
<b>cATP5G1</b>	225	a a GG- GTTCC	ACGAATCAGG	Ag a g c g c GAA	TTGCTGC AAA	GGCGTTGGCT
		*****	*****	*****	*****	*****
alignment position		4 0 1 . . . . .	4 1 1 . . . . .	4 2 1 . . . . .	4 3 1 . . . . .	4 4 1 . . . . .
<b>P879005</b>	339	CTCCCGGCCT	A- - - - GAA-	- - - TATCTCG	CGGGATCTCA	GCTGTCCTTC
<b>P879006</b>	279	CTCCTTGCCA	G- - - - GAAG	CAACATCTCG	CGGGATGTCG	GTGGTCCTTC
<b>P879007</b>	276	CTCCCTGCCA	A- - - - GAAG	CAACGTCTCG	CGGGATGTCG	GTGGTCCTTA
<b>cATP5G1</b>	274	CTCCCGGCCT	c a g g a g GAA-	- - - CGTCTCG	CGGGATCTCA	GCCCTCCTTC
		*****	*****	*****	*****	*****
alignment position		4 5 1 . . . . .	4 6 1 . . . . .	4 7 1 . . . . .	4 8 1 . . . . .	4 9 1 . . . . .
<b>P879005</b>	380	GGCC C c c c c	c t c a g c g CAA	CTAC CAATCC	CAACATGCAA	CGCGCCC CGT
<b>P879006</b>	324	AGTCCTTGGA	CA- - - - GGA	CTAC AAAGCC	CAACATGCAA	TGCGCCC CA
<b>P879007</b>	321	AGTCCTCGGA	CG- - - - GGA	CTAC AAAGCC	CAATATGCAA	TGCGCTC CA
<b>cATP5G1</b>	320	GGGCCTCTGA	CC- - - - CGA	CTAC AAATCC	CGTCATCAA	CGTGCCT GA
		*****	*****	*****	*****	*****
alignment position		5 0 1 . . . . .	5 1 1 . . . . .	5 2 1 . . . . .	5 3 1 . . . . .	5 4 1 . . . . .
<b>P879005</b>	430	GGCCCAAGCG	CCCGAATGAA	GGCTCGGGGC	CAAAGTCATG	TGTCTGACTC
<b>P879006</b>	369	GGTCCAAGCG	GCCGAATGAA	GGCCTGGAGC	CCTTATCACG	TGT CAGCTTC
<b>P879007</b>	366	GGTCCAAGCG	GCCGAATGAA	GACTCGGAGC	CCACGTTACG	TGTCCGCCTC
<b>cATP5G1</b>	365	GGCCCAAGCG	CCCGAATGAA	GGCGCAGGTC	CAAGGTCATG	TGTCTGTCTC

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

**P879005** 480 CGTCACACGT CCCG**TCATCT** **CTCCACGCC** **TTT**TT - - - - -  
**P879006** 419 CGTCAAGCGG CCGG**TGTCA** **CTCCACGCT** **TTT**TT - - - - -  
**P879007** 416 CGTCAAGCGG GCGG**TAGTCA** **CTCCACGCT** **TTT**TT - - - - -  
**cATP5G1** 415 CGTAAGGCGT CCGG**TCATCT** **CTCCACGCC** **TTT**TT t t t t t t t t t t t t t t

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alignment position 6 0 1 . . . . . 6 1 1 . . . . . 6 2 1 . . . . . 6 3 1 . . . . . 6 4 1 . . . . .

**P879005** 515 - - CTTCAGCG **TACACCTTGG** **TCGCCATCTT** **GTGCGGAGG** TTATGGAACC  
**P879006** 454 - - CTTCAGCG **TGCACCTTGG** **TCGCCATTTT** **GTGTTGAAGG** TTGTAGAACC  
**P879007** 451 - - CTTCAGCG **TGCACCTTGG** **TCGCCATTTT** **GTGTTGAAGG** CTGTAGAACC  
**cATP5G1** 465 t t CTGCAGCT **TCCACCTTGG** **CCGCCATTTT** **GTGCGGAGG** TTCTGGAACC

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

**P879005** 563 TCTGAGTCCC GCCAACTCTA TGGT**CGAGCG** TTTCAGGGAT**CGGCCAATCC**  
**P879006** 502 TCTGAGTCTC GTCGACTCTA TGGT**CAAGCA** TTTCGGGAT**CGACCAATCC**  
**P879007** 499 TCTGAGTCTC GTCGACTCTA TGGT**CAAGCA** TTTCGGGAT**CGACCAATCC**  
**cATP5G1** 515 TCTGAGCCC GCCGACTCTA TGGT**TGAGCA** TTTCAGGGAT**CGACCAATCC**

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alignment position 7 0 1 . . . . . 7 1 1 . . . . . 7 2 1 . . . . . 7 3 1 . . . . . 7 4 1 . . . . .

**P879005** 613 **TAAT**CCAGAT CTCGTAGGAA AGCCCGCCT CTAT**CCGCAT** **GGAGGCGGGA**  
**P879006** 552 **TAAC**CCCGAA CTCGGAAAAA GAACCCGCCT TTAT**CCGCAA** **GGAGGCGGGA**  
**P879007** 549 **TAAT**CACGAT CTCGGAAAAA GACCCGCCT TTAT**CCGCAA** **GGAGGCGGGA**

**cATP5G1** 565 **GAAGCCAGAT** GTCGGAGGAA AACCCCGCCT TCGC**CCGCAG** **GGAAGCGGGA**  
 \* \* \* \* \*  
 \* \* \* \* \*  
 \* \* \* \* \*  
 \* \* \* \* \*  
 \* \* \* \* \*  
 \* \* \* \* \*

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

**P879005** 663 **ATTGCCACG**A AGCTCCTGTG GA**GGGAGAGG** **AAGCAGCTGC** GGA**AAAGCCA**  
**P879006** 602 **ATTGCCACG**A AGCTCCTGTG GA**GAGAGAGG** **AAGAAGCTGA** AGA**AAAGCCA**  
**P879007** 599 **ATTGCCACG**A AGCTCCCGTG GA**GAGAGAGG** **AAGAAGCTGA** AA**AAAGCCA**  
**cATP5G1** 615 **ACTGCCACG**A AGCTCCTGTG GA**GAGAGAGG** **AAGAAGCTGC** CG**AAAGCCA**  
 \* \* \* \* \*  
 \* \* \* \* \*  
 \* \* \* \* \*  
 \* \* \* \* \*  
 \* \* \* \* \*  
 \* \* \* \* \*

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

**P879005** 713 **TAA**GAg t g g - GGAATCGATG ACG**TCAACCA** **ATGGGGAC**GC GGGGATATTA  
**P879006** 652 **TAA**GAAGGAT GGAGTTGATG ACG**CCAGCCA** **ATTGGAA**CGT GGAGAGATAA  
**P879007** 649 **TAA**GAAAAGAT GAAGTTGATG ACG**CCAGCCA** **ATTGGAA**CGT GAGGAGATAA  
**cATP5G1** 665 **TAA**GAAAAGGA GGACTTGAGG ACG**TTAACCA** **ATGAGGAT**GC GGGAGGATTC  
 \* \* \* \* \*  
 \* \* \* \* \*  
 \* \* \* \* \*  
 \* \* \* \* \*

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

**P879005** 762 **CGGCCAATGA** **GAAT**GGAGAA GGTC**CAGGAC** **ACGTGGGT- G** **GGGg a A**GCCTC  
**P879006** 702 **CGACCAATGG** **GAGT**GAAGGG ACT**CCGA- AC** **ACGTGGGTGG** **GGG- - A**GCCTC  
**P879007** 699 **CGGCCAATGG** **GAGT**GGAGGG ACC**CCGA- AC** **ACGTGGGTGG** **GGG- - A**GCCTC  
**cATP5G1** 715 **CAGCCAATGA** **GAGT**GGGGGG ATCC**CGGGAC** **ACGTGGGT- G** **GGG- - A**GCCTC  
 \* \* \* \* \*  
 \* \* \* \* \*  
 \* \* \* \* \*  
 \* \* \* \* \*

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

**P879005** 811 AGCGCTGAGA CCAAG**GGCTA** **AAGCTGGGAG** GT**GAGTCTGT** **CACCTTGAGC**  
**P879006** 749 AGCGCTCAGA CCAAG**GGCTA** **AAGCTGGGAG** GT**GAGTCA**GT **CACCTTGAGC**

**P879007** 746 AGCGCTGAGA CCAAGGGCTA AAGCTGCGAG GTGAGTCAGT CACCTTGAGC  
**cATP5G1** 762 AGCGCTGAGA CCTAGAGCTA AAGcGGGAG GTGAGTCAGT CACCTTGAGC  
 \* \* \* \* \*  
 \* \* \* \* \*  
 \* \* \* \* \*  
 \* \* \* \* \*  
 \* \* \* \* \*  
 \* \* \* \* \*  
 \* \* \* \* \*  
 \* \* \* \* \*

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

**P879005** 861 CGGGCGAGCG CTGTGGGCCA AGCAGGGGT T GCAGGGT AGT AGGAGTGCAC  
**P879006** 799 AGGGAGTGTG CTGTGGGCCG AGCAGGGGCT GCAGGGGAGT GGGAGTGCAC  
**P879007** 796 AGGGAGTGTG CTGTGGGCCG AGCAGGGGCT GCAGGGGAGT GGGAGTGCAC  
**cATP5G1** 812 CGGGCAAGCG CCGTGgtcgg attAGGGGCC GCGGGGCTGT GGGAGTGCAC  
 \* \* \* \* \*  
 \* \* \* \* \*  
 \* \* \* \* \*  
 \* \* \* \* \*  
 \* \* \* \* \*  
 \* \* \* \* \*

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

**P879005** 911 GTGACTTGGG GCCGGGAGCC AGCAATAGGC AGGGT TGTGG GCTGGGCAGT  
**P879006** 849 GTGACTTGGG GCTGGGAGAC AGGGGTCCGC AAGGCCGTGG GTTGTGCCAC  
**P879007** 846 GTGACTTGGG GCCCGGAGAC AGGG- TCCGC TAGGCCGTGG GCTGTGCCAT  
**cATP5G1** 862 GTGACTTGGG GCCGGAAGCC AGCGATCGGC AGGGGTGTGG GCTGGGCCGT  
 \* \* \* \* \*  
 \* \* \* \* \*  
 \* \* \* \* \*  
 \* \* \* \* \*  
 \* \* \* \* \*

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

**P879005** 961 GTGGAGGGGT ATTTCCCCC AGTGCTGGGA GAGGCt atgg caatctagaT  
**P879006** 899 GTGGAGCAC C ATTTGCCTCC AGGGATAGGG AAGGAGGACT AgAGTCTTT/  
**P879007** 895 GTGGAGCAGC ATTTGCCTCC AGGGATAGGG AAGGAGGACT AaAGTCTTT/  
**cATP5G1** 912 GTGG- GGGGC ATTTGCCCC AGGGCCGGGA GAAGCgctagtgccc- - - T  
 \* \* \* \* \*  
 \* \* \* \* \*  
 \* \* \* \* \*

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

**P879005** 1011 ATGGCCTTAT CAATGAATGT TAATTACCAA CGGTAATGAA CGATTGACTC

```

P879006 949 A - - GCCTTAT CAATTAAATGT TAATTACCAA CGGTAATGAG CGATAAACGC
P879007 945 A - - GCCTTAT CAATTAAATGT TAATTACCAA CGGTAATGAG CGATAAACGC
cATP5G1 957 ATA TCCTTAA CAATTAAATGT TAATTACCAA - - GTAATGAG CGATTAGCTC
* * * * *
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* * * * *
* * * * *

```

```

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

```

```

P879005 1061 cc t CCGCTGG GGC GGGTCGG G GACTGCTGT GT AAGATGGG CAGGATCCTC
P879006 997 - - - CCGCTGG GGAGAGTAGG GGACAGCAGT GT AACTTGGG CAGGATCCTC
P879007 993 - - - CCGCTGG GGAGAGTAGG GGACAGCTAT GT AACATGGG CAGGATCCTC
cATP5G1 1005 tc c c a c c g a GGC GGGCCGA GGACAGCTGT GT AAAATGGG CAGCACTCTC
* * * * *
* * * * *
* * * * *
* * * * *
* * * * *

```

```

alignment
position 1201. . . . . 1211. . . . . 1221. . . . . 1231. . . . . 1241. . . . .

```

```

P879005 1111 CGCGACACCT GCCCAGTATC CGCCTCC - - AGTCTTCCCG AGAGACCATTT
P879006 1044 CACGACGTCT G- CCAGTTTC TGCCTCC - - GGTCTTCCCG GGAGACCATTT
P879007 1040 CACGACGTCT G- CCAGTTTC TGCCTCC - - AGTCTTCCCG GGAGATCATTT
cATP5G1 1055 CCCGGCACCG ACCCAGTATC TGCCTCCt a a AGCCTTCCCG GGAGACCATTT
* * * * *
* * * * *
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* * * * *

```

```

alignment
position 1251. . . . . 1261. . . . . 1271. . . . . 1281. . . . . 1291. . . . .

```

```

P879005 1158 CCCTTTTCGC A ACATTTCCTT CCTGGGGGCTT GGGCa c a t TT CCTTGACTTC
P879006 1090 CCTTTTTCGC A ACATTTCCTT CTTGGGGGCTT GAGCCACCTC CTTTTATTTC
P879007 1086 CCTTTTTCGC A ACGTTTCCTT CTTGGGGGCTT GAGCCACCTC CTTTTACTTC
cATP5G1 1105 CTCTTTA GC A ACATTTCCTT CCTGGGGGTTT GGCCCTCCTT CCTCTGCTGC
* * * * *
* * * * *
* * * * *
* * * * *
* * * * *

```

```

alignment
position 1301. . . . . 1311. . . . . 1321. . . . . 1331. . . . . 1341. . . . .

```

```

P879005 1208 CGATCTCCAT GACTTTGCTT - TGAAGACCC a - - - - -
P879006 1140 CGATCTCGGT TGCTGTCCTT CTGCAGACCC GCTGC GCAGA g AGTGGTTGA

```

```

P879007 1136 CGTTCTTGAT TGCTGTCCTT CTGCAGACCC GCTGCGCAGA a AGTGGTTGA/
cATP5G1 1155 AGATCTACGT GACCTTCCTT - TGCAGACCC c t t t c - - - - -
* * * * *
* * * * *
* * * * *

```

```

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

```

```

P879005 1238 - - - - - C TGCTCT GTCC CTCT GACCTC TAATGCCCTC CTC AGCTGGC
P879006 1190 CCCC GGAATC TGCTCT GTCC TTCT GACCTC TAATGCCCTC CTT AGCTGGC
P879007 1186 CCCC GGAATC TGCTCT GTCC TTCT GACCTC TAATGCCCTC CTT AGT TGG
cATP5G1 1189 - - - - - - - GC GCT GTTC CTCT GACCTC TAATGCCCTC CTC AGCTGGC
* * * * *
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* * * * *
* * * * *

```

```

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

```

```

P879005 1279 GCACG GTGCA AGGAA GAGCG TGG- - - - - - - - - - - - - - -
P879006 1240 GTAT- - - - - AGGAA GAGGG TTGGGGG- GA AC GATTGGA- GGTGGATGGC
P879007 1236 GTAT- - - - - AGGAA GAGGG TTGGGGG a GA AC GATTGGA- GGTGGATGGC
cATP5G1 1228 GCACG GTGCA AGGAA GAA CG TGGt c c c g g g a g g g c g g g c g GGGTGAAGGC
* * * * *
* * * * *
* * * * *
* * * * *

```

```

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

```

```

P879005 1302 - - - - - - - - - - - - - - - - - - - - -
P879006 1282 GACAACAGGA GGT TGCCAGT - - - - - - - - - - -
P879007 1279 AACGACAGGA GGT TGCCAGT At c - - - - - - - - - - -
cATP5G1 1278 GACGCCGAA GGT CGCCACT A a g c a a a c g a c t a g g c t g t g g a t g a a t c t t
* * * * *
* * * * *

```

```

alignment
position      1 5 0 1 . . . . . 1 5 1 1 . . . . . 1 5 2 1 . . . . . 1 5 3 1 . . . . . 1 5 4 1 . . . . .

```

```

P879005 1302 - - - - - - - - - - - - - - - - - - - - -
P879006 1302 - - - - - - - - - - - - - - - - - - - - -
P879007 1302 - - - - - - - - - - - - - - - - - - - - -
cATP5G1 1328 t t t t t t t t t t t t t t t c c c t c t g c a g a c t g a g a a a a t g c a g a c c a c c

```

```

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

```

```

P879005 1302 - - - - - - - - - - - - - - - - - - - - -
P879006 1302 - - - - - - - - - - - - - - - - - - - - -
P879007 1302 - - - - - - - - - - - - - - - - - - - - -
cATP5G1 1378 g g g g c a t t a c t c a t t c c t c c g g c t c t g g t a a g c t g c g g c t c c g g g t g a t

```



```

alignment
position      1 6 0 1 . . . . . 1 6 1 1 . . . . . 1 6 2 1 . . . . . 1 6 3 1 . . . . . 1 6 4 1 . . . . .
P879005 1302 - - - - -
P879006 1302 - - - - -
P879007 1302 - - - - -
cATP5G1 1428 c t g t a g t g c c a g g t g t g g g a c c t g t c g a t g t t t a a t g a a t g a a c t g a g a g

```

```

alignment
position      1 6 5 1 . . . . . 1 6 6 1 . . . . . 1 6 7 1
P879005 1302 - - - - -
P879006 1302 - - - - -
P879007 1302 - - - - -
cATP5G1 1478 g a g c c t g g c a t c c a g a g g a t g 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>P879006</b> (1301 bp)	<b>P879007</b> (1301 bp)	<b>cATP5G1</b> (1500 bp)
<b>P879005</b> (1301 bp)	0.411 58 %	0.415 59 %	0.473 63 %
<b>P879006</b> (1301 bp)		<u>1.000</u> <u>89 %</u>	0.311 57 %
<b>P879007</b> (1301 bp)			0.304 53 %

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	dialign.seq <input type="text"/>
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 Task: *DiAlign TF*: Multiple alignment plus TF sites  
working on promoters.seq (4 seq.)**

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

DiAlign professional TF Release 3.1 December 2004

Tue May 24 21:11:02 2005

## Solution parameters:

**Sequence file:** [promoters.seq](#) (4 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 4 (100.0 %) sequences)  
**Family matches:** yes  
**MatInspector library:** Matrix Family Library Version 5.0 (February 2005)  
**Selected groups** (core/matrix sim):

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

## Aligned Sequences:

No.	Sequence Name	Sequence Description	Length
1	P879005	sym=ATP5G1 loc=Loc5116 taxid=9606 spec=Homo sapiens chr=17  ctg=NT_010783 str=(+) start=5622941 end=5623941 len=1001  tss=501  comm=ATP synthase, H+ transporting, mitochondrial F0 complex, subunit c (subunit 9), isoform 1; (NM_005175/501/bronze;)	1001 bp
2	P879006	sym=Atp5g1 loc=Loc11951 taxid=10090 spec=Mus musculus  chr=11 ctg=NT_039521 str=(-) start=7475581 end=7476581  len=1001 tss=501  comm=ATP synthase, H+ transporting, mitochondrial F0 complex, subunit c (subunit 9), isoform 1; (NM_007506/562/bronze;)	1001 bp
3	P879007	sym=Atp5g1 loc=Loc29754 taxid=10116 spec=Rattus norvegicus  chr=10 ctg=NW_047338 str=(-) start=167149 end=168149  len=1001 tss=501  comm=ATP synthase, H+ transporting, mitochondrial F0 complex, subunit c, isoform 1; (NM_017311/565/bronze;)	1001 bp
4	P879008	sym=na loc=Loc419992 taxid=9031 spec=Gallus gallus chr=27  ctg=NW_060665 str=(-) start=111543 end=112543 len=1001  tss=501 comm=similar to P1 subunit; (XM_418114/501/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.

VSEGRF VSECAT VSPCAT

```

alignment
position      1 . . . . . 1 1 . . . . . 2 1 . . . . . 3 1 . . . . . 4 1 . . . . .
P879005      1 a a a c c t c c a - - - - - CGG TGGGAATTAC TGC AAAGGCa t c g g c t c t c c
P879006      1 - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
P879007      1 - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
P879008      1 c g c t g g g c c g c c g g c t c CGC TGGGCAGGGC TGGACAGGCc g t g c t t c a a c
                    * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * *
    
```

```

alignment
position      5 1 . . . . . 6 1 . . . . . 7 1 . . . . . 8 1 . . . . . 9 1 . . . . .
P879005      43 c g g c c t a g a a t a t c TCGCGG GATCTCAGCT GTCCTTGGGC CCCCc c c c t c
P879006      1 - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
P879007      1 - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
P879008      51 a a a a c a c a a g g a c a t g t t t c a g t g t c g a a g c g a t c t t t t t a g g a g c g a
                    * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * *
                    * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * *
                    * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * *
                    * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * *
    
```

```

alignment
position      10 1 . . . . . 1 1 1 . . . . . 1 2 1 . . . . . 1 3 1 . . . . . 1 4 1 . . . . .
P879005      93 a g c g c a - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
P879006      31 - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
P879007      28 - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
P879008      101 a t g g g a a a a g GGAGAGGCCG ACACGGC g g c c g c a a c a g c c t c c g g c g c a c
                    * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * *
                    * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * *
                    * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * *
                    * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * *
                    * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * *
                    * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * *
    
```

```

alignment
position      15 1 . . . . . 1 6 1 . . . . . 1 7 1 . . . . . 1 8 1 . . . . . 1 9 1 . . . . .
P879005      132 CCCAAGCGCC CGAATGAAGG CT CGGGGCCA AAGTCATGTG TCTGACTGCG
P879006      71 TCCAAGCGGC CGAATGAAGG CCTGGAGCCC TTATCACGTG TCAGCTTGCG
P879007      68 TCCAAGCGGC CGAATGAAGA CT CGGAGCCC ACGTTACGTG TCCGCCTGCG
P879008      151 c g g a g a g t a c c g t g a g a g g a c a g c t g a g c a c a g - - - - - - - - - - - - - - - - - - - -
                    * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * *
                    * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * *
                    * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * *
                    * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * *
                    * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * *
                    * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * *
                    * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * *
    
```

```

alignment
position      20 1 . . . . . 2 1 1 . . . . . 2 2 1 . . . . . 2 3 1 . . . . . 2 4 1 . . . . .
P879005      182 TCACACGTCC CGTCATCTCT CCCACGCCTT TTTCTTCAGC GTACACCTTG
P879006      121 TCAAGCGGCC GGTTGTCACT CCCACGCTTT TTTCTTCCGC TTGCACCTTG
P879007      118 TCAAGCGGCC GGTaGTCACT CCCACGCTTT TTTCTTCCGC TTGCACCTTG
P879008      184 - - - - - - - - - - - - - - - - CCCACGCTg c t a c g c c g - - - - - - - - - -
    
```

```
*****
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*****
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*****
```

alignment position 25 1 . . . . . 2 6 1 . . . . . 2 7 1 . . . . . 2 8 1 . . . . . 2 9 1 . . . . .

**P879005** 232 GTCGCCATCT TGTGc g c g AG GTTATGGAAC CTCTGAGTCC CGCCAACCTCT  
**P879006** 171 GTCGCCATTT TGTGTTGAAG GTTGTAGAAC CTCTGAGTCT CGTCGACTCT  
**P879007** 168 GTCGCCATTT TGTGTTGAAG GCTGTAGAAC CTCTGAGTCT CGTCGACTCT  
**P879008** 202 - - - - - - - - - - - - - - - - - - - C CACCACCTCT  
\*\*\*\*\*  
\*\*\*\*\*  
\*\*\*\*\*  
\*\*\*\*\*  
\*\*\*\*\*  
\*\*\*\*\*  
\*\*\*\*\*  
\*\*\*\*\*  
\*\*\*\*\*

alignment position 30 1 . . . . . 3 1 1 . . . . . 3 2 1 . . . . . 3 3 1 . . . . . 3 4 1 . . . . .

**P879005** 282 ATGGT CGAGC - - - GTTTC A GGGATCGGCC AATCGTAAATC CAGATCTCGT  
**P879006** 221 ATGGT CAAGC - - - ATTTTCG GGATTCGACC AATCGTAAACC CCGAACTCGG  
**P879007** 218 ATGGT CAAGC - - - ATTTTCG GGATTCGACC AATCGTAAATC ACGATCTCGG  
**P879008** 213 GTGGT CAc c t c t a t GGTTTCG AGGAGCGGCC c c a c g c g c c t c a t g g t c c t c  
\*\*\*\*\*  
\*\*\*\*\*  
\*\*\*\*\*  
\*\*\*\*\*  
\*\*\*\*\*  
\*\*\*\*\*  
\*\*\*\*\*  
\*\*\*\*\*

alignment position 35 1 . . . . . 3 6 1 . . . . . 3 7 1 . . . . . 3 8 1 . . . . . 3 9 1 . . . . .

**P879005** 328 AGGAAAGCCC CGCCTCTATC CGCATGGAGG CCGGAATTGC CACGAAGCTC  
**P879006** 267 AAAAAGAACC CGCCTTTATC CGCAAAGGAGG CCGGAATTGC CACGAAGCTC  
**P879007** 264 AAAAAGACCC CGCCTTTATC CGCAAAGGAGG CCGGAATTGC CACGAAGCTC  
**P879008** 263 t g g a a a c c - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -  
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alignment position 40 1 . . . . . 4 1 1 . . . . . 4 2 1 . . . . . 4 3 1 . . . . . 4 4 1 . . . . .

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P879005 378 CTGTGGAGGG AGAGGAAGCA GCTGCGGAAA GCCAATAAGA g t g g g g a a T C
P879006 317 CTGTGGAGAG AGAGGAAGAA GCTGAAGAAG ACCAATAAGA AGGATGGA GT
P879007 314 CCGTGGAGAG AGAGGAAGAA CCTGAAAAAG ACCAATAAGA AAGATGAAGT
P879008 272 - - - - - - - - - - - - - - - - - - - - - - - - - - - - T C
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alignment position 451 . . . . . 461 . . . . . 471 . . . . . 481 . . . . . 491 . . . . .

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P879005 428 - GATGACGTC AACCAATGGG GACGC GGGGA TATT A- - - - - - - - - - - -
P879006 367 TGATGACGCC AGCCAATTGG AACGT GGAGA GATTA A- - - - - - - - - - - -
P879007 364 TGATGACGCC AGCCAATTGG AACGT GAGGA GATTA A- - - - - - - - - - - -
P879008 274 - CAGGCCGTC AGCCAATCGC AAA GC GC GTA GCGAA a a t a a c t a a c c a a t g
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alignment position 501 . . . . . 511 . . . . . 521 . . . . . 531 . . . . . 541 . . . . .

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P879005 462 - - - - - - - - - - - - - - - - - - - - - - - - - - - -
P879006 402 - - - - - - - - - - - - - - - - - - - - - - - - - - - -
P879007 399 - - - - - - - - - - - - - - - - - - - - - - - - - - - -
P879008 323 g a a g c t c g c a t c a t g g c a c g g t t c t c c c g c c c c g t g c t g c t a t c c c g g a

```

alignment position 551 . . . . . 561 . . . . . 571 . . . . . 581 . . . . . 591 . . . . .

```

P879005 462 - - - - - - - - - - - - - - - - CGG CCAATGAGAA TGGAGa a g g t
P879006 402 - - - - - - - - - - - - - - - - CGA CCAATGGGAG T Ga AGGGACT
P879007 399 - - - - - - - - - - - - - - - - CGG CCAATGGGAG TGGAGGGACC
P879008 373 t g c t a g t g g g a g g a g c t t g c t g g a c t g CGG CCAATGGGg a g c g c g g a t g t
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alignment position 601 . . . . . 611 . . . . . 621 . . . . . 631 . . . . . 641 . . . . .

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P879005 485 c c a g g ACACG T - - - - - - - - - - - - - - - - - -
P879006 425 CCGA- ACACG T - - - - - - - - - - - - - - - - - -
P879007 422 CCGA- ACACG T - - - - - - - - - - - - - - - - - -
P879008 423 t g t c c a g a g t g c c g c g c g c c g c g c g c a g c g g t a g c c a a t c g g c g c g g a g
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alignment position	651 . . . . .	661 . . . . .	671 . . . . .	681 . . . . .	691 . . . . .				
<b>P879005</b>	496	-----	-----	----- GG	GTGGGGGAaG	CTGAGCGCTG			
<b>P879006</b>	435	-----	-----	----- GG	GTGGGGGA - G	CTGAGCGCTC			
<b>P879007</b>	432	-----	-----	----- GG	GTGGGGGA - G	CTGAGCGCTG			
<b>P879008</b>	473	g a c g c t g g g g	g a c a c g g c a a	g g t g a g g	c g GG	GTGGGGGC - G	Cg g g c g c g c t		
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alignment position	701 . . . . .	711 . . . . .	721 . . . . .	731 . . . . .	741 . . . . .				
<b>P879005</b>	518	AGACC AAGGG	CTAAAGCTGG	GAGGTGAGTc	t GTCACCTTG	AGC - - CGGGC			
<b>P879006</b>	456	AGACC AAGGG	CTAAAGCTGG	GAGGTGAGTC	AGTCACCTTG	AGC - - AGGGA			
<b>P879007</b>	453	AGACC AAGGG	CTAAAGCTGC	GAGGTGAGTC	AGTCACCTTG	AGC - - AGGGA			
<b>P879008</b>	522	c t c t c t t c a c	a g c c g t c a c c	g t c g c a g c c c	c g a g a g g a c a	c c g t g CAGGT			
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alignment position	751 . . . . .	761 . . . . .	771 . . . . .	781 . . . . .	791 . . . . .				
<b>P879005</b>	566	GAGCGCTGTG	GGCC AAGCAG	GGGTTGCAGG	G TAGTAGGAG	TGCAGGTGAC			
<b>P879006</b>	504	GTGTGCTGTG	GGCCGAGCAG	GGGCTGCAGG	GGAGTGGGAG	TGCAGGTGAC			
<b>P879007</b>	501	GTGTGCTGTG	GGCCGAGCAG	GGGCTGCAGG	GGAGTGGGAG	TGCAGGTGAC			
<b>P879008</b>	572	GGGGTCTGCG	TGCGGCCCCG	GGGCTGt g a g	c a g g c a c c g t	g a - - - - -			
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alignment position	801 . . . . .	811 . . . . .	821 . . . . .	831 . . . . .	841 . . . . .				
<b>P879005</b>	616	TTGGGGCCGG	GAGc c a g c a a	t a g g c a g GGT	TGTGGGCTGG	GCAGTGTGGA			
<b>P879006</b>	554	TTGGGGCTGG	GAGACAGGGg	TCCGCAAGGC	CGTGGGTTGT	GCCACGTGGA			
<b>P879007</b>	551	TTGGGGCCCG	GAGACAGGG-	TCCGCTAGGC	CGTGGGCTGT	GCCATGTGGA			
<b>P879008</b>	614	-----	-----	-----	-----	-----			



```
alignment
position      1 0 0 1 . . . . . 1 0 1 1 . . . . . 1 0 2 1 . . . . . 1 0 3 1 . . . . . 1 0 4 1 . . . . .
P879005 816 C a c c t g c C C A G T A T C C G C C T C C A G T C T T C C C G A G A G A C C A T T C C C T T T C G
P879006 749 C G T C T G - C C A G T T T C T G C C T C C G G T C T T C C C G G G A G A C C A T T C C T T T T C G
P879007 745 C G T C T G - C C A G T T T C T G C C T C C A G T C T T C C C G G G A G A T C A T T C C T T T T C G
P879008 614 - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
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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 . . . . .
P879005 866 C A A C A T T T C C T T C C T G G G G C T T G G G C a c a t T T C C T T G A C T T C C G A T C T C C
P879006 798 C A A C A T T T C C C T C T T G G G G C C T G A G C C A C C T C C T T T T A T T T C C G A T C T C G
P879007 794 C A A C G T T T C C C T C T T G G G G C C T G A G C C A C C T C C T T T T A C T T C C G T T C T T G
P879008 614 - - - - - - - - - - C C T G G G G C T T G G c c g g t g g g g t g g t g c c t g g c c g g g c t
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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 . . . . .
P879005 916 A T G A C T T T G C T T T G A A G - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
P879006 848 G T T G C T G T C C T T C T G C A G A C C C G C T G C G C A G A g A G T G G T T G A C C C C G G A A
P879007 844 A T T G C T G T C C T T C T G C A G A C C C G C T G C G C A G A a A G T G G T T G A C C C C G G A A
P879008 652 g t a c c - - - - C T T C G A T 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 . . . . .
P879005 937 A C T G C T C T G T C C C T C T - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
P879006 898 T C T G C T C T G T C C T T C T - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
P879007 894 T C T G C T C T G T C C T T C T - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
P879008 669 T C T G C T G T C C C C T G C T c c g g c c g g g a c t c g g t t g t g c t g a g g t g g t t t t 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>P879005</b>	953	- - - - -	- - - - -	- - - - -	- - - - -
<b>P879006</b>	914	- - - - -	- - - - -	- - - - -	- - - - -
<b>P879007</b>	910	- - - - -	- - - - -	- - - - -	- - - - -
<b>P879008</b>	719	g g g t g t t t a g	a a t g a g g a a g	g g g a g a a c c g	c g g a t c t c c t g a t c t g c a g g
alignment position	1 2 5 1 . . . . .	1 2 6 1 . . . . .	1 2 7 1 . . . . .	1 2 8 1 . . . . .	1 2 9 1 . . . . .
<b>P879005</b>	953	- - - - -	- - - - -	- - - - -	- - - - -
<b>P879006</b>	914	- - - - -	- - - - -	- - - - -	- - - - -
<b>P879007</b>	910	- - - - -	- - - - -	- - - - -	- - - - -
<b>P879008</b>	769	g g t g g g c c g c	g a g g c g g a t g	t a g c a g c a c t	g g g g t t c c t a a t t c c t t c t t
alignment position	1 3 0 1 . . . . .	1 3 1 1 . . . . .	1 3 2 1 . . . . .	1 3 3 1 . . . . .	1 3 4 1 . . . . .
<b>P879005</b>	953	- - - - -	- - - - -	- - - - -	G A C C T C T A A T G C C C T
<b>P879006</b>	914	- - - - -	- - - - -	- - - - -	G A C C T C T A A T G C C C T
<b>P879007</b>	910	- - - - -	- - - - -	- - - - -	G A C C T C T A A T G C C C T
<b>P879008</b>	819	c t c a t g a t t a	g t a a t a g g t a	a a g c a a g a t g	c a g a c G G C T T C T T T G G C T C T
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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 . . . . .
<b>P879005</b>	968	C C T C A G C T G G	g g c a c g g t g c	a A G G A - - - - -	A G A G C G T g g - - - - -
<b>P879006</b>	929	C C T T A G C T G G	G G T A T - - - - -	A G G A - - - - -	A G A G G G T T G G G G G - G A
<b>P879007</b>	925	C C T T A G T T G G	A G T A T - - - - -	A G G A - - - - -	A G A G G G T T G G G G G a G A
<b>P879008</b>	869	C C T C A G C T c t	c c g g c t c t g g	t a a g a a c t c t	g c a g A G A G G T G T A G T G G - T G
		* * * * *	* * * * *	* * * * *	* * * * * * * * * * * * * *
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alignment position	1 4 0 1 . . . . .	1 4 1 1 . . . . .	1 4 2 1 . . . . .	1 4 3 1 . . . . .	1 4 4 1 . . . . .
<b>P879005</b>	1002	- - - - -	- - - - -	- - - - -	- - - - -
<b>P879006</b>	963	A C G A T T G G A G	G T G G A T G G G G	A C A A C A G G A G	G T T G C C A G t - - - - -
<b>P879007</b>	960	A C G A T T G G A G	G T G G A T G G G A	A C G A C A G G A G	G T T G C C A G t a t c - - - - -
<b>P879008</b>	918	C T T A G T G G G G	C T G T G T G G c t	g g g a t c a g g a	c g t g a c t c t g g g c a g c c c t g

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alignment
position      1 4 5 1 . . . . . 1 4 6 1 . . . . . 1 4 7 1 . . . . . 1 4 8 1
P879005 1002 - - - - -
P879006 1002 - - - - -
P879007 1002 - - - - -
P879008 968 g t t g a g a g g g g g t c c c a t g a g g c c a t t t a c a c a
    
```

### 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>P879006</b> (1001 bp)	<b>P879007</b> (1001 bp)	<b>P879008</b> (1001 bp)
<b>P879005</b> (1001 bp)	0.458 65 %	0.450 63 %	0.009 16 %
<b>P879006</b> (1001 bp)		<u>1.000</u> <u>92 %</u>	0.005 14 %
<b>P879007</b> (1001 bp)			0.007 14 %

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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[Frequently asked questions](#) [Your Results](#) [Your Sequences](#) [Your Protocol](#) [Help](#)

**GEMS Launcher Task: *DiAlign TF*: Multiple alignment plus TF sites  
working on C5-ATP5G2 (3 seq.)**

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

DiAlign professional TF Release 3.1 December 2004

Tue May 31 00:27:39 2005

## Solution parameters:

**Sequence file:** [C5-ATP5G2](#) (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)  
**Selected groups**

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

(core/matrix sim):

## Aligned Sequences:

No.	Sequence Name	Sequence Description	Length
1	P879011	P879011 sym=ATP5G2 loc=Loc517 taxid=9606 spec=Homo sapiens chr=12 ctg=NT_029419 str=(-) start=16212672 end=16213672 len=1001 tss=501 comm=ATP synthase, H+ transporting, mitochondrial F0 complex, subunit c (subunit 9), isoform 2; (AK130971/501/gold;)	1001 bp
2	mSTP5G2	mSTP5G2 m6_dna range=chr15:102731087-102731883 5'pad=0 3'pad=0 revComp=TRUE strand=? repeatMasking=none	797 bp
3	P879015	P879015 sym=Atp5g2 loc=Loc171082 taxid=10116 spec=Rattus norvegicus chr=7 ctg=NW_047785 str=(-) start=631146 end=632146 len=1001 comm=ATP synthase, H+ transporting, mitochondrial F0 complex, subunit c (subunit 9), isoform 2; (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\$NRF1
V\$NRF1
V\$SETSF
V\$NRF2
V\$ZBPF
V\$EVI1

alignment position	1 . . . . .	11 . . . . .	21 . . . . .	31 . . . . .	41 . . . . .
<b>P879011</b>	1 a g c - - - - -	- - - - -	- - - - -	- - - - -	- - - - -
<b>mSTP5G2</b>	1 t t - - - - -	- - - - -	- - - - -	- - - - -	- - - - -
<b>P879015</b>	1 c g g g a c t c g t	g c c c g g a a g c	c c c c g c c c a c	c g c c a c c g g g	g g a g g g g c g g
alignment position	51 . . . . .	61 . . . . .	71 . . . . .	81 . . . . .	91 . . . . .
<b>P879011</b>	4 - - - - -	- - - - -	- - - - -	- - - - -	- - - - -
<b>mSTP5G2</b>	3 - - - - -	- - - - -	- - - - -	- - - - -	- - - - -
<b>P879015</b>	51 g c g a a a g g g c	a c t g a a g c a a	a g c a g g g g c t	t g g g g a g a g c	c c c t c g c g g g
alignment position	101 . . . . .	111 . . . . .	121 . . . . .	131 . . . . .	141 . . . . .
<b>P879011</b>	4 - - - - -	- - - - -	- - - - -	- - - - -	- - - - -
<b>mSTP5G2</b>	3 - - - - -	- - - - -	- - - - -	- - - - -	- - - - -
<b>P879015</b>	101 c g g c t g c a c a	t t c c a g c t t g	c a c c c c c c t t	t c c c c a g c a a	g t c t g a c a g a
alignment position	151 . . . . .	161 . . . . .	171 . . . . .	181 . . . . .	191 . . . . .
<b>P879011</b>	4 - - - - -	- - - - -	- - - - -	- - - - -	- - - - -
<b>mSTP5G2</b>	3 - - - - -	- - - - -	- - - - -	- - - - -	- - - - -
<b>P879015</b>	151 g g t a a a c t g g	t c g c c t g g g g	t g a c c t t g c a	c c c t a c t a c	a g g c a a t a a g
alignment position	201 . . . . .	211 . . . . .	221 . . . . .	231 . . . . .	241 . . . . .
<b>P879011</b>	4 - - - - -	- - - - -	- - - - -	- - - - -	- - - - -
<b>mSTP5G2</b>	3 - - - - -	- - - - -	- - - - -	- - - - -	- - - - -
<b>P879015</b>	201 t g t g g t t a t t	c c t a a t t g a t	c c c a g g a c t c	a c a a a a g g g a	g a t a c a g g c c
alignment position	251 . . . . .	261 . . . . .	271 . . . . .	281 . . . . .	291 . . . . .
<b>P879011</b>	4 - - - - -	- - - - -	- - - - -	- - - - -	- - - - -
<b>mSTP5G2</b>	3 - - - - -	- - - - -	- - - - -	- - - - -	- - - - -
<b>P879015</b>	251 t t g t t t a c c c	t c a a g t t t c t	g a c t c g c a g a	t g t t g g g g t t	t t t t t t t t g t
alignment position	301 . . . . .	311 . . . . .	321 . . . . .	331 . . . . .	341 . . . . .
<b>P879011</b>	4 - - - - -	- - - - -	- - - - -	- - - - -	- - - - -
<b>mSTP5G2</b>	3 - - - - -	- - - - -	- - - - -	- - - - -	- - - - -
<b>P879015</b>	301 t t g t t t g t t t	g t t t t g t t t t	g t t t t t t t t c	a t g c t c t g c t	c a t c a g c g a g
alignment position	351 . . . . .	361 . . . . .	371 . . . . .	381 . . . . .	391 . . . . .
<b>P879011</b>	4 - - - - -	- - - - -	- - - - -	- - - - -	- - - - -
<b>mSTP5G2</b>	3 - - - - -	- - - - -	- - - - -	- - - - -	- - - - -
<b>P879015</b>	351 a t a g g g a a a a	c a a g a a a t a a	g t t a a a g c c g	a a a t A G C C G T	G A C A T T T T G 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>mSTP5G2</b> (797 bp)	<b>P879015</b> (1001 bp)
<b>P879011</b> (1001 bp)	0.714 <u>59 %</u>	0.435 34 %
<b>mSTP5G2</b> (797 bp)		<u>1.000</u> 54 %

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 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 31 22:39:23 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)  
**Selected groups**

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

(core/matrix sim):

## Aligned Sequences:

No.	Sequence Name	Sequence Description	Length
1	P978262	sym=ATP5G3 loc=Loc518 taxid=9606 spec=Homo sapiens chr=2 ctg=NT_005403 str=(-) start=26255279 end=26256279 len=1001 tss=501 comm=ATP synthase, H+ transporting, mitochondrial F0 complex, subunit c (subunit 9) isoform 3; (NM_001689/501/bronze;)	1001 bp
2	P978265	sym=Atp5g3 loc=Loc228033 taxid=10090 spec=Mus musculus chr=2 ctg=NT_039207 str=(-) start=14746017 end=14747017 len=1001 comm=ATP synthase, H+ transporting, mitochondrial F0 complex, subunit c (subunit 9), isoform 3; (CompGen promoter)	1001 bp
3	P978269	sym=Atp5g3 loc=Loc114630 taxid=10116 spec=Rattus norvegicus chr=3 ctg=NW_047656 str=(-) start=2899390 end=2900390 len=1001 comm=ATP synthase, H+ transporting, mitochondrial F0 complex, subunit c (subunit 9) isoform 3; (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\$HOXF	V\$ECAT	V\$HOXH	V\$MYTI	V\$XBBF	V\$RORA	V\$SEREF	USEREF	V\$SFIF	V\$DMTF	V\$NRF1	USNRF1
	V\$SEGRF	V\$ZBPF	V\$HESF									
alignment position	1 . . . . .	1 1 . . . . .	2 1 . . . . .	3 1 . . . . .	4 1 . . . . .							
<b>P978262</b>	1 g c t t t g c t g g	g g a c c c t a g t	t t c c t g t t a a	g t a g t g a a t g	a c c c t t c t t t							
<b>P978265</b>	1 t a c a g - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -
<b>P978269</b>	1 t t a a a a a - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -
alignment position	5 1 . . . . .	6 1 . . . . .	7 1 . . . . .	8 1 . . . . .	9 1 . . . . .							
<b>P978262</b>	51 c c t c c c g c c a	g c c a c a g t c c	T A T T T C A C A G	A G G A A G A G A A	T G A C C A G C A A							
<b>P978265</b>	6 - - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -
<b>P978269</b>	9 - - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -
alignment position	1 0 1 . . . . .	1 1 1 . . . . .	1 2 1 . . . . .	1 3 1 . . . . .	1 4 1 . . . . .							
<b>P978262</b>	101 G T C A A C T - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -
<b>P978265</b>	9 T T T A T C T G A G	A C A T T T C T G C	A T C C A T C T G G	T T T G T T C a a A	G T T A T C A G A A							
<b>P978269</b>	39 C T T A T C T G A G	A T A T T T C T G C	A T T C A T C T G G	T T T G T T C - - A	G T T A C C A G A A							
	*	*	*	*	*	*	*	*	*	*	*	*
	*	*	*	*	*	*	*	*	*	*	*	*
	*	*	*	*	*	*	*	*	*	*	*	*
alignment position	1 5 1 . . . . .	1 6 1 . . . . .	1 7 1 . . . . .	1 8 1 . . . . .	1 9 1 . . . . .							
<b>P978262</b>	108 - - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -
<b>P978265</b>	59 C T G G g t g c t g	a a t a g A T T T T	G A A A A C T A T T	C A G G C A C T T T	T T t A G T C C G A							
<b>P978269</b>	87 C T G G t g c t g a	- - - - - A T T T T	G A A A A A T A T T	C A G G C A C T T T	T T - A G T C C A A							
	*	*	*	*	*	*	*	*	*	*	*	*
alignment position	2 0 1 . . . . .	2 1 1 . . . . .	2 2 1 . . . . .	2 3 1 . . . . .	2 4 1 . . . . .							
<b>P978262</b>	108 - - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -
<b>P978265</b>	109 A A T G A T G A T A	C A T T A T T A T C	T C T T A A T T C T	c C C A G T T A T A	A T G G T G G A A G							
<b>P978269</b>	131 A A T T A T G A T A	C A T T A T A A T C	T C T T A A T C C T	t C C A A T T A T A	A T G G T G G A A G							
	*	*	*	*	*	*	*	*	*	*	*	*
	*	*	*	*	*	*	*	*	*	*	*	*
	*	*	*	*	*	*	*	*	*	*	*	*
alignment position	2 5 1 . . . . .	2 6 1 . . . . .	2 7 1 . . . . .	2 8 1 . . . . .	2 9 1 . . . . .							
<b>P978262</b>	108 - - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -
<b>P978265</b>	159 G C A G C A G A A C	A C A G T g g t A C	A T G G C T T T A A	T G T C A G C A C T	T G G A A a A C A G							
<b>P978269</b>	181 G C A G C A G A A C	A C A G T a g c A C	A T G G C T T T A A	T C G C A G C A C T	T G C A A g A C A G							
	*	*	*	*	*	*	*	*	*	*	*	*
	*	*	*	*	*	*	*	*	*	*	*	*
	*	*	*	*	*	*	*	*	*	*	*	*
alignment position	3 0 1 . . . . .	3 1 1 . . . . .	3 2 1 . . . . .	3 3 1 . . . . .	3 4 1 . . . . .							

**P978262** 108 - - - - - TCT ACT ACAGAG AAGC  
**P978265** 209 AGGCAGGAGG ATTTCTGTGA GTTGAAGGCT AGCC T a g TCT ACAGAGTTGC  
**P978269** 231 AGGCAGGAAG ATTTCTGTGA GTTGGAGGCT AGTC TGT TCT ACAGAGTTGC  
 \* \* \* \* \*  
 \* \* \* \* \*  
 \* \* \* \* \*

alignment position 351 . . . . . 361 . . . . . 371 . . . . . 381 . . . . . 391 . . . . .

**P978262** 124 A g c a a c t g a t a - - - - -  
**P978265** 259 AAAGCTCTTG AACCGTCATT TGTTCT t c c c a g g a CTTCTA GGTAGGTCCT  
**P978269** 281 AAAGCTCTTG AACCCTCATT TGTTCa t t t c a g g g CTTCTA GTCAGGTCCT  
 \* \* \* \* \*  
 \* \* \* \* \*  
 \* \* \* \* \*

alignment position 401 . . . . . 411 . . . . . 421 . . . . . 431 . . . . . 441 . . . . .

**P978262** 135 - - - - -  
**P978265** 309 CTGAGAAAG ATTTGTCGTC TT a a c a a a g c a a c a a a c a a c a a c a a  
**P978269** 331 CTGAGGAAAT ATTTGCCGTC TT - - - - -  
 \* \* \* \* \*  
 \* \* \* \* \*

alignment position 451 . . . . . 461 . . . . . 471 . . . . . 481 . . . . . 491 . . . . .

**P978262** 135 - - - - -  
**P978265** 359 a a a a c c c t g T TTTAGAGTCT TACAAAGAAA TAATCCC GCT GGAGTTGGTt  
**P978269** 353 - - - - - T TTTAGGTTCT TATAAAGAAA TAAT TCC GCT GGACCTGGTg  
 \* \* \* \* \*  
 \* \* \* \* \*

alignment position 501 . . . . . 511 . . . . . 521 . . . . . 531 . . . . . 541 . . . . .

**P978262** 135 - - - - -  
**P978265** 409 a t g a a g a - - - - - AG C T A A C T A C T T G G A A G G G T G A A A G T G G A C G A  
**P978269** 394 g t g a a g a c c t g a a a t c c t A G C T C G C T A C T T G G A A A G C T A A A A C T G G A C G A  
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alignment position 551 . . . . . 561 . . . . . 571 . . . . . 581 . . . . . 591 . . . . .

**P978262** 135 - - - - -  
**P978265** 448 TCAA g g t t C T C C C T A A C T T A C A T A C T G A G C T C A A G G C C T G C c t G A G C A A C  
**P978269** 444 TCAA a g c c C T C T C T A A C T T A C A T A C T G A G C A C A A G G C C T G C t c G A G C A A C  
 \* \* \* \* \*  
 \* \* \* \* \*  
 \* \* \* \* \*

alignment position 601 . . . . . 611 . . . . . 621 . . . . . 631 . . . . . 641 . . . . .

**P978262** 135 - - - - - AAAG GCCAAATCt t a c a a g g t g c c a a c g t g - - - -  
**P978265** 498 TCACCCTGTT TGAAATAAAA GCCAAATCAG GGTCGGC TTG TAGCTCCCTG  
**P978269** 494 TCACCCTGTC TGAAATAAAA Gt g AAAACAG GGTCGGC TTG CAGCTCTGTG



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alignment position	6 5 1 . . . . .	6 6 1 . . . . .	6 7 1 . . . . .	6 8 1 . . . . .	6 9 1 . . . . .
<b>P978262</b>	165 - - - - -	- - - - -	- - - - -	AAGAA	AAAGGCC CAC TATCCt g c a g
<b>P978265</b>	548 GGAGa a c	CCC TGCCTGGC AC	GTGCAAGGAG	CGAGGCT CAG	Tc t g c g ATAG
<b>P978269</b>	544 GTAGt a t	CCC TGCCTGGC AC	GTGCAAGGAG	AGAGGCT CAG	TACCCa ATAG
	***	***	***	***	***
	***	***	***	***	***
		***	***	***	

alignment position

7 0 1 . . . . .	7 1 1 . . . . .	7 2 1 . . . . .	7 3 1 . . . . .	7 4 1 . . . . .	
<b>P978262</b>	190 c CAACTCAT A	TCAAAAGT TA	a t c t g t t a g	t c c t c t c t g c	c g g g g t g a a t
<b>P978265</b>	598 - CGACAACAA	CTAAA AAT TA	TCTGCAC CGT	TAGT a a CACT	AACAAA GC CA
<b>P978269</b>	594 - CGACACAAA	TTAAA AAT TA	TCTTCAC CGT	TAGT g g CACT	AACAAT GC CA
	*****	*****	*****	*****	*****
	*****	*****	*****	*****	*****

alignment position

7 5 1 . . . . .	7 6 1 . . . . .	7 7 1 . . . . .	7 8 1 . . . . .	7 9 1 . . . . .	
<b>P978262</b>	240 c t a c a g t t t t	t c t t t TTGTC	TCCCTCTTGC	CCCATCACC a	- - - - -
<b>P978265</b>	647 AGAG- - - - -	- - - - - TCGTC	TTCAGTGTG-	- - CT TTT CAT	TTCACTGGCC
<b>P978269</b>	643 GGAG- - - - -	- - - - - TTGTC	TCCAGTGTGC	TCCT TTT CCT	TTCACTGGCT
	***	***	***	***	***
	***	***	***	***	***
		***	***	***	***

alignment position

8 0 1 . . . . .	8 1 1 . . . . .	8 2 1 . . . . .	8 3 1 . . . . .	8 4 1 . . . . .	
<b>P978262</b>	280 - - - - -	- - - - - GGT	GGTTGTC GTT	GTCC TTC CG	GCT <b>AGT Tg CC</b>
<b>P978265</b>	683 GCCAGCCGGT	CACGGAGGG	GCCTGT CATT	GTCC TCC TCT	GAG <b>AGT Tg CC</b>
<b>P978269</b>	682 GCCAGCC TGT	TACGGAGGG-	- CCTGT CATT	GTCC TCC TCT	GCT <b>GGT Tg CC</b>
	*****	*****	*****	*****	*****
	*****	*****	*****	*****	*****
	*****	*****	*****	*****	*****
	*****	*****	*****	*****	*****
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alignment position

8 5 1 . . . . .	8 6 1 . . . . .	8 7 1 . . . . .	8 8 1 . . . . .	8 9 1 . . . . .
<b>P978262</b>	313 <b>AATAAAGTTG</b>	<b>TTACAAAGTG</b>	<b>ACCTTGAGTG</b>	<b>TCTT</b> CCt t g g t g c a c c c g a a
<b>P978265</b>	<b>AATAAAGTTG</b>	<b>TTACAAAGTG</b>	<b>ACCTTGAGCG</b>	<b>TCTT</b> CC- - - - -
<b>P978269</b>	<b>AATAAAGTTG</b>	<b>TTACAAAGTG</b>	<b>ACCTTGAGCG</b>	<b>TCTT</b> CC- - - - -
	*****	*****	*****	*****
	*****	*****	*****	*****
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	*****	*****	*****	*****

\* \* \* \* \*

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

**P978262** 363 a c C C C G C C T T **CTT CATCCGG** **GTG** C T G C G G C G C G A A T A A G A G C C G **G A C C G C**

**P978265** 769 - - C C C G C C T T **CTCCATCCGG** **GTG** C T G C G G C G C G G A T A A G A G C C G **C A C C G C**

**P978269** 766 - - C C C G C C T T **CTCCATCCGG** **GTG** C T G C G G C A C G G A T A A G A G C C G **C A C C G C**

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\* \* \* \* \*

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

**P978262** 413 **G C T T G C G C A T** **T** G A G T C C C **AC** **T C C T T C G A C C** **T C T G C C G** C A G C C C **G T - - - G C**

**P978265** 817 **G C T T G C G C g C** **C** C A G C C C C **AC** **T G C T T C G A C C** **T C T G C C G** C C G C C A **C T - - - G C**

**P978269** 814 **G C T T G C G C A C** **C** C A G C C C C **AC** **T G C T T C G A C C** **T C T G C C G** C C G C t g c t g **c c G C**

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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 . . . . .

**P978262** 460 **C G C C G C C G C C** **t c c t - - -** G G G A A G G T A A G T G G A G G G C A C A G G g a g c c c g g

**P978265** 864 **C G C C G C C T C G** **G G A** G G T A A G C G A A G G T A A A C G G A G G G C G C G G G g c - - - - -

**P978269** 864 **C G C C G C C T C C** **G G A** G G T A A G C G G A G G T A A A C G G A G G G C G c g - - - - -

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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 . . . . .

**P978262** 506 C C T **G G C C A G G** **G C G G A G C G G c** **g c e e a g** T A G G G A C C A T T C A T T G T G C C G G C

**P978265** 908 C C G G G C C G G G **G C G G A G C G G G** **T C T - - - C C C** G G C C T G T C C A C C G G G C T T G C

**P978269** 904 - - G G G C C G G G **G C G G A G C G G G** **T C T - - - T C G** G C C C T G T C C A C T A G A C T T G T

\* \* \* \* \*  
\* \* \* \* \*  
\* \* \* \* \*

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

**P978262** 556 G C C T C A C **T G G** **g c a c g G G G C C** **C A** A G C T G A C G G C G T G C A C G G G A G C C T G C G G

**P978265** 955 G C T T C C **C G G G** **C A C - - G C G G C** **C A C** G C T G A C C G C C T G C G C G G G G C C C T C G -

**P978269** 949 G A C T C C **C G G G** **C A C - - G C G G C** **C A C** G C C G A C G G T C T G C G C G G G T C C C T C G G

```

* * * * *
* * * * *
* * * * *
* * * * *
alignment
position      1 1 5 1 . . . . . 1 1 6 1 . . . . . 1 1 7 1 . . . . . 1 1 8 1 . . . . . 1 1 9 1 . . . . .
P978262 606 GGCCtgggtgggaagaaacaggcccctggagggcacttgacccttaagccctc
P978265 1002 - - - - -
P978269 997 GGCCg - - - - -
* * * * *

alignment
position      1 2 0 1 . . . . . 1 2 1 1 . . . . . 1 2 2 1 . . . . . 1 2 3 1 . . . . . 1 2 4 1 . . . . .
P978262 656 t t t t c c t c c g c a g a g a g g a a g c g g g a g a g g a g c c c a c g t c g c c t g t c a c c
P978265 1002 - - - - -
P978269 1002 - - - - -

alignment
position      1 2 5 1 . . . . . 1 2 6 1 . . . . . 1 2 7 1 . . . . . 1 2 8 1 . . . . . 1 2 9 1 . . . . .
P978262 706 c a a t a t c t c c a g c c g c g c a g t c c c g a a g a g t g t a a g a t g t t c g c c t g c g c
P978265 1002 - - - - -
P978269 1002 - - - - -

alignment
position      1 3 0 1 . . . . . 1 3 1 1 . . . . . 1 3 2 1 . . . . . 1 3 3 1 . . . . . 1 3 4 1 . . . . .
P978262 756 c a a g c t c g c c t g c a c c c c t c t c t g g t g c g t a g c c c a g g c a g g g t c g g g g
P978265 1002 - - - - -
P978269 1002 - - - - -

alignment
position      1 3 5 1 . . . . . 1 3 6 1 . . . . . 1 3 7 1 . . . . . 1 3 8 1 . . . . . 1 3 9 1 . . . . .
P978262 806 g g a t t g a g g g g t g g g c g t t t t g g c c t a g a g c g t c c a c g t t g t t g a a t g g g
P978265 1002 - - - - -
P978269 1002 - - - - -

alignment
position      1 4 0 1 . . . . . 1 4 1 1 . . . . . 1 4 2 1 . . . . . 1 4 3 1 . . . . . 1 4 4 1 . . . . .
P978262 856 g c a a c c t t c g g g c g g g g c a c a c c g c c t c t c g g g a a c g g c t t t c t c c t t a
P978265 1002 - - - - -
P978269 1002 - - - - -

alignment
position      1 4 5 1 . . . . . 1 4 6 1 . . . . . 1 4 7 1 . . . . . 1 4 8 1 . . . . . 1 4 9 1 . . . . .
P978262 906 c c t a t t a a c c c a t t g c c g t t t t c t t c c t a a t c t t a g g g c a t c t c a g c c c t
P978265 1002 - - - - -
P978269 1002 - - - - -

alignment
position      1 5 0 1 . . . . . 1 5 1 1 . . . . . 1 5 2 1 . . . . . 1 5 3 1 . . . . . 1 5 4 1 . . . . .
P978262 956 c t c c t t g c c a c t a g g g c g a g g c a g a g c a g c c g a g g c c t a g c t g t c a
P978265 1002 - - - - -
    
```

P978269 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.

	P978265 (1001 bp)	P978269 (1001 bp)
P978262 (1001 bp)	0.194 27 %	0.193 28 %
P978265 (1001 bp)		<u>1.000</u> <u>80 %</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**

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**GEMS Launcher Task: *DiAlign* TF: Multiple alignment plus TF sites  
working on C5-ATP5H (3 seq.)**

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

DiAlign professional TF Release 3.1 December 2004

Tue May 31 23:42:02 2005

## Solution parameters:

**Sequence file:** [C5-ATP5H](#) (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)  
**Selected groups** (core/matrix sim):

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

## Aligned Sequences:

No.	Sequence Name	Sequence Description	Le
1	P880080	P880080 sym=ATP5H loc=Loc10476 taxid=9606 spec=Homo sapiens chr=17 ctg=NT_010641 str=(-) start=6968827 end=6969827 len=1001 tss=501 comm=ATP synthase, H+ transporting, mitochondrial F0 complex, subunit d; (NM_006356/501/silver;)	100
2	P880083	P880083 sym=Atp5h loc=Loc71679 taxid=10090 spec=Mus musculus chr=11 ctg=NT_039521 str=(-) start=26819896 end=26820902 len=1007 tss=501,507 comm=ATP synthase, H+ transporting, mitochondrial F0 complex, subunit d; (AK088617/507/gold;AK002376/501/gold;)	100
3	rATP5H	rATP5H n3_dna range=chr10:105513408-105514236 5'pad=0 3'pad=0 revComp=TRUE strand=? repeatMasking=none	8:

## 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\$PLAG
V\$EGRF
V\$MAZF
V\$ZBPF
V\$SP1F
V\$HEN1
V\$YY1F
V\$AP2F
V\$SETF
U\$NRF2
V\$MYB

alignment position	1 . . . . .	1 1 . . . . .	2 1 . . . . .	3 1 . . . . .	4 1 . . . . .
<b>P880080</b>	1 c - - - - -	- - - - -	- - - - -	- - - - -	- - - GCGCCGC
<b>P880083</b>	1 c a c g a a g t a g	g t a c c g c c c a	c g t t g a g c c g	g a c c c a g c g g	g c g GCCCCGC
<b>rATP5H</b>	1 - - - - -	- - - - -	- - - - -	- - - - -	- - - - -
					* * * * *
					* * * * *
alignment position	5 1 . . . . .	6 1 . . . . .	7 1 . . . . .	8 1 . . . . .	9 1 . . . . .
<b>P880080</b>	9 CGCCCCCTGC	CCGCTCGGGT	GGTCCGGGAC	C c GGCTCCAG	CGGCTGCGCC
<b>P880083</b>	51 CGCCTCCCGT	CCGCTCCGGA	GGTCCGGGCC	C g GGCTCCAG	CGGCTGCGCC
<b>rATP5H</b>	1 - - - - -	- - - - -	- - - - -	- - - - -	- - - - -
	* * * * *	* * * * *	* * * * *	* * * * *	* * * * *
	* * * * *	* * * * *	* * * * *	* * * * *	* * * * *
alignment position	1 0 1 . . . . .	1 1 1 . . . . .	1 2 1 . . . . .	1 3 1 . . . . .	1 4 1 . . . . .
<b>P880080</b>	59 AC GGC GG C a g	c c g GGC GG CC	GT GC CC G CG G	GGC GT G G G GC	C A G C C G G G C C
<b>P880083</b>	101 GC GGC GG C g g	g c t GGC GG CC	GT GT CC G CG G	GGT GT C G G GC	C C G C A G G G C C
<b>rATP5H</b>	1 - - - - -	- - - - -	- - - - -	- - - - -	- - - - -
	* * * * *	* * * * *	* * * * *	* * * * *	* * * * *
	* * * * *	* * * * *	* * * * *	* * * * *	* * * * *
alignment position	1 5 1 . . . . .	1 6 1 . . . . .	1 7 1 . . . . .	1 8 1 . . . . .	1 9 1 . . . . .
<b>P880080</b>	109 t GGGC TG GGG	GGC CC G CG GA	CT GG GCC ACC	C CC GTC GC CC	A c c c C A C T C C
<b>P880083</b>	151 a GGGC TG GGG	GGT CC G CG GC	CC G A G C C G C C	G C C G T C G C C C	A t c g C A C T G C
<b>rATP5H</b>	1 - - - - -	- - - - -	- - - - -	- - - - -	- - - - -
	* * * * *	* * * * *	* * * * *	* * * * *	* * * * *
	* * * * *	* * * * *	* * * * *	* * * * *	* * * * *
alignment position	2 0 1 . . . . .	2 1 1 . . . . .	2 2 1 . . . . .	2 3 1 . . . . .	2 4 1 . . . . .
<b>P880080</b>	159 C G C C G C C C C C	T C C C A G C C C C	G C C A T c G C C G	G G T C C A G C T G	C A G T T C C G C C
<b>P880083</b>	201 T G C C A C C C C C	T C C C A G C C C C	G C C A c T G C C G	G G T C C A G C T G	C A G C T C C G C C
<b>rATP5H</b>	1 - G C C A C C C C C	T C C C A G C C C C	G C C A T T G C C G	G G T C C A G C T G	C A G C T C C G C C
	* * * * *	* * * * *	* * * * *	* * * * *	* * * * *
	* * * * *	* * * * *	* * * * *	* * * * *	* * * * *
	* * * * *	* * * * *	* * * * *	* * * * *	* * * * *
	* * * * *	* * * * *	* * * * *	* * * * *	* * * * *
	* * * * *	* * * * *	* * * * *	* * * * *	* * * * *
	* * * * *	* * * * *	* * * * *	* * * * *	* * * * *
	* * * * *	* * * * *	* * * * *	* * * * *	* * * * *
	* * * * *	* * * * *	* * * * *	* * * * *	* * * * *
	* * * * *	* * * * *	* * * * *	* * * * *	* * * * *
	* * * * *	* * * * *	* * * * *	* * * * *	* * * * *
alignment position	2 5 1 . . . . .	2 6 1 . . . . .	2 7 1 . . . . .	2 8 1 . . . . .	2 9 1 . . . . .
<b>P880080</b>	209 A T C T T G G A C C	G C C G C c g c c a	c c g c t g c T G C	C C G C G C G C A G	C C G G G C C G G C
<b>P880083</b>	251 A T C T T G G G C C	G C C G C - - - -	- - - - - T G C	C C G C G C G C C G	C C G G G C C G G C
<b>rATP5H</b>	50 A T C T T G G G C C	G C C G C - - - -	- - - - - T G C	C C G C C C G C C G	C C G G G C C G G 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>P880083</b> (1007 bp)	<b>rATP5H</b> (829 bp)
<b>P880080</b> (1001 bp)	0.514 49 %	0.417 51 %
<b>P880083</b> (1007 bp)		<u>1.000</u> <u>76 %</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 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

Wed Jun 1 22:20:06 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)  
**Selected groups** (core/matrix sim):

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

## Aligned Sequences:

No.	Sequence Name	Sequence Description	Length
1	P937000	sym=ATP5I loc=Loc521 taxid=9606 spec=Homo sapiens chr=4  ctg=NT_037622 str=(-) start=657542 end=658598 len=1057  tss=501,557  comm=ATP synthase, H+ transporting, mitochondrial F0 complex, subunit e; (AK000656/557/gold;NM_007100/501/silver;)	1057 bp
2	P937002	sym=Atp5k loc=Loc11958 taxid=10090 spec=Mus musculus chr=5  ctg=NT_039308 str=(-) start=31053274 end=31054277 len=1004  tss=501,504  comm=ATP synthase, H+ transporting, mitochondrial F1F0 complex, subunit e; (AK011342/547/gold;NM_007507/544/bronze;)	1004 bp
3	P937003	sym=Atp5k loc=Loc140608 taxid=10116 spec=Rattus norvegicus  chr=14 ctg=NW_047419 str=(+) start=1519276 end=1520276  len=1001 tss=501  comm=ATP synthase, H+ transporting, mitochondrial F1F0 complex, subunit e; (NM_080481/547/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\$NRF1 USNRF1 V\$SETF USNRF2 V\$SRORA V\$EV1 V\$SSF1F V\$SSPIF

alignment position 1 . . . . . 11 . . . . . 21 . . . . . 31 . . . . . 41 . . . . .
P937000 1 a a g g a c c t g c c c g g g g a g c - - - - -
P937002 1 t g a a c a t t a c c t g t a a a g c c c a a t g g a a a t t a g g a g c T C T G G G C G A G A A A
P937003 1 - - - - - T C T G G G T G A G A A A
\*\*\*
\*\*\*
\*\*\*

alignment position 51 . . . . . 61 . . . . . 71 . . . . . 81 . . . . . 91 . . . . .
P937000 20 - - - - -
P937002 51 A C A C T G G T C G G A G G A C A T A T G T G T C C a a t g c c g g a a a T T G C A G G A A A G C C
P937003 14 A C A C T G G C C A G A G G A C A T A T G C G T C C g a g g c t g g a a g T T G C A G G A A A G C C
\*\*\*
\*\*\*
\*\*\*
\*\*\*
\*\*\*

alignment position 101 . . . . . 111 . . . . . 121 . . . . . 131 . . . . . 141 . . . . .
P937000 20 - - - - - C A
P937002 101 C T G G A A G G T T G C T G A C C T C T C A G G A A G g G C C A A T A C A A G T T C T G T A A T C T
P937003 64 C T G G A A G G T T G C T G A C C T C T C A G G A A G a G C C A A T A C A A G T T C T G T A A T C T
\*\*\*
\*\*\*
\*\*\*
\*\*\*
\*\*\*

alignment position 151 . . . . . 161 . . . . . 171 . . . . . 181 . . . . . 191 . . . . .
P937000 22 C C T G C A C T C G G C T C A C A C T C C G C T C C C A G G A C C C C a g g t c c c t - - - - -
P937002 151 C A T G C C C a a a - - - - - C C C A C C G C A C C C A A T G G G C C
P937003 114 C C T G C C C T G T C T C C C C C T C C G C C C C C C C C C C C G C A T C C A T T G G G C C
\*\*\*
\*\*\*
\*\*\*

alignment position 201 . . . . . 211 . . . . . 221 . . . . . 231 . . . . . 241 . . . . .
P937000 66 - - - - -
P937002 181 G C T G G A G T C G G C C A G G T G T g C T C G T C T G T T C C A A G A G A T A A A G G G A T T G T
P937003 164 G C C C C C G T C G G C C A G G T G T t C T T G T C T G T T C C A A G A G A C G A A G G A A T T G T
\*\*\*
\*\*\*
\*\*\*

alignment position 251 . . . . . 261 . . . . . 271 . . . . . 281 . . . . . 291 . . . . .
P937000 66 - - - - - G C C C A G G C C A C C C T C G G G T G G G C G C G G T C C G C G G G G C T G G A C c
P937002 231 T T G C G T G C T C C A G T C C A C A A C A G G T G G G C G A C A G A T T C C A G G G C T G G T C a
P937003 214 T T G C T T G G T C T A G T C C A C A A C A G G T G G G C G A C G G A T T C C A G G G C T T G T g g
\*\*\*
\*\*\*
\*\*\*
\*\*\*

alignment position 301 . . . . . 311 . . . . . 321 . . . . . 331 . . . . . 341 . . . . .
P937000 109 c g c c c g - - - - -

```
P937002 281 g TCA TTACAC GCCGGTGCTG AAGT AACGAG GCTCTGTGTC a CCACCCTTT
P937003 264 t TCT TACAC  GTCGATGCGG AAGT AACGAG GCTCTGCGTC t CCACCCTTC
      * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * *
      * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * *
      * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * *
```

```
alignment position 3 5 1 . . . . . 3 6 1 . . . . . 3 7 1 . . . . . 3 8 1 . . . . . 3 9 1 . . . . .
P937000 115 - - - AGCCGCC CTGACCTCAG GCCTCCGACG CTCCGCGCAA GAAGa c a g a g
P937002 331 T GAAGCCAGC TTACTACTAAC AGCC TAGAc t t c c t a c c t - G GAGAGTAGTA
P937003 314 T GAAGCCATC TTGCACTAAC AGCC CAGAGA CTTCGCACGG GAAAGCGGTA
      * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * *
      * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * *
      * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * *
```

```
alignment position 4 0 1 . . . . . 4 1 1 . . . . . 4 2 1 . . . . . 4 3 1 . . . . . 4 4 1 . . . . .
P937000 162 t g c g c c c c g g c c c g c a g t c t g g g g t g t g g a c a c a c g g c c a g g a c g c g g a c
P937002 380 ACCA- - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
P937003 364 ACCA- - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
      * * * *
```

```
alignment position 4 5 1 . . . . . 4 6 1 . . . . . 4 7 1 . . . . . 4 8 1 . . . . . 4 9 1 . . . . .
P937000 212 g g c g g g g c c t c g g c a g c a g c g c g g g a a a c a g c g g a c c c c c a g c c c t g c g
P937002 384 - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
P937003 368 - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
```

```
alignment position 5 0 1 . . . . . 5 1 1 . . . . . 5 2 1 . . . . . 5 3 1 . . . . . 5 4 1 . . . . .
P937000 262 g g g a a a g g a a a c c c c c c g c c c a c t c g g c g c a g a t c c c g c c t c a c g c a g c a
P937002 384 - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
P937003 368 - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
```

```
alignment position 5 5 1 . . . . . 5 6 1 . . . . . 5 7 1 . . . . . 5 8 1 . . . . . 5 9 1 . . . . .
P937000 312 a c t g c g c a g g c g c a g c c g a t g a t c c t c c g c g c a c t c c c c a g c c t t t g t g c
P937002 384 - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
P937003 368 - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
```

```
alignment position 6 0 1 . . . . . 6 1 1 . . . . . 6 2 1 . . . . . 6 3 1 . . . . . 6 4 1 . . . . .
P937000 362 g c g t g c g c c t c a c g t g a c g t c a c c G C C G C G C G G G G C G C G C A G T C A C C C T
P937002 384 - - - - - - - - - - - - - - - - - - - G C C c c g T G G G A A C G C T C G G C T A T C C T
P937003 368 - - - - - - - - - - - - - - - - - - - G C C T C T T G G G A A C G C A C T G C T A T C C T
      * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * *
      * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * *
      * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * *
      * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * *
      * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * *
```

```
alignment position 6 5 1 . . . . . 6 6 1 . . . . . 6 7 1 . . . . . 6 8 1 . . . . . 6 9 1 . . . . .
P937000 412 T C G G T C G C C A G G G G C g c g g c c c c c g c t c t c t c g c c g c t g A C G G C G C A T
P937002 410 C C A G T C G C T A G G G G C A G C g c t t t c a C T - - - - - - - - - - - G C G G C G C A T
P937003 394 C C A G T C G C T A G G G G A A G C a t t t g c g C T - - - - - - - - - - - A C G G C G C A T
      * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * *
      * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * *
      * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * *
      * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * *
      * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * *
```



```

P937002 677 g - AG CAATC- - - - -
P937003 664 C a AG CAATC- - - - -
      * * * * *
      * * * * *
      * * * * *
      * * * * *
  
```

```

alignment position 1 0 0 1 . . . . . 1 0 1 1 . . . . . 1 0 2 1 . . . . . 1 0 3 1 . . . . . 1 0 4 1 . . . . .
P937000 735 a c c c c c a CCC CTCCTGCGAC C TCT GC CCA G CGACCCCGCC CCCCCTCC - -
P937002 685 - - - - - CCG GCCCTGCAAC C CTT GC ACA CACACCCGCC CGTACTCCCT
P937003 673 - - - - - CCC GGCCTGCAAC C CTT GC ACA CACACCCGCC a t t gCTCCCT
      * * * * *
      * * * * *
      * * * * *
      * * * * *
  
```

```

alignment position 1 0 5 1 . . . . . 1 0 6 1 . . . . . 1 0 7 1 . . . . . 1 0 8 1 . . . . . 1 0 9 1 . . . . .
P937000 783 - - - - - TCCCGCGACC C CCGTCC- CG CGAGCCCGT TTCGCGCCGc
P937002 728 C TCC CAGTAC TCCTCGATGT C CGA C C c T G CGATCCCTT GTTCCCTCGG
P937003 716 T TCC CAGTCC TCCTCCATCT C CGA C C - T G CGATCCCTT GTCCCACCGG
      * * * * *
      * * * * *
      * * * * *
  
```

```

alignment position 1 1 0 1 . . . . . 1 1 1 1 . . . . . 1 1 2 1 . . . . . 1 1 3 1 . . . . . 1 1 4 1 . . . . .
P937000 822 c t c t g a c c a a c c - - - - - TCTTTCGC AGCTCGGCCG CTACTCCGCC
P937002 778 T GTGCCTTCT ACTATAAt GT T T T C T T C T G C AGTTCGGCCG GTACTCCGCT
P937003 765 T GTT CCTTCT GCTCTAAc GT T T T G T T C T G C AGTTCGGCCG GTACTCCGCT
      * * * * *
      * * * * *
      * * * * *
      * * * * *
      * * * * *
      * * * * *
      * * * * *
      * * * * *
      * * * * *
  
```

```

alignment position 1 1 5 1 . . . . . 1 1 6 1 . . . . . 1 1 7 1 . . . . . 1 1 8 1 . . . . . 1 1 9 1 . . . . .
P937000 862 C TGT TCCTCG Gt g TGGCCTA C GGAGC CACG CGCTACAGTG AGT g a c c g c g
P937002 828 C TGA TCATCG GCATGGCATA C GGCGC C AAG CGCTACAGTG AGT TTGGGGA
P937003 815 C TGA TCCTCG GCATGGCATA C GGCGC C AAG CGCTACAGTG AGT TTGGGGA
      * * * * *
      * * * * *
      * * * * *
      * * * * *
      * * * * *
      * * * * *
      * * * * *
      * * * * *
      * * * * *
      * * * * *
  
```

```

alignment position 1 2 0 1 . . . . . 1 2 1 1 . . . . . 1 2 2 1 . . . . . 1 2 3 1 . . . . . 1 2 4 1 . . . . .
P937000 912 g g c g g g g c c g g g g c g g g g t - - - - - - - - - - - - - - - CTGCTC
P937002 878 C CGG GAGAAC GGGATTCCGG Gt g a a a g - - - - - GCTGTGT GACTACTGCTC
P937003 865 T TGG GAGGC GGGATTCCGG G g a g a g a c a c c t a GCTGTGT GACTACTGCTC
  
```

```

* * * * *
* * * * *
* * * * *
alignment position 1 2 5 1 . . . . . 1 2 6 1 . . . . . 1 2 7 1 . . . . . 1 2 8 1 . . . . . 1 2 9 1 . . . . .
P937000 937 G G c t t t c c t g t g g a g c t c c t g t - - - - - - - - - - - - - - - - - - - - - - - - - - -
P937002 922 G A G C C T G C A G T T C C T T G G G A G G G a g a t g a t g c c a g g c c c t A G A G G G G G G C
P937003 915 G G G C C A G C A C C T C C T C G G G A G G G a a a t a a t t c t a g g c c - - A G A G G G G A G C
* * * * *
* * * * *
* * * * *
alignment position 1 3 0 1 . . . . . 1 3 1 1 . . . . . 1 3 2 1 . . . . . 1 3 3 1 . . . . . 1 3 4 1 . . . . .
P937000 959 - - - - - - - - - G C T A T T T G G A G A A a c t c c a g c t c t g g a a g g g g g c t t g g g a
P937002 972 A G G T G G G A A C A G C T A T C T G G A G A T T T T G G A g t c - - - - - - - - - - - - - - - - -
P937003 963 A G G T G G G G A C A G C T A T C C G G A G A T T C T G G A g t c g g c t t t - - - - - - - - - - -
* * * * *
* * * * *
* * * * *
alignment position 1 3 5 1 . . . . . 1 3 6 1 . . . . . 1 3 7 1 . . . . . 1 3 8 1 . . . . . 1 3 9 1 . . . . .
P937000 998 c g c a t g c g a g g c t g c a g g a c c g t g t c c t c c a c c g a g c g t g a c c c c g a t a g
P937002 1005 - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
P937003 1002 - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -

alignment position 1 4 0 1 . . . . .
P937000 1048 t g g a a t c a g c
P937002 1005 - - - - - - - - -
P937003 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>P937002</b> (1004 bp)	<b>P937003</b> (1001 bp)
<b>P937000</b> (1057 bp)	0.151 25 %	0.168 33 %
<b>P937002</b> (1004 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	
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 Task: *DiAlign* TF: Multiple alignment plus TF sites  
working on C5-ATP5J (3 seq.)**

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

DiAlign professional TF Release 3.1 December 2004

Wed Jun 1 00:46:06 2005

## Solution parameters:

**Sequence file:** [C5-ATP5J](#) (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)  
**Selected groups** (core/matrix sim):

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

## Aligned Sequences:

No.	Sequence Name	Sequence Description	Len
1	P977923	P977923 sym=ATP5J loc=Loc522 taxid=9606 spec=Homo sapiens chr=21 ctg=NT_011512 str=(-) start=12769355 end=12770355 len=1001 tss=501 comm=ATP synthase, H+ transporting, mitochondrial F0 complex, subunit F6; (NM_001685/544/silver;)	100
2	P977924	P977924 sym=Atp5j loc=Loc11957 taxid=10090 spec=Mus musculus chr=16 ctg=NT_039625 str=(-) start=19651782 end=19652782 len=1001 tss=501 comm=ATP synthase, H+ transporting, mitochondrial F0 complex, subunit F; (NM_016755/596/silver;)	100
3	P977926	P977926 sym=Atp5j loc=Loc94271 taxid=10116 spec=Rattus norvegicus chr=11 ctg=NW_047354 str=(-) start=24323700 end=24324800 len=1101 tss=1001 comm=ATP synthase, H+ transporting, mitochondrial F0 complex, subunit F6; (NM_053602/1194/silver;)	110

## 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\$MAZF
V\$SPIF
V\$ZBPF
V\$PLAG
V\$PAX8
V\$SNAP
V\$CLOX
V\$SETF
V\$FKHD
V\$AP2F
V\$AHRR





**P977923** 350 CGGTCCCCCG GGGCTCCAGG CCgctcg - - - - -  
**P977924** 238 CGCTCGGCCA GCGCGCCGAG CCTGGACCGc gcccgt GC GA CGGGCGACTC  
**P977926** 141 CGCACCGTCA GCGCGCAGAG CCTGGACCGt gcccgtg - GC GA CGGGCGACTC  
 \* \* \* \* \*  
 \* \* \* \* \*

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

**P977923** 377 - - - - - CCCC CCGCCCTCC  
**P977924** 288 CGCCGCGTCC CGCAACGCGG CCGgGGCCAC GCCGCTC CCG CGCCCTCC  
**P977926** 190 CGCAGCGTCC CGCAGC GCGG CCGcGGCCAC GCCGCTT CCG CGCCCTCC  
 \* \* \* \* \*  
 \* \* \* \* \*  
 \* \* \* \* \*

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

**P977923** 391 CCTTCGCTCC CCGCACAG- C TCTCCGCCC CTCCCACCC GGCTCCCTCA  
**P977924** 338 CCTCGGCTTC CCGCACAGCC TCTCCGCCC CTCCCACCA GGCTCCCTCA  
**P977926** 240 CCTCGGCTTC CCGCACAGCC TCTCCGCCC CTCCCACCC GGCTCCCTCA  
 \* \* \* \* \*  
 \* \* \* \* \*  
 \* \* \* \* \*  
 \* \* \* \* \*  
 \* \* \* \* \*  
 \* \* \* \* \*

alignment position 5 0 1 . . . . . 5 1 1 . . . . . 5 2 1 . . . . . 5 3 1 . . . . . 5 4 1 . . . . .

**P977923** 440 AGTCTCCACG AACGGAAATG GGAGTCACAG CGCCGGGGA- CCAGCGGAA  
**P977924** 388 AGTCTCCACG AACGGAAATG GGAGTCGCAG CGCCGGGGAc CCAGCGGAA  
**P977926** 290 AGTCTCCACG AACGGAAATG GGAGTCACAG CGCCGGGGA- CCAGCGGAA  
 \* \* \* \* \*  
 \* \* \* \* \*  
 \* \* \* \* \*  
 \* \* \* \* \*  
 \* \* \* \* \*  
 \* \* \* \* \*  
 \* \* \* \* \*  
 \* \* \* \* \*

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

**P977923** 489 CAAAAACAG AGGCGGC CGC GGGGGGGCc c t t g t g g GGGA AAA GGCCCC  
**P977924** 438 CAAAAACAG AGGCGGC CGC GGGGGGGg a c - - - - - - - - - - AAGCCCC  
**P977926** 339 CAAAAACAG AGGCGGC CGC GGGGGGGCt g c g g c - - GGGG GAA AAGCCCC

```
* * * * *
* * * * *
* * * * *
* * * * *
* * * * *
* * * * *
* * * * *
* * * * *
```

alignment position 60 1 . . . . . 61 1 . . . . . 62 1 . . . . . 63 1 . . . . . 64 1 . . . . .

```
P977923 539 GAACGAGGCC GGC CCGCGAG GGCCCGCGCT CCCCTCTCC CCGg c g GCCC
P977924 476 GAACCAGGCC G- CCGCGCG GGCCCGCGCT CCCCGCCAGC CCGCG- TCCC
P977926 387 GAACCAGGCC GG- CCGCGCG GGCCCGCGCT CCCCGCCAGC CCGCA- GCCC
* * * * *
* * * * *
* * * * *
```

alignment position 65 1 . . . . . 66 1 . . . . . 67 1 . . . . . 68 1 . . . . . 69 1 . . . . .

```
P977923 589 CA- CTCACC CACTCCGGAAT CGGCCCTGT C GCCCCGCCC GCaC- TCCAC
P977924 524 CAa CTCACC A GCTCCGGAAT TCGTCCCGT G GCCCTAGCCC GCGc t TCCAC
P977926 435 CA- CTCACC A GCTCCGGAAT CCGGCCCGT G GCCCTCGCCC GCGC- TCCAC
* * * * *
* * * * *
* * * * *
```

alignment position 70 1 . . . . . 71 1 . . . . . 72 1 . . . . . 73 1 . . . . . 74 1 . . . . .

```
P977923 637 AGCCGGCT GA GAACGGCAGC GGCGAGGGCT CCAc g t g CAG CGTCTCTCC
P977924 574 AGCCGGCT GG GAACGGCGGC GGCGCGGGCT CCAGGTACAG CGCTCTCTCC
P977926 483 AGCCGGCT GG GAACGGCGGC GGCGCGGGCT CCAGGTACAG CGTCTCTCTC
* * * * *
* * * * *
* * * * *
```

alignment position 75 1 . . . . . 76 1 . . . . . 77 1 . . . . . 78 1 . . . . . 79 1 . . . . .

```
P977923 687 GGTAAGACCT GCAGCTCCCG C GACTAGa AG TGTGAGGTCC CAGGGCCCTT
P977924 624 GGCGAGCCGC GCCGCTCCCG C GAGTAGCAG GGTAAAGTCC CGGGGCCCTT
P977926 533 GGTAAGACGC GCCGGTCCCG C GAGTAGCAG TGTGAGGCC CGGGGCCCTT
* * * * *
* * * * *
* * * * *
```



\*\*\*\*\*

```

alignment
position      1 0 5 1 . . . . . 1 0 6 1 . . . . . 1 0 7 1 . . . . . 1 0 8 1 . . . . . 1 0 9 1 . . . . .
P977923 959 CT CGGAGGGG AGC TTGAACT AGGGGAAAGG CCA c t c a a a g a g c - - - - -
P977924 914 CT CCGAAGGG AGC TTGAACT AGGGGACAGG CCA g a a t ACG CATGCGTAC A
P977926 794 CT CCGTAGGG AGC TTGAATT AGGGGACAGG CCA a a g c ACG CATGCGTAC A
* * * * *
* * * * *
* * * * *
* * * * *
* * * * *
* * * * *
* * * * *
* * * * *

```

```

alignment
position      1 1 0 1 . . . . . 1 1 1 1 . . . . . 1 1 2 1 . . . . . 1 1 3 1 . . . . . 1 1 4 1 . . . . .
P977923 1002 - - - - -
P977924 964 GT GCAGT GTc T CC AAGAGGG AAAAGGGGGT GAAGT TAA - - - - -
P977926 844 GT GCAGT GTt T CC AAGAGGG AAAAGAGGGT GAAGT TAAgt g t a g g a a g a
* * * * *
* * * * *

```

```

alignment
position      1 1 5 1 . . . . . 1 1 6 1 . . . . . 1 1 7 1 . . . . . 1 1 8 1 . . . . . 1 1 9 1 . . . . .
P977923 1002 - - - - -
P977924 1002 - - - - -
P977926 894 t g g c g g a g t c t t a g c t g a g g g a c c c g g a a g c a c t t a c c c t c c a c t t c c t c

```

```

alignment
position      1 2 0 1 . . . . . 1 2 1 1 . . . . . 1 2 2 1 . . . . . 1 2 3 1 . . . . . 1 2 4 1 . . . . .
P977923 1002 - - - - -
P977924 1002 - - - - -
P977926 944 c t c c t g t t t g g c t t c t g t c t c a c c t a g a g g c g t c c g g t c g c a g a c t c t c t

```

```

alignment
position      1 2 5 1 . . . . . 1 2 6 1 . . . . . 1 2 7 1 . . . . . 1 2 8 1 . . . . . 1 2 9 1 . . . . .
P977923 1002 - - - - -
P977924 1002 - - - - -
P977926 994 t c g a g g c g c t t c c t g t c c g g t g a g c g t c g a a c g a c t g a a g c g g t g g c c c a

```

```

alignment
position      1 3 0 1 . . . . . 1 3 1 1 . . . . . 1 3 2 1 . . . . . 1 3 3 1 . . . . . 1 3 4 1 . . . . .
P977923 1002 - - - - -
P977924 1002 - - - - -
P977926 1044 t a g t g c a t t g c g a t g g c g g g t a g g c g t g t g t a g g c g g a g c c a g g g c c g g a

```

```

alignment
position      1 3 5 1 . . . .
P977923 1002 - - - - -
P977924 1002 - - - - -
P977926 1094 a g t a g a 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>P977924</b> (1001 bp)	<b>P977926</b> (1101 bp)
<b>P977923</b> (1001 bp)	0.487 52 %	0.577 55 %
<b>P977924</b> (1001 bp)		<u>1.000</u> <u>76 %</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	

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**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

Wed Jun 1 22:45:23 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)  
**Selected groups** (core/matrix sim):

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

## Aligned Sequences:

No.	Sequence Name	Sequence Description	Length
1	P848677	sym=ATP5L loc=Loc10632 taxid=9606 spec=Homo sapiens chr=11  ctg=NT_033899 str=(+) start=21834233 end=21835233 len=1001  tss=501  comm=ATP synthase, H+ transporting, mitochondrial F0 complex, subunit g; (NM_006476/501/bronze;)	1001 bp
2	P848678	sym=Atp5l loc=Loc27425 taxid=10090 spec=Mus musculus chr=9  ctg=NT_039473 str=(-) start=4369214 end=4370255 len=1042  tss=501,502,507,510,511,513,516,517,520,527,532,535,542  comm=ATP synthase, H+ transporting, mitochondrial F0 complex, subunit g; (AK008321/510/gold;AK008251/516/gold;AK019320/514/gold; AK011046/538/gold;AK011038/538/gold;AK008183/516/gold; AK008087/530/gold;AK008169/505/gold;AK009612/523/gold; AK019252/516/gold;AK019350/516/gold;AK019343/545/gold; AK009471/516/gold;AK019192/516/gold;AK008002/545/gold; AK019274/516/gold;AK005321/505/gold;AK019355/516/gold; AK009465/516/gold;AK009806/516/gold;AK008012/519/gold; AK009468/516/gold;AK011099/513/gold;AK008030/519/gold; AK005175/535/gold;AK011842/545/gold;AK008036/505/gold; AK005380/504/gold;NM_013795/520/bronze;)	1042 bp



**P848679** 162 CCTCGATTTTC C - - - At a TT TTCTGAAAAG CTACGAAACT GCCGCAAGCT  
 \* \* \* \* \*  
 \* \* \* \* \*  
 \* \* \* \* \*  
 \* \* \* \* \*

alignment position 251 . . . . . 261 . . . . . 271 . . . . . 281 . . . . . 291 . . . . .

**P848677** 202 AA a t a g c g g a g g t c g g c GCC AAGAAAAGCA CTGc a g g t t c a g g g CGCATG  
**P848678** 206 AATGTGGc GA TCAA- - GCC AAGAAAACCA ATAA- - - - - - - - CGCATG  
**P848679** 208 AATGTGGa GA TGAA- - GCA AAGAAAATCA ATGA- - - - - - - - CGCATG  
 \* \* \* \* \*  
 \* \* \* \* \*  
 \* \* \* \* \*

alignment position 301 . . . . . 311 . . . . . 321 . . . . . 331 . . . . . 341 . . . . .

**P848677** 252 CGCATT T - CC g c t c c t t g c c g g t t TTCCGG ACCT CTACGA GTGGCTGCC  
**P848678** 243 CGCATT T c CC CCACT TC ACC GATCTTCCGG ACCA ACATGA ATAGCTGTCC  
**P848679** 245 CGCATT T - CC CCACT TC AAC GATCTTCCGG CCCA CCATGA ATAGCTGTCC  
 \* \* \* \* \*  
 \* \* \* \* \*  
 \* \* \* \* \*  
 \* \* \* \* \*

alignment position 351 . . . . . 361 . . . . . 371 . . . . . 381 . . . . . 391 . . . . .

**P848677** 301 CACAAAATGC CTGCt TCTCT GCGGAATCCT ACTGTTCTTC ACATGCTCTC  
**P848678** 293 CAAGT AATGC CTGC- TCCT GAGGAATCTC AGGATTCTTC ACGTGT TATC  
**P848679** 294 CAAGT TATGC CTGG- TTCT GAGGAATCTC GTTATTCTCC ACGTGT TATC  
 \* \* \* \* \*  
 \* \* \* \* \*  
 \* \* \* \* \*  
 \* \* \* \* \*

alignment position 401 . . . . . 411 . . . . . 421 . . . . . 431 . . . . . 441 . . . . .

**P848677** 351 T a a t a c c a t c - TT- TTCATA TCCACTTTCT CTTC CATGTT GAAAAATTAA  
**P848678** 342 GC GCC TCATT T Tt t TTTATA TCTAGGTTTT TACTTGg a g T GAACAAAGTA  
**P848679** 343 TT GCC TCATT TTA- TTTATA TCTACGTTTT TACTTGTGCT GAACAAAGTA  
 \* \* \* \* \*  
 \* \* \* \* \*  
 \* \* \* \* \*

alignment position 451 . . . . . 461 . . . . . 471 . . . . . 481 . . . . . 491 . . . . .

**P848677** 399 AT t g a c a g g c t g g a t t c t g c a a a g a t c t t t g g a c a t t t a a g t a t c t t c g -  
**P848678** 392 AACTGACTAA TGAGATGCCA CAAACA g GGA ATCAATACCT ATATGT TTTG  
**P848679** 392 ATCTGACTAA TGAGATGCCA CAAACA c GGA AGCAATGCCT ATATAT TTTG  
 \* \* \* \* \*  
 \* \* \* \* \*  
 \* \* \* \* \*





		* *							
alignment position	701	...	711	...	721	...	731	...	741
<b>P848677</b>	646	g c a c a c g g g c	g g c a g g g a g g	c c t g c g a t g g	C C T G A G A G G A	A G A A G C G G G C			
<b>P848678</b>	634	- - - - -	- - - - -	- - - - -	C G C G A G G G G A	G G G A T T G T G C			
<b>P848679</b>	633	- - - - -	- - - - -	- - - - -	C G T G A G G G G A	A G G A G T G T G C			
					* * * * *	* * * * *			
					* * * * *	* * * * *			
					* * * * *	* * * * *			
					* * * * *	* * * * *			
alignment position	751	...	761	...	771	...	781	...	791
<b>P848677</b>	696	T G C G a a g a c C	C G A G G G G C C T	G C G G G T G C C G	G G G C G G g a t g	g c c t g c a g g t			
<b>P848678</b>	654	T G C G G C A - - C	C A A G G G G C C g	t - G G G C G T C G	G G A G G G C t t C	C A G G A G G C C A			
<b>P848679</b>	653	T G C G G C A - - C	C A A G G G G C C C	G C G G G C G T C G	G G A G G G C c a C	C A G G A G G C A A			
		* * * * *	* * * * *	* * * * *	* * * * *	* * * * *			
		* * * * *	* * * * *	* * * * *	* * * * *	* * * * *			
		* * * * *	* * * * *	* * * * *	* * * * *	* * * * *			
		* * * * *	* * * * *	* * * * *	* * * * *	* * * * *			
alignment position	801	...	811	...	821	...	831	...	841
<b>P848677</b>	746	g g a g g g a g c a	g g a a g c a g g t	t g g c g a c t c t	t t t c t a g c c t	t c c a C T C G T C			
<b>P848678</b>	701	C T G T A A G G C C	G C A G C - - - -	- - - - -	- - - - -	- - - - C T C G C C			
<b>P848679</b>	701	C T G C A A A G C C	C C A G T - - - -	- - - - -	- - - - -	- - - - C T C G C C			
		* * * * *	* * * * *			* * * * *			
		* * * * *	* * * * *			* * * * *			
		* * * * *	* * * * *			* * * * *			
alignment position	851	...	861	...	871	...	881	...	891
<b>P848677</b>	796	T G A C C T G C a g	a t t g g g t t c t	c t a c A C A A C C	T A G A A G T T C C	T G A A T T C T A A			
<b>P848678</b>	722	T G G C C T G C c c	g c G G C T G C T T	- - - - A G A G C T	C A C A A G C T G C	A G G G T C C T A G			
<b>P848679</b>	722	T G G C C T G t c c	c t G G C T G C C T	- - - - A G G G C G	C A C A A G C T G T	T G G G C C C T A A			
		* * * * *	* * * * *	* * * * *	* * * * *	* * * * *			
		* * * * *	* * * * *	* * * * *	* * * * *	* * * * *			
		* * * * *	* * * * *	* * * * *	* * * * *	* * * * *			
alignment position	901	...	911	...	921	...	931	...	941
<b>P848677</b>	846	C C A C G A C T G G	G A A G A G A - - G	G T A G T G T G a a	g g a a G C C C G G	C G T T G C C C G G			
<b>P848678</b>	768	C T C G G C C G G G	G A g c g a g t g G	G T C G T G T a a c	t c - T G C C C G G	C C T C A C T C C G			
<b>P848679</b>	768	C C G G G C C T G T	T A A G T G T - - G	G T C G T G T G g t	t t t T G C C C G G	C C T C A C T C C G			
		* * * * *	* * * * *	* * * * *	* * * * *	* * * * *			
		* * * * *			* * * * *	* * * * *			
					* * * * *	* * * * *			
					* * * * *	* * * * *			
alignment position	951	...	961	...	971	...	981	...	991
<b>P848677</b>	894	C A G C T G C A A C	C A T T A C G C C C	C C T G a g a t c g	c t a a g a g c a g	g g a t c t a g a g			
<b>P848678</b>	817	C C G C G A A C G C	C G T G A T G C C C	C C T T A C C G T G	C C G - - - - -	- - - - -			
<b>P848679</b>	816	C C G C G A A C G C	C A T G A C G C C C	C C T T A C C G T G	C C G - - - - -	- - - - -			
		* * * * *	* * * * *	* * * * *	* * * * *	* * * * *			
		* * * * *	* * * * *	* * * * *	* * * * *	* * * * *			
		* * * * *	* * * * *	* * * * *	* * * * *	* * * * *			

```

*****
alignment
position    1 0 0 1 . . . . . 1 0 1 1 . . . . . 1 0 2 1 . . . . . 1 0 3 1 . . . . . 1 0 4 1 . . . . .
P848677 944 g g g a t g g t t c t g t t a GGAGA GCT AAG AAAA GGAA Gg g - - - - -
P848678 850 - - - - - GGAGA GTT GGG AAGG Ga g g t - - - C GGT AAC AGGG
P848679 849 - - - - - GGAGA TCT AGG AAGG GGAG Ga c g a C GGT AAC AGGG
          * * * * *
          * * * * *
          * * * * *

alignment
position    1 0 5 1 . . . . . 1 0 6 1 . . . . . 1 0 7 1 . . . . . 1 0 8 1 . . . . . 1 0 9 1 . . . . .
P848677 981 - - - - -
P848678 881 GAGAG a g a g G T CACAC ATCA GAC CTC ATAG CTGGTCT GCG TCT CAGCG Aa
P848679 884 GAGAG - - - G T CACAC ATCA GAC CTT ATAG CTGATCT GGG TCT CAGTG Aa
          * * * * *
          * * * * *
          * * * * *
          * * * * *

alignment
position    1 1 0 1 . . . . . 1 1 1 1 . . . . . 1 1 2 1 . . . . . 1 1 3 1 . . . . . 1 1 4 1 . . . . .
P848677 981 - - - - - CAGA AAC GTG AAA- - - - - GTAA
P848678 931 g t a - TTT GAA AGCCATC AGA AATTTT AAAG a c g g g t g a g a g a t c t t TGAA
P848679 930 g t t g TTAGAA AGTCACC AGA AATTTT AAA- - - - - TGAA
          * * * * *
          * * * * *
          * * * * *
          * * * * *

alignment
position    1 1 5 1 . . . . . 1 1 6 1 . . . . . 1 1 7 1 . . . . . 1 1 8 1 . . . . . 1 1 9 1 . . . . .
P848677 998 A t c a - - - - -
P848678 980 AGTTATGTTT GCTTACC ATC CTGGTTAGAG CCTAGAG a a t t c t g c g t c c g
P848679 963 AGTTATGTTT GCTTACC ATC CTGGTCAGAT GCTAGAG a a - - - - -
          * * * * *
          * * * * *
          * * * * *
          * * * * *

alignment
position    1 2 0 1 . . . . . 1 2 1 1
P848677 1002 - - - - -
P848678 1030 a t g a a g g g a a t t t
P848679 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>P848678</b>	<b>P848679</b>
	<b>(1042 bp)</b>	<b>(1001 bp)</b>

<b>P848677</b> (1001 bp)	0.175 42 %	0.166 42 %
<b>P848678</b> (1042 bp)		<u>1.000</u> <u>84 %</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

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**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**

**Wed Jun 1 23:14:51 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)  
**Selected groups** (core/matrix sim):

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

## Aligned Sequences:

No.	Sequence Name	Sequence Description	Length
1	P978665	sym=ATP5O loc=Loc539 taxid=9606 spec=Homo sapiens chr=21 ctg=NT_011512 str=(-) start=20948942 end=20950528 len=1587  tss=501,587  comm=ATP synthase, H+ transporting, mitochondrial F1 complex, O subunit (oligomycin sensitivity conferring protein); (AK124187/587/gold;NM_001697/501/silver;)	1587 bp
2	P978667	sym=Atp5o loc=Loc28080 taxid=10090 spec=Mus musculus chr=16 ctg=NT_039625 str=(-) start=26829146 end=26830647 len=1502  tss=501,502  comm=ATP synthase, H+ transporting, mitochondrial F1 complex, O subunit; (AK005309/520/gold;NM_138597/519/bronze;)	1502 bp
3	P978669	sym=Atp5o loc=Loc192241 taxid=10116 spec=Rattus norvegicus chr=11 ctg=NW_047354 str=(-) start=31958531 end=31960031  len=1501 tss=501  comm=ATP synthase, H+ transporting, mitochondrial F1 complex, O subunit (oligomycin sensitivity conferring protein); (NM_138883/585/bronze;)	1501 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.



```
*****
*****
*****
*****
alignment
position      3 5 1 . . . . . 3 6 1 . . . . . 3 7 1 . . . . . 3 8 1 . . . . . 3 9 1 . . . . .
P978665 242 G C C A G T G A C G C T G G T A A T A A C T G T G A A A T G g a a c a a a t g c c a c c a t a t t t
P978667 308 G T C A A C G A T G T T G A C G A T G C A T g T G C A A A G A - - - - - - - - - - - - - - - - - -
P978669 237 G G C A G A G A T G T T G A C G A T G C A T A T G C A A A G A - - - - - - - - - - - - - - - - - -
*****
*****
*****
alignment
position      4 0 1 . . . . . 4 1 1 . . . . . 4 2 1 . . . . . 4 3 1 . . . . . 4 4 1 . . . . .
P978665 292 A T C T A A A T G T A A A t t t t a a a a c t g g g g a c a g c a a a t c c a t t c t a c a g t g a
P978667 339 G T T T A A A T C T A A A C C T A A T T T C A - - - - - - - - - - - - - - - - - - - - - - - -
P978669 268 A T C T A A A T G T A A A C C T A G T T T C A - - - - - - - - - - - - - - - - - - - - - - - -
*****
*****
*****
alignment
position      4 5 1 . . . . . 4 6 1 . . . . . 4 7 1 . . . . . 4 8 1 . . . . . 4 9 1 . . . . .
P978665 342 g c g c c g c t t g g c c a g t a a c a a t G A C T T C A T T T - - - - T C a g a t g c a g t c g
P978667 362 - - - - - - - - - - - - - - - - - - - - G A C T T A A T T T - - - - T C - - - - - - - - - - - -
P978669 291 - - - - - - - - - - - - - - - - - - - - G A T T T A A T T t t c c g a T C - - - - - - - - - - - -
*****
*****
*****
alignment
position      5 0 1 . . . . . 5 1 1 . . . . . 5 2 1 . . . . . 5 3 1 . . . . . 5 4 1 . . . . .
P978665 387 a a g c c c t g T G G C T C C A C C C C G A G G G T C C A G C C c t t a c c a c t g - - C T A A G A
P978667 374 - - - - - - T G G T T C C G G T T C A C G A G T C C A G C C G G A C C G C G G C A g g t a c G C
P978669 308 - - - - - - T T G T T C G G G T T C A A G A G T C T A G C G G G A C C A C G G C A c C T A T G C
*****
*****
*****
*****
*****
alignment
position      5 5 1 . . . . . 5 6 1 . . . . . 5 7 1 . . . . . 5 8 1 . . . . . 5 9 1 . . . . .
P978665 435 A C T A C A A C T C C C A G C C C G A G G G A G G T c t c t g c g c c t g c g g c c t g a c g c c c
P978667 416 A C T A C A A C T C C C A G C A T G C A A G A G G T T C T T A C C C A C A C t c c c g G G C T C C T
P978669 350 A C T A C A A C T C C C A G C G T G C A A G A G G T T C T T A C C C A C A C g c c c c G G C T C C T
*****
*****
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*****
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*****
*****
alignment
position      6 0 1 . . . . . 6 1 1 . . . . . 6 2 1 . . . . . 6 3 1 . . . . . 6 4 1 . . . . .
```

**P978665** 485 t A C G C C T A C A **CTTCCCAGAG** **AACTAGCGG** **TTACGC** **CAA-** **CGCGCGCGT**  
**P978667** 466 G A C G C G T A C A **TTTCCCAGAA** **AGCCGAGCGA** **TCACGC** t g g c g **CGCGCGCGT**  
**P978669** 400 G G T G C G T T C A **TTTCCCAGAA** **AACCGAGCGA** **TCACGCCG** A - **CGCGCGCA T**

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\* \* \* \* \*  
\* \* \* \* \*

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

**P978665** 533 **GCGCCCT** T G C G C g t t t c - T C T C T T C C C A C T **CGGGTTTGAC** **CTACAGCC** G C  
**P978667** 516 **GCGCTCT** G G C G C C A G T A G T C T C T T T T C A T **TGGGTTTGAC** **CTACAGCC** G C  
**P978669** 448 **GCGCTCT** G G C A T C A C T A G T C T C T T - - - A C T **TGGGTTTGAC** **CTACAGCT** G C

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\* \* \* \* \*  
\* \* \* \* \*

alignment position 7 0 1 . . . . . 7 1 1 . . . . . 7 2 1 . . . . . 7 3 1 . . . . . 7 4 1 . . . . .

**P978665** 582 **CCGGGAGAAG** **ATGGCTGCC** C A G C A G T G T C C G G G C T C T C C C G G C A G G T g a  
**P978667** 566 **CCGGGAAAAG** **ATGGCCGCG** C T G C A G C G T C C G G A C T G T C T C G A C A G G T A C  
**P978669** 495 **CCGGGAAAAG** **ATGGCCGCA** C A G C A A C A T C C G T G C T G T C C C G A C A G G T A C

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\* \* \* \* \*  
\* \* \* \* \*

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

**P978665** 632 g a g a a a g g t g g t c c t g a g a g c c a **GTGGGAG** **GATCCCTC** C T G G G A T G A C C C  
**P978667** 616 A A G C T G - - - - - - - - - - - - - - **GCGGGAG** **GCTCCCTC** C C A G G G T T G C G C  
**P978669** 545 A A G C T G a - - - - - - - - - - - - - - **CGGGAG** **GGTCCCTC** C T G G G G T T C C C C

\* \* \* \* \*  
\* \* \* \* \*

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

**P978665** 682 G T A C C a a a c c t c g a g c a c C A G G G T G C G A T G C T T C G G C T G G G G a a g t c t g g  
**P978667** 649 G T C C C C G G C T C C C A t C G - C C G C G T G T G A G G C C G T G G C T G A G G G G T C A G G C  
**P978669** 578 G T C C C C G A C T C C C A g C G - C T G C G T G T G A G G C T G T G G C T G A G G G G T C A A G C



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alignment
position      8 5 1 . . . . . 8 6 1 . . . . . 8 7 1 . . . . . 8 8 1 . . . . . 8 9 1 . . . . .
P978665 732 c a g t c t t - CA AGGTTATGGG ACCTGGCGAG TGg g a g c g a c t c a g g a c g a c
P978667 698 AGCCCg c CCA GGGTCGTGGG GCCCGGCGAC TG- - - - - - - - - - - - - - - - - -
P978669 627 CGCCC a - CCA GGGTCGTGGG GCCCGGCCAT Tt - - - - - - - - - - - - - - - - - -
* * * * *
* * * * *
* * * * *

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```

alignment
position      9 0 1 . . . . . 9 1 1 . . . . . 9 2 1 . . . . . 9 3 1 . . . . . 9 4 1 . . . . .
P978665 781 c c a g c g t t t g t c c c c c g g g a t g c c t a c g g g g CAGTAGGCG CGGGGCTGc g
P978667 730 - - - - - - - - - - - - - - - - - - - - - - - - - - - CAGGCAGCG TGGGGC GGAT
P978669 658 - - - - - - - - - - - - - - - - - - - - - - - - - - - CAGGAAGCG TGGGGCTGAT
* * * * *
* * * * *

```

```

alignment
position      9 5 1 . . . . . 9 6 1 . . . . . 9 7 1 . . . . . 9 8 1 . . . . . 9 9 1 . . . . .
P978665 831 c g t g c c g t a a c c t t g g c g t c t t c c g a g c a c a g c c c c t g g a a g c t g c t a g c
P978667 749 CCGCGTTTCG TCCCC- GT- - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
P978669 677 TCGCGTTTTT TCCCCc GT- - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
* * * * *
* * * * *
* *
* *

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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 . . . . .
P978665 881 c t g a g g g c g c g c a g g a g a g g g g g t c t g c c c t t c g c t g a a t t c c GGGGAAGC
P978667 766 - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
P978669 695 - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
* * * * *
* * * * *
* * * * *

```

```

alignment
position     1 0 5 1 . . . . . 1 0 6 1 . . . . . 1 0 7 1 . . . . . 1 0 8 1 . . . . . 1 0 9 1 . . . . .
P978665 931 GGCATGGACT a g c c c c a a a t c a g c t t - - - - - - - - - - - - - - - - - - - - - - - -
P978667 774 GGCACGGATT TCTCTGTCCT GACCTTGACA t c c a g g a c t c a c TGCATAGC
P978669 703 GGCACGAATT GCGCTATCTT GACCTTGACA t c c a a g a g t c g a TGCATAGC
* * * * *
* * * * *
* * * * *
* * * * *

```

```

alignment
position     1 1 0 1 . . . . . 1 1 1 1 . . . . . 1 1 2 1 . . . . . 1 1 3 1 . . . . . 1 1 4 1 . . . . .
P978665 958 - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
P978667 824 GGAGCAGCTG GCAAGGGC AT GGGAGAGAGc a c TGGGGAGA GTACATGCC T
P978669 753 TGAGCAGCTG GCAAAA GC AT GGGAGAGAGa a t TGGGGAAA GCACACGTCT

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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 . . . . .
P978665 963 G CCATTGTGG TAAAACCTGT CAGAGATCAC T t a c t a g t a a t g c t a a g GA A
P978667 874 GT CCTTGCTG GTAAAACCTa - - AGGGCTGCC TGCTGCTT a g g a t t - TTGAC
P978669 803 AG CCTTGTTG GTAAAACCTG C CAGGGCTAGC TGCTGCTT g g c a g t a TTGAC
* * * * *
* * * * *

```

```

alignment
position    1 2 0 1 . . . . . 1 2 1 1 . . . . . 1 2 2 1 . . . . . 1 2 3 1 . . . . . 1 2 4 1 . . . . .
P978665 1013 TATTTGTAAA ACACAT TTCA CAGTTTTATA AATAAa a t g a g g c c g a a a a g
P978667 921 TGTTGGAAAA GCGCAT CCCC TGTGTTTATA AAGAA g g g g g g a AAGGGCTA A
P978669 853 TGTTTCGTAAA GCGCAT TCCA TGTGTTTATA AAGAA g g a a g a AAGGGTTA 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 . . . . .
P978665 1063 t t t a a a t g a g TCTTTGGCTG c t CAGTCAGT AAGTGGTAGA A - - TTGa g a
P978667 971 AC g t CTCC - - CCTTTGGCTG G- CAGCTGGT GAGTGATG g c g a g c TTGCA A
P978669 903 AC - - CTCT - - TCTTTGGCTG G- CAGCCAGT AAGTGGTGAG A - - TTGCA A
* * * * *
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* * * * *

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alignment
position    1 3 0 1 . . . . . 1 3 1 1 . . . . . 1 3 2 1 . . . . . 1 3 3 1 . . . . . 1 3 4 1 . . . . .
P978665 1110 t t t g a a c c c a c g g a a t c a c c c a g a a g a t c g a g t t t g a a a a a a t g t t a t g c
P978667 1018 CAGGCCAAGT CCAGCAGAAC CTGGAATTGG GTGGa a a a a a a t a c g t g c c t
P978669 945 CGGGCCAAGT CCAGCAGAAA CTGGAATTGG GTGGa - - - - - - - - - - - - - - - - - - - - - - -
* * * * *
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* * * * *

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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 . . . . .
P978665 1160 t g t t t g t g c t g c a t c t c a c c a t g g t g c t t t a c a t a t c a t g a c c c c t t c c t
P978667 1068 g g g TCATCTG CCATGATAAT TT T g t a t c g a c a g c c g t c a t g g t t t t c a t c
P978669 980 - - - TCATCTG CCCTGATGAT TT T a a t t t - - - - - - - - - - - - - - - - - - - - - - -
* * * * *
* * * * *

```

```

alignment
position    1 4 0 1 . . . . . 1 4 1 1 . . . . . 1 4 2 1 . . . . . 1 4 3 1 . . . . . 1 4 4 1 . . . . .
P978665 1210 g g c a t c t t a g GTAATTTTTT CATAA g c a t t - - - - - - - - - - - - - - - - - - - - - - -
P978667 1118 t g c a c c a t a - - - - - - - - - - CAGAATTATT ACTAAGGC GT TAGAAAGt TT
P978669 1005 - - - - - - - - - - G T A C T T A A T T C A T A A T T T T T A T C A A G G C C T G A G A A A G C T T

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* * * * *
alignment
position      1 4 5 1 . . . . . 1 4 6 1 . . . . . 1 4 7 1 . . . . . 1 4 8 1 . . . . . 1 4 9 1 . . . . .
P978665 1247 CT T A A T C C T C A C A A G C A G T T T T G A T A A A A C A C G T T C C A t a g c t g g a g t a t
P978667 1157 T T T A A C C C T C A T A G C C A G T T C C A A T C G A G T A C A T T C T A g t C T A G A G A G A C
P978669 1045 T T T A A C C C T C A T A G C C A G T T C T A G T C G A G T A C A c c - - - - C T A G A G A T G C
* * * * *
* * * * *
* * * * *
* * * * *
alignment
position      1 5 0 1 . . . . . 1 5 1 1 . . . . . 1 5 2 1 . . . . . 1 5 3 1 . . . . . 1 5 4 1 . . . . .
P978665 1297 t t g a a g g t g a c c t g t g a t C T G T G A C C T G T G C G C T T G C A - G G T G A T T T T T A
P978667 1207 T A G T A T A t G A - - - - - C T G T G A C C T G T G C C C T C G C A A A A C G C T T T T T A
P978669 1090 G A G T A T A - G A - - - - - C A G T G A C C T G T G C C C T T G A G A G G T G C T T T T T A
* * * * *
* * * * *
* * * * *
* * * * *
alignment
position      1 5 5 1 . . . . . 1 5 6 1 . . . . . 1 5 7 1 . . . . . 1 5 8 1 . . . . . 1 5 9 1 . . . . .
P978665 1346 A A C T G t g t a t t c c a g c t c t g t c t t t t g a t g g g c a g g a t a g t g t c t c t c a g
P978667 1249 A A C T G g A T T C C - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
P978669 1131 A A t g g c A T T C C - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
* * * * *
* * * * *
* * * * *
* * * * *
alignment
position      1 6 0 1 . . . . . 1 6 1 1 . . . . . 1 6 2 1 . . . . . 1 6 3 1 . . . . . 1 6 4 1 . . . . .
P978665 1396 a a c t a A G G C T T C T t g t c a g a t c a a a c t c t g c g g c a g t a c t c a a a a - - - -
P978667 1260 - - - - A G G C T G C T C C A G T G A C A G A C A C A G T G C C T G a a g c c t g G T G C T G T A
P978669 1142 - - - - A G G C T T C T C C A G T G A C A G A C T C A G T G C C T G - - - - - - G T G C T A T A
* * * * *
* * * * *
* * * * *
* * * * *
alignment
position      1 6 5 1 . . . . . 1 6 6 1 . . . . . 1 6 7 1 . . . . . 1 6 8 1 . . . . . 1 6 9 1 . . . . .
P978665 1441 - - A A T T C A T C T T T A T T T T C A G A T A G C A T T T G C A T T C C g a g g a g g g t a c g t
P978667 1305 T C A A G A G A T C T T T G G T C T T A G A T A G C A T T T C A G T T C C T A A G C A A G T A G G T
P978669 1180 T G A A A A G A T C T T T G G T G T T T G A T A T C A C T T C A A T T C C T T A G C A C A T A G G T
* * * * *
* * * * *
* * * * *
* * * * *
alignment
position      1 7 0 1 . . . . . 1 7 1 1 . . . . . 1 7 2 1 . . . . . 1 7 3 1 . . . . . 1 7 4 1 . . . . .
P978665 1489 c t g t t g c a - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
P978667 1355 T T C C T T G A A T T A A G A C T G G A C T C a t t t c A T G T T C A T T A A A G T T T T T C T C A
P978669 1230 T T A C T C G A A T C A A G G C T G G C C T C c t c t t A T G T T C A T T A A A G T T T T T C C C A

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*****
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alignment
position  1 7 5 1 . . . . . 1 7 6 1 . . . . . 1 7 7 1 . . . . . 1 7 8 1 . . . . . 1 7 9 1 . . . . .
P978665 1510 AGGGT CT GTT - AATAGAAAc g c c a a a a t t t t g g t - - - - - - - - - - - - -
P978667 1405 AAGGT GATGT - AATATAAAT CCTCCGCTTT CATAAAGCAT T c t t c c CAAA
P978669 1280 AAGGT GATa g a AATATAAAT CCTCCACTTT GCTAAAGCAT T t t c c t CAAA
*****
*****
*****

alignment
position  1 8 0 1 . . . . . 1 8 1 1 . . . . . 1 8 2 1 . . . . . 1 8 3 1 . . . . . 1 8 4 1 . . . . .
P978665 1543 - - - - - - - - - - TAAA- - - - - - - - - - TATT TTTGAAACAT GCACTCCTTC
P978667 1454 TGTGATAAAG CTCTTAA- - - - - - - - - - TTAT TTTGAAAAAT TCCACTTTGC
P978669 1330 TGTGATAAAG CTCTTg a c t t t t t t t TTTT TTTTTTAAAT TCAATTTTGA
*****
*****

alignment
position  1 8 5 1 . . . . . 1 8 6 1 . . . . . 1 8 7 1 . . . . . 1 8 8 1 . . . . . 1 8 9 1 . . . . .
P978665 1571 GAAGT TAGTG TTTTt c t - - - - - - - - - - - - - - - - - - - - - - -
P978667 1495 GAAGT TAG- - - - - - - - - - - - - - - - - - - - - - - - - - - - -
P978669 1380 GAAGC TAGCA TTTTt c t t t c t c a a c t a c c c a g g g a g g a a g g c a g t t g a a a g
*****
*****

alignment
position  1 9 0 1 . . . . . 1 9 1 1 . . . . . 1 9 2 1 . . . . . 1 9 3 1 . . . . . 1 9 4 1 . . . . .
P978665 1588 - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
P978667 1503 - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
P978669 1430 a c a g t t t c t g a a g c a g t t t g g g g t g a c t c t c a a t a g g g a a t g t a t a g g t a

alignment
position  1 9 5 1 . . . . . 1 9 6 1 . . . . . 1 9 7 1
P978665 1588 - - - - - - - - - - - - - - - - - - - - - - -
P978667 1503 - - - - - - - - - - - - - - - - - - - - - - -
P978669 1480 a t a a g g a g c a g t t c c c a g t c a 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.

	P978667 (1502 bp)	P978669 (1501 bp)
P978665 (1587 bp)	0.150 31 %	0.152 31 %
P978667 (1502 bp)		<u>1.000</u> <u>67 %</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"/>

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

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GEMS Launcher 4.1.1

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**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 Jun 3 22:12:33 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)  
**Selected groups** (core/matrix sim):

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

## Aligned Sequences:

No.	Sequence Name	Sequence Description	Length
1	P973053	sym=ATP5S loc=Loc27109 taxid=9606 spec=Homo sapiens chr=14  ctg=NT_026437 str=(+) start=31778252 end=31779652 len=1401  tss=601  comm=ATP synthase, H+ transporting, mitochondrial F0 complex, subunit s (factor B); (NM_015684/501/silver;)	1401 bp
2	P973055	sym=Atp5s loc=Loc68055 taxid=10090 spec=Mus musculus chr=12  ctg=NT_039551 str=(+) start=14615676 end=14617088 len=1413  tss=601,613  comm=ATP synthase, H+ transporting, mitochondrial F0 complex, subunit s; (AK009141/501/gold;NM_026536/513/silver;)	1413 bp
3	P973058	sym=na loc=Loc362749 taxid=10116 spec=Rattus norvegicus  chr=6 ctg=NW_047760 str=(+) start=38712374 end=38713774  len=1401  comm=similar to mitochondrial ATP synthase regulatory component factor B; (CompGen promoter)	1401 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\$ZBPF	V\$SP1F	V\$SEGRF	V\$MINI	V\$ECAT	V\$PCAT	V\$ZF5F	V\$GLIF
alignment position	1 . . . . .	1 1 . . . . .	2 1 . . . . .	3 1 . . . . .	4 1 . . . . .			
<b>P973053</b>	1 g a g c t a - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -
<b>P973055</b>	1 t g - - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -
<b>P973058</b>	1 g a g g c a g t g g	t g a t a c a c a c	c t t t a a t c c c	a g c a a g g t g g	a g a c a a g a c a			
alignment position	5 1 . . . . .	6 1 . . . . .	7 1 . . . . .	8 1 . . . . .	9 1 . . . . .			
<b>P973053</b>	7 - - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -
<b>P973055</b>	3 - - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -
<b>P973058</b>	51 c a g g a a a t c	t t t g a g t t c a	a g g c c a g c c t	g g t t g a c a a g	a c a g c c a g g a			
alignment position	1 0 1 . . . . .	1 1 1 . . . . .	1 2 1 . . . . .	1 3 1 . . . . .	1 4 1 . . . . .			
<b>P973053</b>	7 - - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -
<b>P973055</b>	3 - - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -
<b>P973058</b>	101 t a c a a a g a g a	g g c c c t a t g t	g g a a g a c a g	t c a g a a a c a g	g c a t g a a g g g			
alignment position	1 5 1 . . . . .	1 6 1 . . . . .	1 7 1 . . . . .	1 8 1 . . . . .	1 9 1 . . . . .			
<b>P973053</b>	7 - - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -
<b>P973055</b>	3 - - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -
<b>P973058</b>	151 g a a g g g a a a a	a g g g a g g a a g	a t g g a g a a g g	g a g g g g a g g g	g a g g g g a g g g			
alignment position	2 0 1 . . . . .	2 1 1 . . . . .	2 2 1 . . . . .	2 3 1 . . . . .	2 4 1 . . . . .			
<b>P973053</b>	7 - - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -
<b>P973055</b>	3 - - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -
<b>P973058</b>	201 g g a g a g g a a g	a t t g g g a g a g	g t g g g g t g g c	a t g t g c c t t t	a a t t c c a g c g			
alignment position	2 5 1 . . . . .	2 6 1 . . . . .	2 7 1 . . . . .	2 8 1 . . . . .	2 9 1 . . . . .			
<b>P973053</b>	7 - - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -
<b>P973055</b>	3 - - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -
<b>P973058</b>	251 c t t g g a a a g g	a g g g g c a g g t	t g a t c g c t t g	a g a c a t t g g a	g t c t g c c t g a			
alignment position	3 0 1 . . . . .	3 1 1 . . . . .	3 2 1 . . . . .	3 3 1 . . . . .	3 4 1 . . . . .			
<b>P973053</b>	7 - - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -
<b>P973055</b>	3 - - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -
<b>P973058</b>	301 t c t a c a g g g c	t a a a t a g g g a	a a c c t a g t t t	c a a a g g a a a a	c a a a c c a c t a			
alignment position	3 5 1 . . . . .	3 6 1 . . . . .	3 7 1 . . . . .	3 8 1 . . . . .	3 9 1 . . . . .			
<b>P973053</b>	7 - - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -
<b>P973055</b>	3 - - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -
<b>P973058</b>	351 c c a t t t a g c a	t g a c c a t t a g	a c t a a a a t t t	g a t g t g g c t t	a a a c a a a a g c			

alignment position	4 0 1 . . . . .	4 1 1 . . . . .	4 2 1 . . . . .	4 3 1 . . . . .	4 4 1 . . . . .
<b>P973053</b>	7 - - - - -	- - - - -	- - - - -	- - - - -	- - - - -
<b>P973055</b>	3 - - - - -	- - - - -	- - - - -	- - - - -	- - - - -
<b>P973058</b>	401 a a g g c g c c c c	t c t c c a g a g t	c t t t c c a c a c	c t c t a t c t g c	c a c t a a a t c c
alignment position	4 5 1 . . . . .	4 6 1 . . . . .	4 7 1 . . . . .	4 8 1 . . . . .	4 9 1 . . . . .
<b>P973053</b>	7 - - - - -	- - - - -	- - - - -	- - - - -	- - - - -
<b>P973055</b>	3 - - - - -	- - - - -	- - - - -	- - - - -	- - - - -
<b>P973058</b>	451 a t t c g c a c a g	c t c a c c t t g c	c t c a a a c a a t	c a a a a a c t t c	c c c c t g t a a a g
alignment position	5 0 1 . . . . .	5 1 1 . . . . .	5 2 1 . . . . .	5 3 1 . . . . .	5 4 1 . . . . .
<b>P973053</b>	7 - - - - -	- - - - -	- - - - -	- - - - -	- - - - -
<b>P973055</b>	3 - - - - -	- - - - -	- - - - -	- - - - -	- - - - -
<b>P973058</b>	501 c t t t c a c a c a	g a a a a c t g t a	t t t g c c a a g g	c a g c c c a c g g t	g g t c a a c t g
alignment position	5 5 1 . . . . .	5 6 1 . . . . .	5 7 1 . . . . .	5 8 1 . . . . .	5 9 1 . . . . .
<b>P973053</b>	7 - - - - -	- - - - -	- - - - -	- - - - -	- - - - -
<b>P973055</b>	3 - - - - -	- - - - -	- - - - -	- - - - -	- - - - -
<b>P973058</b>	551 a g t t g c t t c t	c a t g a g g a c a	a c t c t a a t g t	g t g c a a g g a a	c t t g a c c c a c
alignment position	6 0 1 . . . . .	6 1 1 . . . . .	6 2 1 . . . . .	6 3 1 . . . . .	6 4 1 . . . . .
<b>P973053</b>	7 - - - - -	- - - - -	- - - - -	- - - - -	- - - - -
<b>P973055</b>	3 - - - - -	- - - - -	- - - - -	- - - - -	- - - - -
<b>P973058</b>	601 t g a a g c c a a g	t t c t g g a t t t	t c c a a g c a a c	a c g g g a t g c t	a g c t a a g a a a
alignment position	6 5 1 . . . . .	6 6 1 . . . . .	6 7 1 . . . . .	6 8 1 . . . . .	6 9 1 . . . . .
<b>P973053</b>	7 - - - - -	- - - - -	- - - - -	- - - - -	- - - - -
<b>P973055</b>	3 - - - - -	- - - - -	- - - - -	- - - - -	- - - - -
<b>P973058</b>	651 c a g c a t a c t t	a t a t t t g c a g	t a t g c t g g g t	c t t t t t a a c c t	t a a a a c c AC
					**
					**
					**
					**
					**
					**
alignment position	7 0 1 . . . . .	7 1 1 . . . . .	7 2 1 . . . . .	7 3 1 . . . . .	7 4 1 . . . . .
<b>P973053</b>	7 - - - - -	- - - - -	- - - - -	- - - - -	- - - - -
<b>P973055</b>	5 C A C C T A G G G G	C C A G A C T A G G	A T C C T A G T C A	C C A G T C A C c c	t t t a g A G T G G
<b>P973058</b>	701 C A C C T A G C G G	C C A G A C T A G G	A T C C T A T T C A	C C A C T C A C c c	a c - - - A G T G G
	** ** ** ** **	** ** ** **~	** ** ** **~	** ** ** **~	** ** ** **~
	** ** ** **~	** ** ** **~	** ** ** **~	** ** ** **~	** ** ** **~
	** ** ** **~	** ** ** **~	** ** ** **~	** ** ** **~	** ** ** **~
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**P973058** 934 CAGGTT CAGT TGGAGACACC TCTGAGGGGA GCAGCg AGTG CAGGCC GC CG  
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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 . . . . .

**P973053** 207 g g a g g a c c a g c g g c CACTCA CCTGGT GCT G GCGCT- - - GC GGCTACCTCC

**P973055** 293 CCTCT- - - - - CACTTA CCTGGT GCT G GAGCTt c t GC GGCCACCCCC

**P973058** 984 CCTCT- - - - - CACCTA CCTGGT ACT G GAGCT- - - GC GACCACCCCT

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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 . . . . .

**P973053** 254 ACACAGC GGT CTTGGCCTCC CAGACGCGAA CCCGCACGCC CCAGGGGAGC

**P973055** 334 GCACAGTAGC CCGGGCACCC CGGACGCCGG TCCACTTGCG CGGAGGAAGC

**P973058** 1022 GCAGAGTAGC CCGAGCACCC CGGACACCGG CCCGCTAGCG CGGAGGAAGC

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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 . . . . .

**P973053** 304 CACCGGC GA a a a g c c c g CCG GCCCGTCCGC AGGCACCAAC CAAATAACGC

**P973055** 384 CCCAGCCAC GCa g t a c CCG GCCAGTCCGC AGACACCGCC TACGTAGCGC

**P973058** 1072 CCCAGCAAC Gc t g c a c c c a a t CCGTCCGC AGACACCTCC CACATAACGC

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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 . . . . .

**P973053** 354 AGCGc t GGC A CCATCCCCTA CGCACGCTCC CCTCCCTCAG C g c t c a g a g

**P973055** 434 AGGGTCGGCC ACATGGCCTG CGCCACCTCC CCTCCCTCCA CCCAGCACc

**P973058** 1122 AGAGTCGGCC ACATGGTCTA CACCGCCTCC TCTTCCTCAA CCTTAGCAGt

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alignment
position      1 4 0 1 . . . . . 1 4 1 1 . . . . . 1 4 2 1 . . . . . 1 4 3 1 . . . . . 1 4 4 1 . . . . .
P973053 585 c t c c c t c c c t c c c t c c g A C G C T G T G A G T A - G A G A A G C T A G G C C C C G A G C C
P973055 661 - - - - - - - - - - - - - - - - A C G C C G T G A G T A a G A G G A G C T A G G G C G A A G G C G
P973058 1348 - - - - - - - - - - - - - - - - A C G C C G T G A G T A - G A G G A A C G A G G G C G G A G G C A
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alignment
position      1 4 5 1 . . . . . 1 4 6 1 . . . . . 1 4 7 1 . . . . . 1 4 8 1 . . . . . 1 4 9 1 . . . . .
P973053 634 G G G c g g g a c t a G G G T G G T G G T T g t g t t C T G C C C T C G C C C G T C G C C A A C G C
P973055 694 G G G A C C - - - - - G G G T G G T G G T T T C C A - - C T C T C C G G G A C C T C C G C C C G C A C
P973058 1380 G G G A C C - - - - - G G G T G G T G G T T T C C A c t - - - - - - - - - - - - - - - - - - - - - - -
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alignment
position      1 5 0 1 . . . . . 1 5 1 1 . . . . . 1 5 2 1 . . . . . 1 5 3 1 . . . . . 1 5 4 1 . . . . .
P973053 684 T G G G C T G A C T G A A A A C C t g g c c c t t t g g g t c g c g c g t c t t c g a c c t t c a c
P973055 737 A G G C T T G A C T G G A C G C C g g c g c t g t t c c g c c a g a g a a g g c t g g g c a t g t c
P973058 1402 - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
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alignment
position      1 5 5 1 . . . . . 1 5 6 1 . . . . . 1 5 7 1 . . . . . 1 5 8 1 . . . . . 1 5 9 1 . . . . .
P973053 734 c g c c a t g c g g a c a t g g g g c c g t g g g a g a a a c t c t g g g c g g g a t t a c g g t g
P973055 787 g g g g t g a c c c c t g g c t c - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
P973058 1402 - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
```

```
alignment
position      1 6 0 1 . . . . . 1 6 1 1 . . . . . 1 6 2 1 . . . . . 1 6 3 1 . . . . . 1 6 4 1 . . . . .
P973053 784 a a a a t t c t t g t t t g g g c g g g c c c t g c g g c t t c t t t C T T C C G G C T C G C C C T
P973055 804 - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
P973058 1402 - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
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```
alignment
position      1 6 5 1 . . . . . 1 6 6 1 . . . . . 1 6 7 1 . . . . . 1 6 8 1 . . . . . 1 6 9 1 . . . . .
P973053 834 C G G C C C C G C C C C C g c c c c g c c c c c g c t c c a g e t c c a g c c g g g t c c t c g c t
P973055 819 C G G C C A C G C C T C C t g g t c g g t t g g c g a c g c t g t g g c c c g g g a g c t g g g g a
P973058 1402 - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
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```
alignment
position      1 7 0 1 . . . . . 1 7 1 1 . . . . . 1 7 2 1 . . . . . 1 7 3 1 . . . . . 1 7 4 1 . . . . .
P973053 884 c g g c c c c g c a c g c g g c c c g c g g t a g a c g g a g g g c c t g g g c a c c c a c c g t c
P973055 869 c t a a g c c a c c t c c t g c - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
P973058 1402 - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
```

alignment position	1751 . . . . .	1761 . . . . .	1771 . . . . .	1781 . . . . .	1791 . . . . .
<b>P973053</b>	934 t c c a t c c c g g	c c c c a g e c c c a	g t c g a g c g t c	c a c t a g a a g g g	CGCTCCCTG
<b>P973055</b>	885 - - - - -	- - - - -	- - - - -	- - - - -	- CGCTCCCTG
<b>P973058</b>	1402 - - - - -	- - - - -	- - - - -	- - - - -	- - - - -
					*****
alignment position	1801 . . . . .	1811 . . . . .	1821 . . . . .	1831 . . . . .	1841 . . . . .
<b>P973053</b>	984 TCc g g c c c t a	a t c c t c g c t c	c t c a c g g a g g	c t c t t t g t c a	c a g c g a a g a C
<b>P973055</b>	894 TC a c t a c c c t	g - - - - -	- - - - -	- - - - -	- - - - - C
<b>P973058</b>	1402 - - - - -	- - - - -	- - - - -	- - - - -	- - - - -
	**				*
alignment position	1851 . . . . .	1861 . . . . .	1871 . . . . .	1881 . . . . .	1891 . . . . .
<b>P973053</b>	1034 TGACAGCCCG CAGTCTTCTG	GACt t CTTTT	ATGGGGCTCC	TGGc g g t g c t	
<b>P973055</b>	906 TGATTGCCCG CAGGT TTCTG	GGC- - CCTTC	ATGGGGCTCC	TGGt t g g t t g	
<b>P973058</b>	1402 - - - - -	- - - - -	- - - - -	- - - - -	- - - - -
	*****	*****	*****	*****	*****
alignment position	1901 . . . . .	1911 . . . . .	1921 . . . . .	1931 . . . . .	1941 . . . . .
<b>P973053</b>	1084 a TTCATT CAG TCATTGATTC	GTCTTG TAAA	TATGGAGCGC	c t g c t c t g t a	
<b>P973055</b>	954 - TTCATTCAA CCACTGACTC	AGCTTG TAAA	TATCGGGCGC	t g a g c t a g g c	
<b>P973058</b>	1402 - - - - -	- - - - -	- - - - -	- - - - -	- - - - -
	*****	*****	*****	*****	*****
	*****	*****	*****	*****	*****
	*****	*****	*****	*****	*****
alignment position	1951 . . . . .	1961 . . . . .	1971 . . . . .	1981 . . . . .	1991 . . . . .
<b>P973053</b>	1134 c t c g a c c c g g	c a c t g g g t a c	c g g a a g a a c c	AGACAGCTCG	GT T T T T G C C A
<b>P973055</b>	1003 g c t g g a t g a a	a g t - - - - -	- - - - -	AGACGGCTCG	GT C T C T G T C G
<b>P973058</b>	1402 - - - - -	- - - - -	- - - - -	- - - - -	- - - - -
				*****	*****
alignment position	2001 . . . . .	2011 . . . . .	2021 . . . . .	2031 . . . . .	2041 . . . . .
<b>P973053</b>	1184 CCATTTA t a a	g t c t g t g t c -	- - - - -	- - - - -	- - - - -
<b>P973055</b>	1036 TCATTTA g t g	t g g t t t t t c c	g g t t t c t a t t	a t t g a c t t g t	a t a t g t g c c t
<b>P973058</b>	1402 - - - - -	- - - - -	- - - - -	- - - - -	- - - - -
	*****				
alignment position	2051 . . . . .	2061 . . . . .	2071 . . . . .	2081 . . . . .	2091 . . . . .
<b>P973053</b>	1203 - - - - -	- - - - -	- - - - -	- - - - -	- - - - -
<b>P973055</b>	1086 a t g c g a g c t t	a t t g c a a c a g	g t a t g t g c a g	g a g t t t g t g a	g a c c a g a a a g
<b>P973058</b>	1402 - - - - -	- - - - -	- - - - -	- - - - -	- - - - -
alignment position	2101 . . . . .	2111 . . . . .	2121 . . . . .	2131 . . . . .	2141 . . . . .
<b>P973053</b>	1203 - - - - -	- - - - -	- - - - -	- - - - -	- - - - -
<b>P973055</b>	1136 g g g a g t a c a g	g a t c g c c t g g	a a c t g g a a a t	t c t g a g c t g c	c a t g t g g g t g

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P973058 1402 - - - - -
alignment
position    2 1 5 1 . . . . . 2 1 6 1 . . . . . 2 1 7 1 . . . . . 2 1 8 1 . . . . . 2 1 9 1 . . . . .
P973053 1203 - - - - -
P973055 1186 c t g g g a a t c t a g g c c c t c a g g t a a g a c c a g t t a a c a g t c t t a a c c a t a g a
P973058 1402 - - - - -

alignment
position    2 2 0 1 . . . . . 2 2 1 1 . . . . . 2 2 2 1 . . . . . 2 2 3 1 . . . . . 2 2 4 1 . . . . .
P973053 1203 - - - - - C T T T T C T T G A G T A C T G A A C c g a g a t a c a g t
P973055 1236 g c c a t c t c t c t a g c c c c a a a C T T T T C T T T A T T A A T T T A C a - - - - -
P973058 1402 - - - - -
                        * * * * *

alignment
position    2 2 5 1 . . . . . 2 2 6 1 . . . . . 2 2 7 1 . . . . . 2 2 8 1 . . . . . 2 2 9 1 . . . . .
P973053 1233 t t t a a a t g t g c t g t g c g g t c t c t g a g c a g c g a c t c a c c t g t g c a g g T C A C
P973055 1276 - - - - - T C T C
P973058 1402 - - - - -
                                                * * * *

alignment
position    2 3 0 1 . . . . . 2 3 1 1 . . . . . 2 3 2 1 . . . . . 2 3 3 1 . . . . . 2 3 4 1 . . . . .
P973053 1283 T T C A C C T G A T T C C C T T T - - - - -
P973055 1280 T G C C C C A G C T T C C C T T c c t t c t c t c a g g c c t t c c t g a c t a a g c c a g c t c
P973058 1402 - - - - -
                        * * * * *

alignment
position    2 3 5 1 . . . . . 2 3 6 1 . . . . . 2 3 7 1 . . . . . 2 3 8 1 . . . . . 2 3 9 1 . . . . .
P973053 1300 - - - - - A T G T A A A A A T g a g g g c g a t g g g c t g t
P973055 1330 a g t c a a c a g g t t c t c c a g g g a g g g A T G A A A A A A T t g a a a a g a a a a g a c a
P973058 1402 - - - - -
                        * * * * *

alignment
position    2 4 0 1 . . . . . 2 4 1 1 . . . . . 2 4 2 1 . . . . . 2 4 3 1 . . . . . 2 4 4 1 . . . . .
P973053 1326 g t a a t c t c t a a a g g a c c t t c t a a c t c t t t a a a a t t g t c a c t g t g c c g g t g
P973055 1380 a t t a g a c a g t a c t a t t a a c a t a a c c c t a g c c c g t - - - - -
P973058 1402 - - - - -

alignment
position    2 4 5 1 . . . . . 2 4 6 1 . . . . . 2 4 7 1 . . . . .
P973053 1376 t t g c t a a c a c t c a t t c t g t a t g c t t g
P973055 1414 - - - - -
P973058 1402 - - - - -
    
```

### 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>P973055</b> (1413 bp)	<b>P973058</b> (1401 bp)
<b>P973053</b> (1401 bp)	0.283 35 %	0.198 23 %
<b>P973055</b> (1413 bp)		<u>1.000</u> <u>41 %</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

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**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 Jun 2 01:38:57 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)  
**Selected groups** (core/matrix sim):

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

## Aligned Sequences:

No.	Sequence Name	Sequence Description	Length
1	P870080	sym=ATPAF2 loc=Loc91647 taxid=9606 spec=Homo sapiens chr=17  ctg=NT_010718 str=(-) start=17539329 end=17540329 len=1001  tss=501  comm=ATP synthase mitochondrial F1 complex assembly factor 2; (NM_145691/511/silver;)	1001 bp
2	P870082	sym=Atpaf2 loc=Loc246782 taxid=10090 spec=Mus musculus  chr=11 ctg=NT_096135 str=(-) start=25500075 end=25501113  len=1039 tss=501,539  comm=ATP synthase mitochondrial F1 complex assembly factor 2; (AK078500/501/gold;NM_145427/539/silver;)	1039 bp
3	P870084	sym=na loc=Loc303190 taxid=10116 spec=Rattus norvegicus  chr=10 ctg=NW_047334 str=(-) start=33521135 end=33522135  len=1001 tss=501  comm=similar to ATP synthase mitochondrial F1 complex assembly factor 2; (XM_220522/525/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\$RXRF	V\$ECAT	V\$NFKB	V\$NRF1	USNRF1	V\$SETF	V\$EBOX	V\$SHIF	V\$STAF	V\$EGRF	V\$SPIF	V\$PAX3														
	V\$COMP	V\$HOXC	V\$PBXC	V\$INSM	V\$BRAC	V\$YY1F	V\$RREB	V\$AREB	V\$IRFF																	
alignment position	1 . . . . .				1 1 . . . . .					2 1 . . . . .		3 1 . . . . .		4 1 . . . . .												
P870080	1 c c g c c g c c g c				g c g g g a g c c g					a g g a g g g t g g		c g g g g a g g g a		g a g g c c g g g g												
P870082	1 c - - - - -				- - - - -					- - - - -		- - - - -		- - - - -												
P870084	1 t - - - - -				- - - - -					- - - - -		- - - - -		- - - - -												
alignment position	5 1 . . . . .				6 1 . . . . .					7 1 . . . . .		8 1 . . . . .		9 1 . . . . .												
P870080	51 c g c g c a c g c g				c g g g g t g g g g					g c g g g a g G G G		C G A C C A C C C G		C C C G C T G C C T												
P870082	2 - - - - -				- - - - -					- - - - - G G G		G A A C C A C C C G		C C C G C T G A G G												
P870084	2 - - - - -				- - - - -					- - - - -		- - - - -		- - - - -												
													*	*	*	*	*	*	*	*	*	*	*	*	*	*
														*	*	*	*	*	*	*	*	*	*	*	*	*
alignment position	1 0 1 . . . . .				1 1 1 . . . . .					1 2 1 . . . . .		1 3 1 . . . . .		1 4 1 . . . . .												
P870080	101 G C G G A G C A A G				C G C T C c g g c C					G C C A C C G G G A		C C C A G G G A C C		T G C G A G C A G G												
P870082	25 C C A G A C C A A G				C G C T C g t g t t					G C C A C C T G G A		C C C G G A G A C C		T G C A A G C A G G												
P870084	2 - - - - -				- - - - - C					G C C A C C T G G A		C C C G A G A C C		T G C A A G C A G G												
	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*
	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*
alignment position	1 5 1 . . . . .				1 6 1 . . . . .					1 7 1 . . . . .		1 8 1 . . . . .		1 9 1 . . . . .												
P870080	151 G C C T C C C A G T				C C T G A G C T G G					G T C C C C T T C C		C G A C T T G C C C		T C G C G - - - -												
P870082	75 G C C T C C C A G a				C C T G A G C T G G					G T C T C C C T T C		C C A C T T G C C C		T C G C G G G t a C												
P870084	33 G C C T C C C A G T				C C T G A G C T G G					G C T C C C C T T C		C C A C T T G C C C		T C G C G G G c t C												
	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*
	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*
alignment position	2 0 1 . . . . .				2 1 1 . . . . .					2 2 1 . . . . .		2 3 1 . . . . .		2 4 1 . . . . .												
P870080	196 - C A C A C A T A C				A C A C A C A C A G					A C A C T C A - - -		- C A G A C A C A C		A - - - - -												
P870082	125 A C A C A C A C A C				A C A C A C A C A C					A C A C A C A - - -		- C A C A C A C A C		A C G C A C G C A C												
P870084	83 A C A C A T A C A C				A C A C A C A C A C					G C A C A C A t g c		a C A C A C A C A C		G C G C A C A C A C												
	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*
	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*

	* * * * *	* * * * *	* * * * *	* * * * *		
alignment position	2 5 1 . . . . .	2 6 1 . . . . .	2 7 1 . . . . .	2 8 1 . . . . .	2 9 1 . . . . .	
<b>P870080</b>	232 - - - - -	- - - - -	- - - - -	- - - - -	- - - - -	
<b>P870082</b>	171 G C A C A C A C A C	A C A C A C G C G C	a t a c a c a c t C	A C T C A C T C A T	A C A C A C G C G C	
<b>P870084</b>	133 T C A C T C A T A C	A C A C A C G C G C	g - - - - -	C A C A C A C A T	A C A C A C A C A C	
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alignment position	3 0 1 . . . . .	3 1 1 . . . . .	3 2 1 . . . . .	3 3 1 . . . . .	3 4 1 . . . . .	
<b>P870080</b>	232 - - - - -	- - - - -	- - - - -	- - - - -	A C A C A C A A C A C	
<b>P870082</b>	221 T C A C A C A C A C	A C G C G C g c g c	t - - - - -	- - - - -	- - - C A C A C A C	
<b>P870084</b>	175 A C A C A C A C A C	T C G C G C a c a c	a c t c a c a c a c	a t a c a c a c A C	A C A C A C A C A C	
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alignment position	3 5 1 . . . . .	3 6 1 . . . . .	3 7 1 . . . . .	3 8 1 . . . . .	3 9 1 . . . . .	
<b>P870080</b>	244 A C A C A G A C A C	A C A C A C A C C C	C G C C C	<b>C T T C C</b>	<b>G A T T G G C T C A</b>	G G C G A G C C T G
<b>P870082</b>	249 A C A C A A A C A C	A C A C A C A C T C	T G C A	<b>G C T T C C</b>	<b>A A T T G G C G C</b>	G G G C G C G C T G G
<b>P870084</b>	225 A C A C A A A C A C	A C A C A C A C T C	T A C T	<b>G C T T C C</b>	<b>A A T T G G C G C</b>	G G A C C C G C C G G
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	* * * * *	* * * * *	* * * * *	* * * * *	* * * * *	* * * * *
alignment position	4 0 1 . . . . .	4 1 1 . . . . .	4 2 1 . . . . .	4 3 1 . . . . .	4 4 1 . . . . .	
<b>P870080</b>	294 G G g G G C G G G A	G C A G G C T C A G	<b>G C G G C G C T T C</b>	<b>C G C C C A T T G G</b>	<b>C G G g</b>	a g g a <b>g a</b>
<b>P870082</b>	299 A G A G G C G G G A	G C A A G C T C A C	<b>G C G G C G C T T C</b>	<b>C G C C C A T T G G</b>	<b>C G G A C</b>	A G A <b>G A</b>
<b>P870084</b>	275 A G A G G C G G G A	G C A A G C T C A C	<b>G C G G C G C T T C</b>	<b>C G C C C A T T G G</b>	<b>C A G A C</b>	A G A <b>G A</b>
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	* * * * *	* * * * *	* * * * *	* * * * *	* * * * *	* * * * *
alignment position	4 5 1 . . . . .	4 6 1 . . . . .	4 7 1 . . . . .	4 8 1 . . . . .	4 9 1 . . . . .	
<b>P870080</b>	344 <b>a a a C A C G T G G</b>	<b>C G C</b> G G T <b>G C G C</b>	<b>G A G C G G C C C G</b>	<b>C T G G G A C T T</b>	G T A G t c t c c t c	
<b>P870082</b>	349 <b>A A G C A C G T G G</b>	<b>C G C</b> A G A <b>G C G C</b>	<b>G A A C G G C C C T</b>	<b>C T G G G A C T T</b>	G T A G T T T T C T T	

**P870084325** **AAGCACGTGG** **TGC**GGT**GCGC** **GAATGGCCCT** **CTGGGACTT**G TAGTTTTCTT  
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alignment position 5 0 1 . . . . . 5 1 1 . . . . . 5 2 1 . . . . . 5 3 1 . . . . . 5 4 1 . . . . .

**P870080394** g CCGAGGC GC GG **CGTGGAGG** **GGGCGGGCG** **A**Gg t g CGTTT GT **GATGCTGA**

**P870082399** C CCGTGGC GC GG **CA TGGAGG** **GGGCGTGGCG** **A**GCA - CGTTT AT **GATGCTGA**

**P870084375** C CCGT a GC GC GG **CA TGGAGG** **GGGCGGGCG** **A**GCA - CGCTT GT **GATGCTGA**

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

**P870080444** **T T GACTGGGG** **g t g t** g - - - - - CGCAG- GAG GCGC GCGGC G GC **ACGGCGC**

**P870082448** **T T GACGGGG** **CGGG**AGT GGC GCGCAgc GGG GCGCACGGCT GC **ACGGCGC**

**P870084424** **T T GACGGGG** **CGGG**GGC GGT AC GCA G- GGG GCGCGTGGCT GT **ACGGCGT**

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alignment position 6 0 1 . . . . . 6 1 1 . . . . . 6 2 1 . . . . . 6 3 1 . . . . . 6 4 1 . . . . .

**P870080487** **GCCGTAGGTG** **T CATGc GGA** **GATGGCGGCG** TCCAAGGGAG GTTGAGGGCT

**P870082498** **GCCGTAGGTG** **T CATGAGGA** **GATGGCGGCG** TGCTGAGGAG GCTGAGGGCT

**P870084473** **GCCGTAGGTG** **T CATGAc GAA** **GATGGCGGCG** TGCTGAGGAG GCTGAGGGCT

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

**P870080537** C T GAg g a g g c g t TGAGAGGT TTCCGTACAG CCGGAC **CGTG** **CGGCTTTGGG**

**P870082548** ATGAAC CCTT GGTGAGAGGT TTCCGTACAG AACCAG **GCGAG** **Gg g - - TGTGG**

**P870084523** T TGAAC CCTT GGTGAGAGGT TTCCGTACGG AACCAG **GCGAG** **GCGTTTGGG**

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alignment
position 7 0 1 . . . . . 7 1 1 . . . . . 7 2 1 . . . . . 7 3 1 . . . . . 7 4 1 . . . . .
P870080587 GA- TCCCATC GCTCTg t g TT TCCTGCTCCA GGT TTCg c g t c t c g c a TCTT
P870082596 GGT TCTCTTC GCTCT- - TT TCCTGTACTC TGT TTCACG CATGTGTCCA
P870084573 GACTCTCTTC GCTCT- - AT TCCTGTACT- - GTT TTCACG TATGGGTCCA
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alignment
position 7 5 1 . . . . . 7 6 1 . . . . . 7 7 1 . . . . . 7 8 1 . . . . . 7 9 1 . . . . .
P870080636 CCCAGACCCT CGGGCGCGAT GTGGAGGAGC TGCCt CCGGC TGCGGGACGG
P870082643 CCCAGGTCCT TGGGCAGGAT GTGGCGAATC TACCCCGGC TGAGGGACCG
P870084618 CCCAAACCCT TGGGCATGAT GTGGCGAATC TACCCCGGC TGAGGGACCG
*****
*****
*****

alignment
position 8 0 1 . . . . . 8 1 1 . . . . . 8 2 1 . . . . . 8 3 1 . . . . . 8 4 1 . . . . .
P870080686 GGGACGCCGT CTCCTGAATC GGCCg g c g GG TGGCC CAGC GCTTCTATGA
P870082693 GTGGCGCGGT CTCTTGGACC GGCCTCTCAG TGACCCACC GTCTCAGTAT
P870084668 GTGGCGCGGT CTCTTGGACC GGCCTCTCAG TGACCCACC GTTTCATGT
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alignment
position 8 5 1 . . . . . 8 6 1 . . . . . 8 7 1 . . . . . 8 8 1 . . . . . 8 9 1 . . . . .
P870080736 GTCCGGGGCC Aa c c a t c c c g t CTCCAGCCC GGGCTTACGC CCCGC CGACA
P870082743 GGC CGGGCC AGCTCCG CAG CCTCCGGCCC GGGCCTATGT CCCGC CAACA
P870084718 GGC CGGGCC AGCTCTGAGG CCTCCAGCCC GGGCCTACGT CCCGC CAACA
*****
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alignment
position 9 0 1 . . . . . 9 1 1 . . . . . 9 2 1 . . . . . 9 3 1 . . . . . 9 4 1 . . . . .
P870080786 GGT AAGAC Ca t g a c a t g t t c - - - - TTTTG GGTGGGGCC GAGCTGGGGT
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P870082793 GGT GAGGC CC GGAC a t a a T G T G A C T T T T T G G T C A G G A G C C A A G T C G G G C T
P870084768 GGT GAGGC CC GGAC t t c - T G T T A C T T T T T G T T C A G G A G C C A A G T C G G G C T
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alignment position 9 5 1 . . . . . 9 6 1 . . . . . 9 7 1 . . . . . 9 8 1 . . . . . 9 9 1 . . . . .

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P870080831 A A G G T G G g c t t c g G G C T T C G G C T G T G C A A A G C G A A G T A A C T G A G G C A G G G
P870082843 C A C C T G G a G G A A - G G T T T C T G A C G T G C A A T G C G G G G T G A C - - A G G C A G G G
P870084817 C A C C T G G c G G A A - G G T T T C C G A C G T G C A G T G C G G G G T G A C T G A G G C A G G G
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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 . . . . .

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P870080881 T T C A G G C T C A T G A G G T T A T G C A G g c c a g t c a g G T C T T T T T A C A G A T G A G A
P870082890 T T C A G G C C T A T G C G A A T A T T T A G A G C A A C A G A G T T C T G T T T C A A T T T G A A
P870084866 T T C A G G C C C A T G A G A A T A T T C A G A G T A A T A G A a c T C T G T T T C A G T T T G A A
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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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P870080931 A A G T G A A G C C C A G A C A A G G G C A G a c - - G A C C C G A G A G G G A A C A G C G A G T C
P870082940 A A A T G A C A T C C A A A C A A G T G C G a g g G T G A C T T T A G G G G A C A C A G C G T G C C
P870084916 A A A T G A C A T C C A A A C C A G T G C G G g a G T G A C T T T A G G G G A C A C A G C G T T T C
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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 . . . . .

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P870080979 A C G C A C g a t a c a g t a a t t g a t a t - - - - - - - - - - - - - - - - - - - - - -
P870082990 C A G G A C A C G A G A T A T t t g g c t c t T G A G G C T T T C T C A a t t t c c t t t a t t t
P870084966 C A G G G T A G G A G A T A T t t g g c - - - T G A G G C T T C T C T C A g 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>P870082</b> (1039 bp)	<b>P870084</b> (1001 bp)
<b>P870080</b> (1001 bp)	0.452 59 %	0.447 55 %
<b>P870082</b> (1039 bp)		<u>1.000</u> <u>85 %</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

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**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 Jun 3 23:28:12 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)  
**Selected groups** (core/matrix sim):

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

## Aligned Sequences:

No.	Sequence Name	Sequence Description	Length
1	P882240	sym=ATPIF1 loc=Loc93974 taxid=9606 spec=Homo sapiens chr=1  ctg=NT_037485 str=(+) start=2673320 end=2674374 len=1055  tss=501,555  comm=ATPase inhibitory factor 1; (AK000934/555/gold;NM_016311/501/bronze; NM_178190/501/bronze;NM_178191/501/bronze;)	1055 bp
2	P882241	sym=Atpi loc=Loc11983 taxid=10090 spec=Mus musculus chr=4  ctg=NT_078437 str=(+) start=34008 end=35058 len=1051  tss=501,551  comm=ATPase inhibitor; (AK011886/551/gold;AK008346/551/gold;NM_007512/501/silver;)	1051 bp
3	P882242	sym=na loc=Loc362620 taxid=10116 spec=Rattus norvegicus  chr=5 ctg=NW_047724 str=(+) start=2519787 end=2520787  len=1001 tss=501  comm=similar to ATPase inhibitor, mitochondrial precursor; (XM_216338/513/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\$MAZF	V\$SEGRF	V\$ZFIA	V\$NRSF	V\$DMTF	V\$SETSF	USNRF2	V\$HNF4	V\$SP1F
alignment position	1 . . . . .	1 1 . . . . .	2 1 . . . . .	3 1 . . . . .	4 1 . . . . .				
P882240	1 a a a g t g t t g g	g a t t a c a g g c	g t g a g c c a c c	g c g c c c a g c c	a g a a c a c t g a				
P882241	1 - - - - -	- - - - -	- - - - -	- - - - -	- - - - -	AGGTCAA	AG A		
P882242	1 a a g c a g g a t a	a a a a a a t t g c	t g a c g a c a g g	a t g a c t a g g a	AGGTCAA	AG A			
						*	*	*	*
						*	*	*	*
						*	*	*	*
						*	*	*	*
						*	*	*	*
alignment position	5 1 . . . . .	6 1 . . . . .	7 1 . . . . .	8 1 . . . . .	9 1 . . . . .				
P882240	51 c - - - - -	- - - - -	- - - - -	- - - - -	- - - - -				
P882241	11 AGGGT TTCTC	T GAGAAAGT G	AC ATTTAAGG	t g a g a g a a g g	c ACTGCAGT G				
P882242	51 AGGGT TTCTC	T GAGAAAGT G	AC ATTTAAGG	t g a g a g g a t a	g ACTGCAGT G				
	*	*	*	*	*				
	*	*	*	*	*				
	*	*	*	*	*				
	*	*	*	*	*				
	*	*	*	*	*				
alignment position	1 0 1 . . . . .	1 1 1 . . . . .	1 2 1 . . . . .	1 3 1 . . . . .	1 4 1 . . . . .				
P882240	52 - - - - -	- - - - -	- - - - -	ACT TCTCA	T AACAAATGA	ACGCGAT	TT a		
P882241	61 GCAAT ATAAC	C AAAGAACAA	GAACACCTCT	T AAGAGAT AA	ACACGAT	TT C			
P882242	101 GCAAT ATAAC	C AAAGAACAA	GAACACCTC-	- AAGAGAT GA	CTACGAT	TT C			
	*	*	*	*	*	*	*	*	*
	*	*	*	*	*	*	*	*	*
	*	*	*	*	*	*	*	*	*
	*	*	*	*	*	*	*	*	*
	*	*	*	*	*	*	*	*	*
alignment position	1 5 1 . . . . .	1 6 1 . . . . .	1 7 1 . . . . .	1 8 1 . . . . .	1 9 1 . . . . .				
P882240	80 t g t a t a t c t a	a g c c a g g g c a	c a TTGGACGT	CGGTATCCTG	GACATCAGC A				
P882241	111 ATATGTAT Aa	a c a g a g G- - - -	TTTGAGGT	CGATATCCAG	GCTGTCGGC A				
P882242	149 ATATGTAT Ag	a g g t a t G- - - -	TTTGAGGT	CGATAACCAG	ACTGTCGGC A				
	*	*	*	*	*	*	*	*	*
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	*	*	*	*	*	*	*	*	*
	*	*	*	*	*	*	*	*	*
	*	*	*	*	*	*	*	*	*
alignment position	2 0 1 . . . . .	2 1 1 . . . . .	2 2 1 . . . . .	2 3 1 . . . . .	2 4 1 . . . . .				
P882240	130 TCCTGGACAC	AGCT - - CCCA	AA CCCCGAAT	T CCCCCATTT	T ATTGAT Gc t				
P882241	156 TCCTAGGCAT	GGCT ACCACA	AACTTTGTGT	T TCCCCAATC	T ATTCAT GT C				
P882242	194 TCCTAAGCAc	a a CT ACCACA	AA CCTTTATT	T CCCCAAT a a	t g t - - - - T C				
	*	*	*	*	*	*	*	*	*
	*	*	*	*	*	*	*	*	*
	*	*	*	*	*	*	*	*	*
	*	*	*	*	*	*	*	*	*
	*	*	*	*	*	*	*	*	*



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alignment
position      2 5 1 . . . . . 2 6 1 . . . . . 2 7 1 . . . . . 2 8 1 . . . . . 2 9 1 . . . . .
P882240 178 a g c a g g c c a g g g a a g g g a a a a c t t c c t t t g g g c TTTGAAT AATAACGACT
P882241 206 CATAGGGCTT GCCATCgtGT ACAT- - - - - - - TTTTAAT AAAATCGACC
P882242 239 CATAGGGATT GCCACCacGT ACAT- - - - - - - TTTTAAT AAAATCGACC
          * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * *
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          * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * *

alignment
position      3 0 1 . . . . . 3 1 1 . . . . . 3 2 1 . . . . . 3 3 1 . . . . . 3 4 1 . . . . .
P882240 228 TTAGAATTGA AATCGTGGGC TGGAGGTGGA CGCCACGCCT CATTCTGATG
P882241 247 TTTGGACGGA AATTGTGCaG TGGGAGTGAA CGAAATGCCT CATTCTAAAG
P882242 280 TTAAGACAAA AATTGTGCGG TGGAAATGAA CAAAATGCCT CATTTGAACG
          * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * *
          * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * *
          * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * *
          * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * *
          * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * *

alignment
position      3 5 1 . . . . . 3 6 1 . . . . . 3 7 1 . . . . . 3 8 1 . . . . . 3 9 1 . . . . .
P882240 278 GGTCC AAGAG CCGAa a t t t c g g c t t c t g g c a c TCTCCTCA CTCAGCTCTC
P882241 297 AGACC AAAAG CCAAg a t t c a - - - - - - - - - - TCTTTTGA CTTTCGCTCTG
P882242 330 AGACC AAAAa t c t c a c g g g t t g g g a t g a - - - - - - - - - - - - - - - - - -
          * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * *
          * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * *
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alignment
position      4 0 1 . . . . . 4 1 1 . . . . . 4 2 1 . . . . . 4 3 1 . . . . . 4 4 1 . . . . .
P882240 328 TAAACTCCTC CATCATTc c t c t t t c c a g t c c t t t g g c c c t a a g c c c t t g c
P882241 335 TAGACTCCTG GGTCATGat g c GTTAGAGCC TTGTTTATTA ACTGTTAACT
P882242 358 - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
          * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * *
          * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * *

alignment
position      4 5 1 . . . . . 4 6 1 . . . . . 4 7 1 . . . . . 4 8 1 . . . . . 4 9 1 . . . . .
P882240 378 t a g c g g t t g g c t AAGAAGAA ACCCGTCTCT TGC TCGGGAT TCGCTGt g a g
P882241 385 A- - - - - - - - - - - - AGGGATAA ATCCGCCTCC CTCTCAACAA ACGCTGCAGA
P882242 387 A- - - - - - - - - - - - ATGCATAA A c c a g a - - - - CTCTCAACAA TCGCTACGGA
          * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * *
          * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * *

alignment
position      5 0 1 . . . . . 5 1 1 . . . . . 5 2 1 . . . . . 5 3 1 . . . . . 5 4 1 . . . . .
P882240 428 c t c c g g g a a g c c c GCCT- - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
P882241 424 T a t - CATAA- - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
P882242 422 T t a g CATAA- - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
          * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * *
          * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * *
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alignment
position      5 5 1 . . . . . 5 6 1 . . . . . 5 7 1 . . . . . 5 8 1 . . . . . 5 9 1 . . . . .
P882240 475 TCA T CCGCCC - CTCCGTC GA CCAGATTGGG TGCT- TGGCC GTCCCTGCCA
P882241 469 TCG TCCCACC TCCCCG GCGT CTAGATTGGC AGT T- CAGCC GCCCTCGCAG
P882242 465 TCG TCCCg CC TCCCCG CCGT CTAGATTGGC GGT Tc CAGCC GCCCTCGCAG
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alignment
position      6 0 1 . . . . . 6 1 1 . . . . . 6 2 1 . . . . . 6 3 1 . . . . . 6 4 1 . . . . .
P882240 523 TTAGC GCGTA ACGAGAGAC t g c t t g c t g CG GCAGAGACGC CAGAGGTGCA
P882241 518 TTAGC GCGCT AGGAGAGAAG CAg CCA- - CG CCCGCAACGC GAGCTGAGCA
P882242 515 TTAGC GCGCT AGGAGAGAAG CAa CCA- - CG CCCGCAACGC GAGCTGAGCA
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alignment
position      6 5 1 . . . . . 6 6 1 . . . . . 6 7 1 . . . . . 6 8 1 . . . . . 6 9 1 . . . . .
P882240 573 GCTCCAGCAG CAATGGCAGT GACGGCGTTG GCGGCGCGGA CGTGGCTTGG
P882241 566 ACGCCGAAGA CAATGGCAGG CTCGGCGTTG GCAGTTCGGG CTCGGTTCGG
P882242 563 ACGCCGAAGA TAATGGCAGG CTCGGCGTTG GCGGTTTCGGG CTCGGCTTCGG
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alignment
position      7 0 1 . . . . . 7 1 1 . . . . . 7 2 1 . . . . . 7 3 1 . . . . . 7 4 1 . . . . .
P882240 623 CGTGTGGGGC GTGAGGACCA TGCAAAGCCG AGGCTTCGGC TCGGATCAGG
P882241 616 TGTCTGGGGT ATGAAGGTCC TGCAAACCCG AGGCTTCGTC TCGGACTCGG
P882242 613 TGTCTGGGGT ATGAAGGTCC TGCAAACCCG AGGCTTCGGC TCGGACTCGG
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alignment
position      7 5 1 . . . . . 7 6 1 . . . . . 7 7 1 . . . . . 7 8 1 . . . . . 7 9 1 . . . . .
P882240 673 TACGCTGCGG CAgtgtcgc tgc t CCAGCC CCGCGGGC GG ATC- - Cc at c
P882241 666 TAGGTGGCGG CACGGCCAG CGC- CCATCG CGGGGc gc ag gt t ct CTCTC
P882242 663 TAGGTGGCGG CACGACCTAC CGC- CCATCG CGGGGTGC GG GTC- - CTCTT

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alignment
position      8 0 1 . . . . . 8 1 1 . . . . . 8 2 1 . . . . . 8 3 1 . . . . . 8 4 1 . . . . .
P882240 721 t t t g c t t - - C C G T A C C T T T A C C A G T G T C C C T G T C T C T C T G C A G T C C G A G
P882241 715 C C T T G T T G T G C C T T T T C T T T T C A C G T C C A C G A C T C T C T T T G C A G T C G G A T
P882242 710 C C T T G T T G T G C C T T T T T T T T a a t - G T C C A C G A C T C T C T C T G C A G T C G G A G
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alignment
position      8 5 1 . . . . . 8 6 1 . . . . . 8 7 1 . . . . . 8 8 1 . . . . . 8 9 1 . . . . .
P882240 768 A a t g t c g a c c g G G G C G C G G G C T C C A T C C G G G A A G C C G G T G G G C C T T C G G
P882241 765 A G C A T G G A T a C G G G C G C T G G C T C C A T C C G A G A A G C T G G T G G A G C C T T C G G
P882242 759 A G C A T G G A T t C G G G C G C T G G C T C C A T C C G A G A A G C T G G T G G G C C T T C G G
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alignment
position      9 0 1 . . . . . 9 1 1 . . . . . 9 2 1 . . . . . 9 3 1 . . . . . 9 4 1 . . . . .
P882240 818 A A A G A G A G A G C A G G C T G A A G A G G A A C G A T A T T T C C G G T G A G G C T A C C G G
P882241 815 A A A A C G A G A A A A G G C T G A A G A G G A T C G G T A C T T C C G G T G A G G C C A C C T G
P882242 809 g A A A C G A G A G A A G G C T G A A G A G G A T C G G T A C T T C C G G T G A G G C C A C C T G
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alignment
position      9 5 1 . . . . . 9 6 1 . . . . . 9 7 1 . . . . . 9 8 1 . . . . . 9 9 1 . . . . .
P882240 868 G T C C C A A G T C C A G C C C T G G A T C T C C C a a t g g c c t t c c a a t c c t t a a a c t g
P882241 865 G T C C C A A G T C C A G C C C C C A G T C G T C C T C C C T G T C C T T T C T A C G C T C T C T G
P882242 859 G T C C C A A G T C C A G C C C C C A A T C G C C C T C C C T G T C C T T T C T A C G C T C T C T G
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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 . . . . .
P882240 918 c c a a T C G C C C C A C C C G T T C C T A C C T G G T G C C T T G G G C G C C C C A T c c c c c a
P882241 915 - - - - T C G C T C C A C C C A T C T T T A C C T G G T C C C T T G G G G C G C C C A T C T T C T G
P882242 909 - - - - T C G C T C C A C C C A T C T T T A C C T G G T C C C C T G G G G C G C C C A T C T T C T G
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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 . . . . .
P882240 968 a C A G A A C T C C C G G G C c c c a a t c c a g t a t a c c c t a a c c c t t g a t g t c c c g a
P882241 961 G C A G A A T T C C A A G G C t G A T G A A G C C A T C G G - - - - - - - - - - - - - - - - -
P882242 955 G C T G A A T T C C A A G G C c G G T G A A G C C T T C C T - - - - - - - - - - - - - - - - -
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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 . . . . .
P882240 1018 c c G T T G C C A C G T A T A G G G C A C T C C C A G T t a c c t g c a c a - - - - - - - - -
P882241 991 - - G T C G C C T C G T A G T C G A G A C T G C T A G T a t c g c a c t g c t g g c c t c c c a g c
P882242 985 - - G T T T C C A C G T A A T C G A G - - - - - - - - - - - - - - - - -
*****
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*****
*****
alignment
position 1 1 5 1 . . . . . 1 1 6 1
P882240 1056 - - - - - - - - - -
P882241 1039 c a g c c t t a a g c c t
P882242 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>P882241</b> <b>(1051 bp)</b>	<b>P882242</b> <b>(1001 bp)</b>
<b>P882240</b> <b>(1055 bp)</b>	0.225 44 %	0.219 43 %
<b>P882241</b> <b>(1051 bp)</b>		<u>1.000</u> <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: <input type="text"/> to: <input type="text"/>
Output file	<input type="text" value="dialign.seq"/>

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

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GEMS Launcher 4.1.1

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**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 Jun 2 01:09:42 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)  
**Selected groups**

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

(core/matrix sim):

## Aligned Sequences:

No.	Sequence Name	Sequence Description	Length
1	P889644	sym=ATPAF1 loc=Loc64756 taxid=9606 spec=Homo sapiens chr=1  ctg=NT_032977 str=(-) start=952928 end=953928 len=1001  tss=501  comm=ATP synthase mitochondrial F1 complex assembly factor 1; (AK026004/527/gold;NM_022745/527/silver;)	1001 bp
2	P889645	sym=Atpaf1 loc=Loc230649 taxid=10090 spec=Mus musculus  chr=4 ctg=NT_039264 str=(+) start=15907741 end=15908968  len=1228 tss=501,728  comm=ATP synthase mitochondrial F1 complex assembly factor 1; (AK032020/733/gold;NM_181040/506/silver;)	1228 bp
3	P889646	sym=na loc=Loc313510 taxid=10116 spec=Rattus norvegicus  chr=5 ctg=NW_047718 str=(+) start=7486974 end=7487974  len=1001 tss=501  comm=similar to ATP synthase mitochondrial F1 complex assembly factor 1; (XM_233402/501/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\$IRFF V\$ZF5F V\$STAF V\$NOLF V\$MOKG V\$SETSF V\$NRFI USNRFI V\$MYOD V\$NEUR V\$MTFI V\$ZBPF  
V\$CDEF V\$IKRS V\$EVI V\$EGRF V\$AREB V\$EBOX

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

**P889644** 1 a t t a c t c t c g - - - - -

**P889645** 1 - - - GCATTGC GTTTTT AAAA AGCTTAGCTT TTAGGTGGAA CTTACTACTT

**P889646** 1 g a g GCATTGC GTTTTT AAAA GGCTCAGCTC TTAGGTGGAA CTTACTACTT

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

**P889644** 11 - - - - - GCCTC AGTTTCCTTA TTTGTAGAT GAGGATAATA

**P889645** 48 TAATGGTTCA CAGCCTGTTT AGCTTCTCCA TCTGTAAAAT GAGGTTAATA

**P889646** 51 TAATGGTTTCG CAGCCGGCTT AGCTTCTCTG TCTGTAAAAT GAGGTTAATA

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

**P889644** 46 - CTGCCACAC AGAGTATGAA GCCgctcagtg - TCCTGCAC ATAGCAACCT

**P889645** 98 TCTACTTTCAT AGGGTATGAG GCCAATGGAA CCTTCTGCAA ATAGACACTC

**P889646** 101 TCTACTTTCAT AGGGTATGAG GCCAATGGAA CCTTCTTCAA ATAGAAACCC

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

**P889644** 94 c a g TAAA GAG AAGCTTgctg ctgtgatata GTTGATGAA AAGACCTTCC

**P889645** 148 A - - TAAA GAG AAGCTTCAGC TAT- - - - - GATGTTTCAG ACATCCTTTC

**P889646** 151 A - - TAAA GAG AA ACTTCAGC TAT- - - - - GATGTTCAA ACATCCTTTC

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

**P889644** 144 ATGCTGAAGG Acggactact acatcgagtg cctggcac TA CAGCGAGTGC

**P889645** 188 CAGCTAAAGA AACTGT - - - - - TA CAGCTAGTGC

**P889646** 191 CAGCTAAAGA AACTGT - - - - - TA CAGCTAGTGC

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alignment
position    5 0 1 . . . . . 5 1 1 . . . . . 5 2 1 . . . . . 5 3 1 . . . . . 5 4 1 . . . . .
P889644 410 G C C C G G A A C C T T G G G C G C G C G G A A C C T C G G T G C C G G A G C G C G G G C G C G G C
P889645 431 A C C C G G A A C C T T G A G C G C G C G G A A C C T C G G T G G C G G A A C G C G G G C C T C G C
P889646 437 A C C C G G A A C C T T G A G C A C G C G G A A C T T C G G T G G C G G A A C T C G G G C C T C G C
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alignment
position    5 5 1 . . . . . 5 6 1 . . . . . 5 7 1 . . . . . 5 8 1 . . . . . 5 9 1 . . . . .
P889644 460 G C A C T C G G A G C G G G A T G G A G C G G G C G C G C G G C G G C C G C G G G C C G A G G C C G A C
P889645 481 G G A C c t t g c g g g a G A T G G A G C A G G C G C G C G G G C C G G G G G C C G A G G C T G A C
P889646 487 G G A C T T A G A G G G C G A T G G A G C A G G C G C G C G G G C C G G C C G G G G C C G A G G C T G A C
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alignment
position    6 0 1 . . . . . 6 1 1 . . . . . 6 2 1 . . . . . 6 3 1 . . . . . 6 4 1 . . . . .
P889644 510 G C G C C t - - G A G G A G G A G G A G G A G G G G G G C G G G C C A T G G C T G C T G T g g t
P889645 531 G C G c c c G A G G A G G A G G A G G G G A G T C G C A G G C G G C C A T G G C G G C g G T A - -
P889646 537 G C G C C a G A G G A G G A G G A G G G G A G G C G C A G G A G G C C A T G G C G G C T G T A - -
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alignment
position    6 5 1 . . . . . 6 6 1 . . . . . 6 7 1 . . . . . 6 8 1 . . . . . 6 9 1 . . . . .
P889644 557 g G T G G C G G C T G C G G G T G G C G C G G G A C C G G C g G T C C T G C A G G T G G C C G G T C
P889645 579 - G T G T C C G C T G C G G G T G G A G C G T G C C C C G C A G T C C T G C A G G T G G C C G G T C
P889646 585 - G T G T C C G C T G C G G G T G G A G C G T G C C C C G C A G T C C T G C A G G T G G C C G G C C
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alignment
position 7 0 1 . . . . . 7 1 1 . . . . . 7 2 1 . . . . . 7 3 1 . . . . . 7 4 1 . . . . .
P889644 607 T C T A C C G G G G C C T G T G C G C G G T G C G C A G C C G C G C C C T G G G C C T G G G G C T C
P889645 628 T C T A C C G A G G C C T G T G T G C a G T G C G C A G C C G C G C C C T G G G G C T G G G G T T C
P889646 634 T C T A C C G A G G C T T G T G T G C G G T G C G C A G C C G C G C C C T G G G G C T G G G G T T C
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alignment
position 7 5 1 . . . . . 7 6 1 . . . . . 7 7 1 . . . . . 7 8 1 . . . . . 7 9 1 . . . . .
P889644 657 G T G T C A C C c G C G C A G C T G C G C G T C T T C C C A G T G C G C C C C G G C T C G G G C C g
P889645 678 G T G T C A C C g G C A C A G T T G C G C G T G T T C C C G G T G C G C C G G G G C T C G G G C C t
P889646 684 G T G T C A C C t G C A C A G T T G C G C G T G T T C C C G G T G C G C C G G G G C T C G G G C C t
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alignment
position 8 0 1 . . . . . 8 1 1 . . . . . 8 2 1 . . . . . 8 3 1 . . . . . 8 4 1 . . . . .
P889644 707 G C C C G A G G G G G G C G C C G A C A G C A G C G G G G T C G G g g c c g a g g c C G A G C T C C
P889645 728 G C C C C C G A G G G A G C A G A C G G C A G T G G G G T C A G - - - - - - - C G A G C T G C
P889646 734 g t c c t C C G G G G G A A C A G A C G G C G G T G G G G T C A G - - - - - - - C G A G C T G C
* * * * *
* * * * *
* * * * *
* * * * *
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```
alignment
position 8 5 1 . . . . . 8 6 1 . . . . . 8 7 1 . . . . . 8 8 1 . . . . . 8 9 1 . . . . .
P889644 757 A G G C C A A C C C T T T C T A C G A C C G C T A C C G C G A C A A G A T C C A G C T G C T G C G C
P889645 769 A A G C G A A C C C C T T C T A C G A C C G C T A C C G g G A C A A G A T C C A G C A G C T G C G C
P889646 775 A A a c t A A C C C T T T C T A C G A C C G C T A C C G C G A C A A G A T C C A G C A G C T G C G C
* * * * *
* * * * *
* * * * *
* * * * *
* * * * *
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					* * * * *	* * * * *	* * * * *	* * * * *	* * * * *
					* * * * *	* * * * *	* * * * *	* * * * *	* * * * *
alignment position	9 0 1 . . . . .	9 1 1 . . . . .	9 2 1 . . . . .	9 3 1 . . . . .	9 4 1 . . . . .				
<b>P889644</b>	807	<b>AGGTGCGGGC</b>	CTGGGT TGGC	TGGAGGC GGG	c a g g a g g c g g	g	AGGAGGGGC		
<b>P889645</b>	819	<b>AGGTGCGGTC</b>	CTGGTC GGG-	TGGGGGT GGG	GACTC - - - -	-	ACGACCGGC		
<b>P889646</b>	825	<b>AGGTGCGGTC</b>	CTGGCC GGGT	TGGGGGT GGG	GACTC - - - -	-	GTGGC GTGC		
		* * * * *	* * * * *	* * * * *	* * * * *		* * * * *		
		* * * * *	* * * * *	* * * * *	* * * * *		* * * * *		
		* * * * *	* * * * *	* * * * *	* * * * *		* * * * *		
		* * * * *	* * * * *	* * * * *	* * * * *		* * * * *		
		* * * * *	* * * * *	* * * * *	* * * * *		* * * * *		
		* * * * *	* * * * *	* * * * *	* * * * *		* * * * *		
		* * * * *	* * * * *	* * * * *	* * * * *		* * * * *		
		* * * * *	* * * * *	* * * * *	* * * * *		* * * * *		
alignment position	9 5 1 . . . . .	9 6 1 . . . . .	9 7 1 . . . . .	9 8 1 . . . . .	9 9 1 . . . . .				
<b>P889644</b>	857	GGCCC GGGCT	GCTGGGCC TT	AGGACAGCCC	TGTGAGGT g g	g c a	CTAGTAC		
<b>P889645</b>	862	GGGCAGAGCT	TCCGGc ATGC	ACTACTCTCC	GGGACGGT GG	G - -	CTTGCCC		
<b>P889646</b>	869	GGGCAGAGCT	TCCGGAATGC	GCTACTGTCC	TGCATGGT GG	G - -	CTGGTAC		
		* * * * *	* * * * *	* * * * *	* * * * *		* * * * *		
		* * * * *	* * * * *	* * * * *	* * * * *		* * * * *		
		* * * * *	* * * * *	* * * * *	* * * * *		* * * * *		
alignment position	1 0 0 1 . . . . .	1 0 1 1 . . . . .	1 0 2 1 . . . . .	1 0 3 1 . . . . .	1 0 4 1 . . . . .				
<b>P889644</b>	907	TGTCC CAGCT	CTTCAGATGA	TGTa g - -	CCA GGCTCCGC GA	GGCT	<b>AGGTCA</b>		
<b>P889645</b>	910	TGGCC CTGCT	ATACCAATAG	TTTGT T T T CCA	AGTTCAGAGA	GGCC	<b>AGGCCA</b>		
<b>P889646</b>	917	TGTCCc a CT	ATACCAATAG	TTTGT T T T CCA	AGTTCAGAGA	GACG	<b>AGGTCA</b>		
		* * * * *	* * * * *	* * * * *	* * * * *		* * * * *		
		* * * * *	* * * * *	* * * * *	* * * * *		* * * * *		
		* * * * *	* * * * *	* * * * *	* * * * *		* * * * *		
		* * * * *	* * * * *	* * * * *	* * * * *		* * * * *		
		* * * * *	* * * * *	* * * * *	* * * * *		* * * * *		
		* * * * *	* * * * *	* * * * *	* * * * *		* * * * *		
		* * * * *	* * * * *	* * * * *	* * * * *		* * * * *		
alignment position	1 0 5 1 . . . . .	1 0 6 1 . . . . .	1 0 7 1 . . . . .	1 0 8 1 . . . . .	1 0 9 1 . . . . .				
<b>P889644</b>	955	<b>CTTGCCCAAG</b>	ATCACACa g c	t a a t t g g t g t	c a g a g c t g g g	a g t c t c t - - -			
<b>P889645</b>	960	<b>CTTGCCTAAA</b>	GTCACATCTC	TGCAGACTCT	TTGGg t c t t t	c c a c a g t c g t			
<b>P889646</b>	967	<b>CTTGCCTAAG</b>	GTCACACC TC	TGCAGAACCT	TTGGa - - - -	- - - - -			
		* * * * *	* * * * *	* * * * *	* * * * *				
		* * * * *	* * * * *	* * * * *	* * * * *				
		* * * * *	* * * * *	* * * * *	* * * * *				
		* * * * *	* * * * *	* * * * *	* * * * *				
		* * * * *	* * * * *	* * * * *	* * * * *				
alignment position	1 1 0 1 . . . . .	1 1 1 1 . . . . .	1 1 2 1 . . . . .	1 1 3 1 . . . . .	1 1 4 1 . . . . .				
<b>P889644</b>	1002	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -			
<b>P889645</b>	1010	c a a a a c a c t c	t t t a a a g c c c	t a t g a a g a a g	a c a g c t c a g a	g a a a g t t g t c			
<b>P889646</b>	1002	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -			
alignment position	1 1 5 1 . . . . .	1 1 6 1 . . . . .	1 1 7 1 . . . . .	1 1 8 1 . . . . .	1 1 9 1 . . . . .				

```

P889644 1002 - - - - -
P889645 1060 c c c t a c t t a g g a a g a t g a a a a t g a a g a c c t t c a g c g a a g g c a t t t g a t t t
P889646 1002 - - - - -

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

P889644 1002 - - - - -
P889645 1110 g c t c a a g g t c a c a t g t t g a g t c a g c a g a t a c c t g c c t g a g a g a t c a a g t t
P889646 1002 - - - - -

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

P889644 1002 - - - - -
P889645 1160 c a c a g g c t c t c c c a g c t t a g g g c c c t g a c t g c c t g g a c a a g g a g a c t g g g
P889646 1002 - - - - -

alignment
position      1 3 0 1 . . . . . 1 3 1 1 . . . . .

P889644 1002 - - - - -
P889645 1210 a t t g t g g c a a a g a c t g a t a
P889646 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>P889645</b> (1228 bp)	<b>P889646</b> (1001 bp)
<b>P889644</b> (1001 bp)	0.340 51 %	0.344 58 %
<b>P889645</b> (1228 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"/>
<input type="button" value="Extract aligned sequences"/>	

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

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