

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

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

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

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

DiAlign professional TF Release 3.1 December 2004

Thu May 5 21:22:57 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)

- ALL user_defined.lib (0.75/Optimized)
- ALL vertebrates.lib (0.75/Optimized)

Selected groups
(core/matrix sim):

Aligned Sequences:

No.	Sequence Name	Sequence Description	Length
1	P977959	sym=COX4I2 loc=Loc84701 taxid=9606 spec=Homo sapiens chr=20 ctg=NT_028392 str=(+) start=421283 end=422483 len=1201 tss=501 comm=cytochrome c oxidase subunit IV isoform 2 (lung); (NM_032609/501/silver;)	1201 bp
2	P977960	sym=Cox4i2 loc=Loc84682 taxid=10090 spec=Mus musculus chr=2 ctg=NT_039210 str=(+) start=3150756 end=3151956 len=1201 tss=501 comm=cytochrome c oxidase subunit IV isoform 2; (NM_053091/501/bronze;)	1201 bp
3	P977961	sym=Cox4b loc=Loc84683 taxid=10116 spec=Rattus norvegicus chr=3 ctg=NW_047658 str=(+) start=33280248 end=33281448 len=1201 tss=501 comm=cytochrome c oxidase, subunit 4b; (NM_053472/530/bronze;)	1201 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\$TEAF
V\$ETSF
V\$NFKB
V\$ZBPF
V\$RORA
V\$TBPF
V\$HIF
V\$HOXF
V\$NKXH
V\$HOME

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alignment position 1 . . . . . 11 . . . . . 21 . . . . . 31 . . . . . 41 . . . . .
P977959          1 a t g a g c c a c c g c g c c c g c c c a a t t t t t c t a t t t t t a - - - - -
P977960          1 a g g c a g a a g g a g g c t t t c c c C T C T C C C C T T A C T G C A C C C C T C T T A G G G T G
P977961          1 - - - - - - - - - - - - - - - - - - - - - - - - - - - C T C T C C C C T T A A C G C A T C T C T C T T A G G G T G

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P977959 291 a CTACTGTCT GCAGAGG GTC TCCA GA GGc a g g - ACC CCGG T AGGGACa c t
P977960 300 - CTTCTGTCTG GCTGGGG GTC TGCT GA GG T C Cc t a c t c t GG T GA GG ACC CA
P977961 274 - CCTCTGTCA GCTGGGG GTC TGCG GA GG T C Cc c AC ACCGG T GA GG ACC GG
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alignment position 5 0 1 5 1 1 5 2 1 5 3 1 5 4 1
P977959 340 g a t g c a g g a G GC GC TCT GCA GTGC CT CCC C CCAATCTGT G GG CCGGGGt g
P977960 349 GC - - - - - G GG AA ACC GCA GTCC TT TCT C TTTTCC TGT G C CT CTGGGGA
P977961 323 GT - - - - - G GC AA GCT GCA GTCC TT TCT C TTTTCC TGC G C CC CTGGGGA
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alignment position 5 5 1 5 6 1 5 7 1 5 8 1 5 9 1
P977959 390 c c c c a g g g a c g c a g g c t g t g c g c t c c c a c g c c c t g c C G A A G C A G G A C G T
P977960 392 CATGGCT CTG C A A A A G C G A C C g a g g - - - - - C G A G G C G G G A T G T
P977961 366 CGTG GCC CAG C A C A A G C G A C C a - - - - - - - - - - A G G C G G G A T G T
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alignment position 6 0 1 6 1 1 6 2 1 6 3 1 6 4 1
P977959 440 T C C C A C G C - T G G G G C G G C c c c g a g a a a g g c t g t g g g g c g g g c c g g g g c g
P977960 430 T C C C A C G T - G G G G T G G C -
P977961 399 T C C C A C G C g G G G G T G G C -
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alignment position 6 5 1 6 6 1 6 7 1 6 8 1 6 9 1
P977959 489 g g c g c c c g c a c t c a g g t c c c t c c g c a g c g g g t t c t c a g t t g c t c g c t g g g
P977960 447 -
P977961 417 -

alignment position 7 0 1 7 1 1 7 2 1 7 3 1 7 4 1
P977959 539 c a g a c c c a g g t c g c g c t c c c a c t g c c g a g c c c g c g a g g t g a g t g a g t t g g
P977960 447 -
P977961 417 -

alignment position 7 5 1 7 6 1 7 7 1 7 8 1 7 9 1
P977959 589 g g g a g g a c c c c g c c a c c c a a g c c c g c g c g G G T C A G G G G C G C G G C T C G G T C
P977960 447 - G G T C G G A G G C G G G G C G T G T T C
P977961 417 - G G G C G G A G G C G G A G C G T G C T C
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alignment position 8 0 1 8 1 1 8 2 1 8 3 1 8 4 1
P977959 639 T c c t g c c t t c g c c g c t g g g t c a c g c c c c a g t g g t c c c t g t c t t a g a g g g t
P977960 468 T G G T C C -
P977961 438 T G G T C C -
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alignment position 8 5 1 8 6 1 8 7 1 8 8 1 8 9 1

P977959 689 t g g g g g g c t t c t t g t a g g t t a g a g t t g a a g a c t c c t g g g g a g t c t g c a t a
P977960 474 - - - - -
P977961 444 - - - - -

alignment position 9 0 1 9 1 1 9 2 1 9 3 1 9 4 1
P977959 739 t g t g t g c c a t c t c t t t c c c c a a a t a t a g a t t a c a t c c t C C C T C T C T G A T
P977960 474 - - - - - C C C T C T C C G G G T
P977961 444 - - - - - C C t c a g C C T G G T
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alignment position 9 5 1 9 6 1 9 7 1 9 8 1 9 9 1
P977959 789 A T G T G G A G C T C T C C C A C C A C T A A T C A t a a t c a c t g g c c g g a g c - - - - -
P977960 486 C T G C G G T T C C T G C C A G T C A C T C A G C A G G G C A G C T C T g g a t a g t T C C G C C
P977961 456 C T G C G G T T C C T G C C A G T C A C T C A G C A G G G C A G T T C T g g g t a c c T C C G C 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
P977959 833 - - - - -
P977960 536 G C C T C C A G C T T G C A A T T G T G A G T C C A C C T G A G G g G A A G G G T C G C G G G G A
P977961 506 G T C T T C A G C T T G C A A C T G T G A G T C C A C C T G A G G - G A A G G G T C T T G G G G 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
P977959 833 - - - - - C
P977960 586 T G G G A T G T T C G T G G C G G C - - - - - C A C C A C A C A G C
P977961 555 T G G G G T G T T C G T G T G G C c a c c c t a a g c c t t t g c t c c a t C A C C A C A C A 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
P977959 834 C C T C T T T T C C A G A A G T g t g g g c c g c c c c c t c c c a c t t a t c a c c t g t a g t g
P977960 615 C C T C T T T T G C T G A G G T T T - - - - -
P977961 605 C C T C T T T T G C T G A G a - T T - - - - -
* * * * *
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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
P977959 884 t g c c C C C T C C C T C A C T C - - - - - T A T T T G T T G G G T G C C C T C
P977960 633 - - - C C C C C A C T G A C T A - - - - - T C C T T G T C C C G G G C A T C A C
P977961 622 - - - C C C C C A C T G A C c c g t t t t a a t g c t g g g T C C T A G T C C C G G G C A T C G T
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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
P977959 920 T C t c t c c c t a g a t g t g g g a c t c c c c t - - - - - T C T T T T C
P977960 665 A C C G G G C C C A A A A G T G A G G t C T C T T T T C A G A G G A T G G G C T G G T C C T T T T
P977961 668 C C C C G G C C C A G A A A T G G G G c C T C T T T C T A G A G G G T G G G G T G G C C T T T T

alignment position 1 251 1 261 1 271 1 281 1 291

P977959 953 CCCAGAT GTG t g t c t c c ct - - - CCCT CTGA CCCAGT TAA G T C C C C A TCCT
P977960 715 CCTAGAA GTG CT GC CTC TCC TACC CG CTGA CCCAGT TTG G T C C T T A GCCT
P977961 718 CCTAGAA ATG CT GC CTC TCC CACC CG CTGA CCCAGT TTG G T C C T T G GCCT

alignment position 1 301 1 311 1 321 1 331 1 341

P977959 1000 CTAAAGC CCC T c c c a c c a c c a t G G A T G C C A A A C C C T G A G T C T T C C c t g g
P977960 765 CTAAAGC CCC T G - - - - - - - - G G A T A C C A G A C T C T G C A T G T C C C G C G T
P977961 768 CTAAAGC CCC T G - - - - - - - - G G A T G T C A G A C T C T G C A C G T C C C G C G T

alignment position 1 351 1 361 1 371 1 381 1 391

P977959 1050 g g g t g g g a g a c t g g g c t c a g c c a g a c t g g c t a A G C C C A G T C C C C A C C C C A
P977960 804 C - - - - C C G A G T C C G G A G T G A T G G T - - - - - A G G G C A C A G C C T G C C C C
P977961 807 C c c g t t C C G A G T C C G G A G T G A T G G T - - - - - A G G G C A C A G C C T G C C C C

alignment position 1 401 1 411 1 421 1 431 1 441

P977959 1100 A C C A G A T C C A G C A G A G C A G G C c t g t g t G C A C G T A G G C A G C C A A T T A G G G g
P977960 842 T C C T C C T G C A G C G G A G C A G G C A G C - G C A C G T A G G C A G T C A A T T A A G G A
P977961 850 T C C - - T G C A G C G G A G C A G G C A G C - G C A C G T A G G C A G T C A A T T A A G G A

alignment position 1 451 1 461 1 471 1 481 1 491

P977959 1150 g g a a g g g g T G G G G C C A G - - - - - A C C G T C T G t c - - - - - - - - - - -
P977960 891 G A C C - - - T T G G A G C C A G - - - - - A G C T T C T G C T T A G A G G T C T G G G C T A A
P977961 896 G A C C - - - T T G G A G C C A G g c g c a g A G C A T C T G C T T A G A G G T C T G G G C T A A

alignment position 1 501 1 511 1 521 1 531 1 541

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P977959   1178 - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
P977960   931 CAGCCCTGTG Gg a A GGA GGC TCAGGACTTT TCt c t g g g g a a g a c a a t t AG
P977961   942 CCGCCCTGCG Gt g A GGA GGC TCAGGATTTT TCc t c t g g - - - - - - - - - - AG
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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 . . . . .
P977959   1178 - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
P977960   981 TGGAGCTTCC CAAC T - - CT GATGGGAGc a c a t c a C ATC A GAGCACAGGG
P977961   982 TGGGGCTTCC CAAC Tt g g CT GATGGGAGg c t g g - - C ATC A GAGAACGGGG
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alignment position 1 6 0 1 . . . . . 1 6 1 1 . . . . . 1 6 2 1 . . . . . 1 6 3 1 . . . . . 1 6 4 1 . . . . .
P977959   1178 - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
P977960  1028 CTCCCTGTCC TAAACTGTTT ACAT Ct t ACC CAGTAGCTT G ACC TCT TCC C
P977961  1030 CTCCCTGTCC TAAACTGTTT AGAT Ct c ACC CAGTGGCTAG ACC TCT TCC C
          * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * *
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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 . . . . .
P977959   1178 - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
P977960  1078 ACTT TCC AAA TGAT GAAt g g a g a a c c c a a g a g g g c C CCA A AGATCT AGGT
P977961  1080 ACTT CTC AAA CGAC GAAt g a a a a - - - - - - - - - - - C CCA A AGGTCC AGGG
          * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * *
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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 . . . . .
P977959   1178 - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
P977960  1128 CAGCGGT TCC CAAC CTG GGA Gg g g a g t t g g g g g g c g t TGA ACT ACT TT TA
P977961  1118 CAGCGGT TCT CAAC CTG GGA Gt t g a a c g a c t - - - - - - - - - CT TT TA
          * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * *
          * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * *
          * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * *
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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 . . .
P977959   1191 CAGGGGCTC t - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
P977960  1178 CAGGGGT CTC CT AA GAC CGT TGGC - - - - - - - - - - - - - - - - - -
P977961  1155 CAGGGGT CTC CT AA AAC CAC TGGC g t a t c g g g t a t t t a c a g t a g g 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.

	P977960 (1201 bp)	P977961 (1201 bp)
P977959 (1201 bp)	0.079 23 %	0.066 17 %
P977960 (1201 bp)		<u>1.000</u> <u>77 %</u>

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

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

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

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GEMS Launcher 4.1.1

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

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

DiAlign professional TF Release 3.1 December 2004

Tue May 3 22:33:50 2005

Solution parameters:

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

Aligned Sequences:

No.	Sequence Name	Sequence Description	Length
1	P875598	sym=COX4I1 loc=Loc1327 taxid=9606 spec=Homo sapiens chr=16 ctg=NT_010498 str=(+) start=39446895 end=39448095 len=1201 tss=501 comm=cytochrome c oxidase subunit IV isoform 1; (NM_001861/501/silver;)	1201 bp
2	P875602	sym=Cox4i1 loc=Loc12857 taxid=10090 spec=Mus musculus chr=8 ctg=NT_078575 str=(+) start=45821111 end=45822366 len=1256 tss=501,517,556 comm=cytochrome c oxidase subunit IV isoform 1; (AK012583/524/gold;AK019276/579/gold;NM_009941/540/silver;)	1256 bp
3	P875604	sym=Cox4a loc=Loc29445 taxid=10116 spec=Rattus norvegicus chr=19 ctg=NW_047536 str=(+) start=13459368 end=13460568 len=1201 tss=501 comm=cytochrome c oxidase, subunit 4a; (NM_017202/501/bronze;)	1201 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\$ETSF V\$ZF35 V\$TEAF V\$APIR V\$DEAF V\$NRF2 V\$DICE V\$CMYB V\$MYOD V\$RORA V\$SEREF
V\$SEREF V\$SIF1 V\$COUP V\$ZF5F V\$E4FF

alignment position	1 1 1 2 1 3 1 4 1
P875598	1 g g g g c g a g g - - - - -
P875602	1 - - - - -

		* * * * *		* * * * *	* * * * *	* * * * *	
		*					
		*					
alignment position		3 0 1	3 1 1	3 2 1	3 3 1	3 4 1	
P875598	223	- - - - -	- - - - -	CCCGAGGCC	CCTGGGCGCG	C GGC TGAGGC	
P875602	216	c c a c g a c c	CT CC GCT G C A C G	CC GT G A C G C T	CT C G C A C C T C	C G G C C G C G G C	
P875604	289	c a c g a - -	CC C C A C T G C A C G	CT A A G A T G A G	CT C C C A C C A C	C A G C t a c a G C	
			* * * * *	* * * * *	* * * * *	* * * * *	
							**
alignment position		3 5 1	3 6 1	3 7 1	3 8 1	3 9 1	
P875598	253	C T g g a c c c g c	t g c c t g g c c g	c g c g g C G C C T	C A G C C G a g a a	g c g g g a c g a g	
P875602	266	C T C C - - - -	- - - - -	- - - - - C G C C T	C A G C C G G T - -	- - - - -	
P875604	336	C T C C - - - -	- - - - -	- - - - - C G C C T	C A G T C C G C - -	- - - - -	
		* * * *		* * * *	* * * * *		
		* * * *		* * * *	* * * * *		
alignment position		4 0 1	4 1 1	4 2 1	4 3 1	4 4 1	
P875598	303	g c g g c g g c g a	t t g a t g g c g c	g g c c g c g g g c	t g g c g g g g g a	c c c t t c a g g c	
P875602	283	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	
P875604	353	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	
alignment position		4 5 1	4 6 1	4 7 1	4 8 1	4 9 1	
P875598	353	c c g g c c c c g t	t t g g g c c t c g	g c t c c t g g a a	a a g c g a c t c g	c g c c t c t g g g	
P875602	283	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	
P875604	353	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	
alignment position		5 0 1	5 1 1	5 2 1	5 3 1	5 4 1	
P875598	403	a a g c c g c a g c	c c c a g a c t c c	a g t c g c g c t t	c t c g c c c g g c	g CCGCCGGAA	
P875602	283	- - - - -	- - - - -	- - - - -	- - - - -	- CCGCCGGAA	
P875604	353	- - - - -	- - - - -	- - - - -	- - - - -	- CCGCCGGAA	
						* * * * *	
						* * * * *	
alignment position		5 5 1	5 6 1	5 7 1	5 8 1	5 9 1	
P875598	453	a g c a g c c t c t	c c A A - - - -	- - - - -	C G C C T G C C G G	A A A G C A G C C C	
P875602	292	- - - - -	- - A A - - - -	- - - - -	C G T C T G C C G G	A A A G C A G C t g	
P875604	362	- - - - -	- - A g c g t a g t	c g c t a g c t a g	C G T C T G C C A G	A A A G C A G C G C	
			* *		* * * * *	* * * * *	
			*		* * * * *	* * * * *	
alignment position		6 0 1	6 1 1	6 2 1	6 3 1	6 4 1	
P875598	487	GGCC- - - - C	GGCATTTTAC	GACG	TTCG- - - - -	- - - - -	
P875602	314	c t a c c c G C T C	GGCCTTTCGC	GA CA	Gt t a c c	g c c c c g c c c c	g c c t c g t c c t
P875604	400	G G C C t - G C T C	GGCCTTTCGC	GA CA	G C T G - - - - -	- - - - -	- - - - -
		* * * *	* * * *	* * * *	* * * *	* * * *	
			* * * *	* * * *			
alignment position		6 5 1	6 6 1	6 7 1	6 8 1	6 9 1	
P875598	510	- - - - -	- - - - -	- - - - -	- - - - -	CA GCGCTAC CCT	
P875602	364	g c c c c g c c c t	g c c c c g a g c c	g c g c c g c c c c	g c c c c g c c	CC GCCCGCGCT	
P875604	427	- - - - -	- - - - -	- - - - -	- - - - -	CC GCACCGCGAT	
						* * * * *	
alignment position		7 0 1	7 1 1	7 2 1	7 3 1	7 4 1	

P875598 522 T T T CCGC T c c a c g g t g a c c t c c g t g c g g c c g g g t g c g g g c g g a g t c T T C C
P875602 414 C T G A A A C G G A C G G G C T T G G G G C G G G G g c t - - - - - - - - - - - - - - - T C C C
P875604 439 C T G A A G C T G A T G G A C G T G G G C G G G G c t t c t t c - - - - - - - - - - - - - - -

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

P875598 572 T C G A T C C C G T G G T G C T C C G C G G C G C G G C C T **T G C T C T - - - - -**
P875602 446 T G A T T C C C G C G A T G C T T C G C G G C T C C G T C T T G G T C T T C C G G t T G C G G G C C
P875604 471 - G A T T C C C G C G A T G C T T C G C G G C A C C G T C T T G C T C T T C C G G - T G C G G G A C

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

P875598 608 - - - - C T T C C **G G T C G C** G g g a c a c c - - G G G T **G T A G A G G G C G** **G T C G C G G C G G**
P875602 496 **C C G T T C T T C C** **G G T C G C** G A G C A C C C c a G G G T **G T A G A G G G C G** **G T C G C G G C G G**
P875604 519 **C C G C T C T T C C** **G G T C G C** G A G C A C C C **g - G G G T** **G T A G A G G G C G** **G T C G C G G C G G**

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

P875598 651 - - - - - G C A G T G **G C G G C A** **G G T G A g a c a g** g a g - - - - - - - - - - -
P875602 546 T C G C C T G G G C A G C G **G T G G C A** **G G T G A C G G C** T T G G A C G G C G G G T G A G G G T G
P875604 568 T C G C C T G G G C A G C A **G T G G C A** **G G T G A C G G C** C T T T G A C A G C G G G T G A G G G C G

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

P875598 676 - G T G G C C G G - T G C G G C G C C
P875602 596 G C a c g g t c g g g G G C C C G A G G A C C T G G A G C G C C G G G C C G G g A G C G G T G C C
P875604 618 G C g c g g c c a t - G G G C C G A G A T C C T G G A G C G C C G G G C C G G - A G C G G T G C C

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

P875598 693 G C C A G G C C G G G C G G G T C G G G G G C c g g g a g c c a t c a a g t c t g c a c g t c c
P875602 646 T C C G A G A C G C C C C G G A C C C G G G A C T T G A G C **g G C T C G G - - - - -**
P875604 666 T C C G A G G C G C C C C G G A C T C G G G A C T T G A G C **C a G C T 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

P875598 743 g c a g c c t g g c c g c t c g g c t t c a g c a g g a a g c a c c g a a t g g g c c t c g g a g c
P875602 684 -
P875604 704 -

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

P875598 793 c a g g t g a c a t t g a g g c c g g c c c g t g g g g a c t c c g g g c t c g g t g g c t c c a g

P875602	684	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -
P875604	704	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -
alignment position		1 1 0 1	1 1 1 1	1 1 2 1	1 1 3 1	1 1 4 1
P875598	843	g c t c g g g g g g	c c g c c c g a a	g t g c c c g g t c	c a t c t t a c c c	g g t c t c g c a g
P875602	684	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -
P875604	704	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -
alignment position		1 1 5 1	1 1 6 1	1 1 7 1	1 1 8 1	1 1 9 1
P875598	893	c g g c t g c g g a	c c g g c c t c g g	g c a c T G A C C T	T G G A G C G C C C	G C T g g c c g a -
P875602	684	- - - - -	- - - - -	- - - - T G A C C T	T G G G G C G C C C	G C T T C C C c g a
P875604	704	- - - - -	- - - - -	- - - - T G A C C T	T G G G G C G C C C	G C T T C C C g 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
P875598	942	- - - - -	- - - - -	- - - - -	- - - - G G G C T	C A G G C T G C G G
P875602	710	G C G G G T C T G T	T G T C T C G G G T	C C C C g c - - - -	- - - - - T C	C G G C C T G C C G
P875604	729	G C G G A T C T G T	T G T C T T G G G T	C C C C a t t t g c	c g t t c G G T T C	C G G C C T G C C C
		* * * * *	* * * * *	* * * * *	* * * * *	* * * * *
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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
P875598	957	G G A G G C G G G C	C C G C G C T C T G	T G C C t g c a g c	c t c c g c c c t t	g c t c c t t c a a
P875602	748	G G C A C C G G G C	G T T C C C G C T G	T G C C - - - - -	- - - - -	- - - - -
P875604	779	A G C A T C G G G C	G T T C C C G C T C	C G C C - - - - -	- - - - -	- - - - -
		* * * * *	* * * * *	* * * * *		
		* * * * *	* * * * *	* * * * *		
alignment position		1 3 0 1	1 3 1 1	1 3 2 1	1 3 3 1	1 3 4 1
P875598	1007	a a g g t c c c t g	t g c a a c c c c t	c c c g g g t t t t	g c g g g g c t c c	c g g g c g g c g c
P875602	772	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -
P875604	803	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -
alignment position		1 3 5 1	1 3 6 1	1 3 7 1	1 3 8 1	1 3 9 1
P875598	1057	t c g g c t t t c c	a g c c t g g a a g	g c g c c t a t t g	t t t g c t c a c g	c a a g g g c t A G
P875602	772	- - - - -	- - - - -	- - - - -	- - - - -	- - - - - A G
P875604	803	- - - - -	- - - - -	- - - - -	- - - - -	- - - - - A G
						* * * * *
						* * * * *
alignment position		1 4 0 1	1 4 1 1	1 4 2 1	1 4 3 1	1 4 4 1
P875598	1107	G C C C A A G G a g	a g a a g c t a g a	c g c g g g c g t t	c A G C C C T G A C	G T C A T G C T t g
P875602	774	G C C C G A G G G A	C A G C G A C C T G	- - - - -	- A G C C C T G A C	G T C A C G C T A C
P875604	805	G C C C G A G G G A	C A G C G A G C T G	- - - - -	- A G T C C C T G A C	G T C A C G C T A C
		* * * * *	* * * * *		* * * * *	* * * * *
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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
P875598	1157	t t t a T T C T G C	C C C A A G G A G G	G T A T - - - - -	T T c c c c a c a t	c a c t c t c a c c
P875602	813	G G T - T T C T G C	C G C C C C G G G C	G T T G a t t t t t	T T T T T C C C G G	G C T C G G A C G T
P875604	844	G G T - T T C T G C	C G C C A C G G G C	G T T G - - - - -	T T T T T T G C G G	T C T C G G G C G 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		
P875598	1201 a - - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -
P875602	862 T C T T T C T C G G	G G A T C G A A t c	t c - -	A G G G G T	T G T G C T A C A G	T G A G G C G T G G	
P875604	887 T C G C T C T C G G	G G A G C G A A a t	c a a g	A G G G G T	T G T G T T A A A G	T G A G G C G T G G	
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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		
P875598	1202 - - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -
P875602	910 G G C T C G G G T C	G C T G G G G C G G	G T G A C A G G G T	C A T C C A G G T C	G C C T G C G G G A		
P875604	937 A G C T C G G G T C	G C T G G G G C G G	G T G A C A G G G T	C A T C C A G G T C	G C C T G C G G G C		
	* * * * *	* * * * *	* * * * *	* * * * *	* * * * *	* * * * *	* * * * *
	* * * * *	* * * * *	* * * * *	* * * * *	* * * * *	* * * * *	* * * * *
	* * * * *	* * * * *	* * * * *	* * * * *	* * * * *	* * * * *	* * * * *
				* * * * *	* * * * *	* * * * *	* * * * *
alignment position	1 6 0 1	1 6 1 1	1 6 2 1	1 6 3 1	1 6 4 1		
P875598	1202 - - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -
P875602	960 C G C A g g a A C G	G G A A G C G G G C	C A G G G C C T G A	G C C T G G G C G G	C C T C C T C c c g		
P875604	987 C G C A g g g A C G	G G A A G C G C G C	C A G G G C T A G G	G C T T G G G C G G	C C T C C T C c g c		
	* * * * *	* * * * *	* * * * *	* * * * *	* * * * *	* * * * *	* * * * *
	* * * * *	* * * * *	* * * * *	* * * * *	* * * * *	* * * * *	* * * * *
	* * * * *						
	* * * * *						
alignment position	1 6 5 1	1 6 6 1	1 6 7 1	1 6 8 1	1 6 9 1		
P875598	1202 - - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -
P875602	1010 c t t g c C C T T C	G C A G T C T C T G	T A C A A G T C A A	T T T T T A A A A T	A A A A C t c a g t		
P875604	1037 t t g t - C C T T C	G C A G T C T C T G	C G C A A G T C G A	T T T T T A A A A T	A A A A C c a a g t		
		* * * * *	* * * * *	* * * * *	* * * * *	* * * * *	* * * * *
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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		
P875598	1202 - - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -
P875602	1060 - C G C A G G A G G	T G t g c t a c c g	t g c t a t c t a t	c t a t c t a t c t	a t c t a t c t a t		
P875604	1086 c C G C A G G C G G	T G c t c c c a c c	g c c a c a g a g a	g g a a c a g c t c	g t g g t g g c a c		
		* * * * *					
alignment position	1 7 5 1	1 7 6 1	1 7 7 1	1 7 8 1	1 7 9 1		
P875598	1202 - - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -
P875602	1109 c t a - - T A T A T	C T A G T T C T A G	C A G T T T C A G T	C A T t T T T G T C	T T T C T A G T T A		
P875604	1136 c g t g c T A T A C	C G A G T T C T A G	C A G T T T C A G T	C A T - T C T G G C	C T T C T A G T T A		
		* * * * *	* * * * *	* * * * *	* * * * *	* * * * *	* * * * *
		* * * * *	* * * * *	* * * * *	* * * * *	* * * * *	* * * * *
		* * * * *	* * * * *	* * * * *	* * * * *	* * * * *	* * * * *
alignment position	1 8 0 1	1 8 1 1	1 8 2 1	1 8 3 1	1 8 4 1		
P875598	1202 - - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -
P875602	1157 A T T T T T A A G	A a g c c g g a t t	t a t a g t c a t t	g g c c a a a g c c	a t g t a t a t t a		
P875604	1185 A T C T T T A A A A	A g c t g c g - - -	- - - - -	- - - - -	- - - - -		
		* * * * *					
alignment position	1 8 5 1	1 8 6 1	1 8 7 1	1 8 8 1	1 8 9 1		
P875598	1202 - - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -
P875602	1207 c a g c c c t t g g	c t t g a t g t a a	g g a a g t t c a c	c c t g t g c c t t	c g c a t c a g t a		

P875604 1202 - - - - -

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.

	P875602 (1256 bp)	P875604 (1201 bp)
P875598 (1201 bp)	0.300 32 %	0.294 30 %
P875602 (1256 bp)		<u>1.000</u> <u>74 %</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

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

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

DiAlign professional TF Release 3.1 December 2004

Thu May 5 21:49:15 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)

- ALL user_defined.lib (0.75/Optimized)
- ALL vertebrates.lib (0.75/Optimized)

Selected groups
(core/matrix sim):

Aligned Sequences:

No.	Sequence Name	Sequence Description	Length
1	P878122	sym=COX5A loc=Loc9377 taxid=9606 spec=Homo sapiens chr=15 ctg=NT_010194 str=(-) start=46020090 end=46021207 len=1118 tss=501,505,518 comm=cytochrome c oxidase subunit Va; (AK026623/548/gold;AK026615/552/gold;NM_004255/565/silver;)	1118 bp
2	P878123	sym=Cox5a loc=Loc12858 taxid=10090 spec=Mus musculus chr=9 ctg=NT_039474 str=(+) start=3799809 end=3800917 len=1109 tss=501,509 comm=cytochrome c oxidase, subunit Va; (AK018723/552/gold;NM_007747/560/silver;)	1109 bp
3	P878124	sym=Cox5a loc=Loc252934 taxid=10116 spec=Rattus norvegicus chr=8 ctg=NW_047799 str=(+) start=30893983 end=30895083 len=1101 tss=501 comm=cytochrome c oxidase, subunit Va; (NM_145783/525/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.

[VSEGRF](#)
[VSSPIF](#)
[VSMTEF](#)
[VSMOIC](#)
[VSEREF](#)
[USEREF](#)
[VSRARF](#)
[VSMINI](#)
[VSEBOX](#)
[VSAP2F](#)
[VSETSF](#)
[USNRF2](#)
[VSMYOD](#)
[VSNEUR](#)
[VSGREF](#)

alignment position	1	1 1	2 1	3 1	4 1
P878122	1 g - - - - -	- - - - -	- - - - -	- - - - -	CCTGGC TAATTTTGTA
P878123	1 c c a a a t g t t	g a t t a t t g t c t t g	AGTCACT	ACTCCAGTA	TGATTTTTTT

P878124	1	- - - - -	- - - - -	- - - - -	- - - - -	AGACGCC	ACTCCCAGT	A	TGA	a a a a a a a
						*	*	*	*	*
alignment position		5 1	6 1	7 1	8 1	9 1				
P878122	18	T - -	TTTTAG	TAGAGACGGG	g g t t c c t c c a	t g t t g c c c a g	g c t g g t c t t g			
P878123	51	T - -	TTTTCT	GAGACTCAGG	T T G C A T A A G A	G A G C C T G A A A	T T C C t a a t a C			
P878124	28	t t c c	TTTTCT	GAGACTCAGG	A T G C A T A G G A	G A G T T T G A A A	T T C C t a a t c C			
		*	*	*	*	*	*	*	*	*
		*	*	*	*	*	*	*	*	*
		*	*	*	*	*	*	*	*	*
		*	*	*	*	*	*	*	*	*
alignment position		1 0 1	1 1 1	1 2 1	1 3 1	1 4 1				
P878122	65	a a c t c c c g a c	c g 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 c a	AAAGT	GCT	GG		
P878123	98	T T A G C C T G T -	- - - - -	- - - - -	- - - - -	- - - - -	AGAGG	GCT	AG	
P878124	78	T T A G C C T G T -	- - - - -	- - - - -	- - - - -	- - - - -	AGAGG	GCT	GG	
		*	*	*	*	*	*	*	*	*
		*	*	*	*	*	*	*	*	*
		*	*	*	*	*	*	*	*	*
		*	*	*	*	*	*	*	*	*
alignment position		1 5 1	1 6 1	1 7 1	1 8 1	1 9 1				
P878122	115	G A T T A C A G g c	a t g a g c c a C A	G C G C C C G G G C	G C A A A G t a c G	T A T T T T T T A T				
P878123	117	A A T T A T A G C A	T A C A C - - - C A	A C G C G C G G G G	G C A A A G C G - G	T T A T T C T T A T				
P878124	97	G A T T A T A G C A	T A C A C - - - C A	A t a c c t - G G G	G A A A A G C G - G	T T A T T C T T A T				
		*	*	*	*	*	*	*	*	*
		*	*	*	*	*	*	*	*	*
		*	*	*	*	*	*	*	*	*
		*	*	*	*	*	*	*	*	*
alignment position		2 0 1	2 1 1	2 2 1	2 3 1	2 4 1				
P878122	165	T A T A G T T T G T	T G T T A T T G C T	G T C A t t c c t a	t t t t g a g g t g	a t t a a g t g c C				
P878123	163	T A T A G T T T G C	C G T T A T T A t c	G C T A C A A T T C	C A A A T T G T G A	T A G T C T - - - C				
P878124	142	T A C A G T T T A T	C G T T A T T A T T	G C C A C A T T T C	G A T T T C G T G A	T A G T C T - - - C				
		*	*	*	*	*	*	*	*	*
		*	*	*	*	*	*	*	*	*
		*	*	*	*	*	*	*	*	*
		*	*	*	*	*	*	*	*	*
alignment position		2 5 1	2 6 1	2 7 1	2 8 1	2 9 1				
P878122	215	C T C C T G G G C C	T G A C T C G A A C	A A G A T C A C G G	T C G G TTGCT -	- - - - -				
P878123	210	C T C T G T T G G C	G a - - T T C C A A	A T C C A C A T T G	T C C A T T G C T C	ACCCTG	CCTT			
P878124	189	C T C C G T T G G C	G G A T T T C A A A	A T C C A C A T T G	T C C A T T G C T C	G C C C T G	ACTT			
		*	*	*	*	*	*	*	*	*
		*	*	*	*	*	*	*	*	*
		*	*	*	*	*	*	*	*	*
		*	*	*	*	*	*	*	*	*
alignment position		3 0 1	3 1 1	3 2 1	3 3 1	3 4 1				
P878122	254	- CCTCCCTCG	Cctcc a t t c c	t a c t t a c a g g	a t g g c a g c t g	C A C G T C A C C T				
P878123	258	TCCTCCACG	CAGGA A T G T T	C A C T A C G G T C	A C C - - - - -	C G G T C A T C G				
P878124	239	TCCTCCACG	CAGGA A T G T T	C A C T A C A G C C	A G C - - - - -	C A G G T C A T C G				
		*	*	*	*	*	*	*	*	*
		*	*	*	*	*	*	*	*	*
		*	*	*	*	*	*	*	*	*
		*	*	*	*	*	*	*	*	*
alignment position		3 5 1	3 6 1	3 7 1	3 8 1	3 9 1				
P878122	303	G A C C A G a g a c	a a g g c g g g a c	g c g a g g c t a a	c a G T T T G T C C	T C A G C G C G C C				
P878123	301	G A C C A G C T T T	G G C G C G G C G C	C G A C G T G - - -	- - G T T T G T C C	T C C A C G - G C C				

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P878124 282 G ACC AG CAC T  GACTC GGC GC  AGAC GTG - - - - GT TT GTCC TCG AC GCG CC
      * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * *
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      * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * *

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

P878122 353 GCCGTAGCC CCGCCGcgc cggcgcgcggtggctcctcccgccACGC
P878123 345 GCCGTAGCCG CCGGC GAC CG CATG GCG CCC CACC C GCTTC CGT - - AGGC
P878124 327 GCCGTAGTGA CCGGC GAC CG CATG GTG CCC CACC C GCTTC CGT - - AGGC
      * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * *
      * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * *
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alignment
position    4 5 1 . . . . .   4 6 1 . . . . .   4 7 1 . . . . .   4 8 1 . . . . .   4 9 1 . . . . .

P878122 403 GCCA GAGTC G CAGTGGGCGG GCCTacgTGC TCCGCCGcctgtgagccct--
P878123 392 GCGAGCTCCG CAGTGGGCGG GCCTTA-TGC TCCGCCCAGC GTGCGTCGCT
P878124 374 GCGAGCTCTG CAGAGGGCCG GCCTTA-TGC TCCGCCCAGC GTGCGTCGCT
      * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * *
      * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * *
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alignment
position    5 0 1 . . . . .   5 1 1 . . . . .   5 2 1 . . . . .   5 3 1 . . . . .   5 4 1 . . . . .

P878122 451 - - - - - GTCC GGCCCCCGCc c g c t c c g g a g c a a C C C G C G A G C T T A C A C C G
P878123 441 GCGT GAGTCC GGCCCCCGCG AACTGCTGTACCGCCGCGA GCTCACACCG
P878124 423 GCGT GAGTCC GGCCCCCa a G AACTGCTGTGCCCGCGA GCTCACACCG
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      * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * *
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alignment
position    5 5 1 . . . . .   5 6 1 . . . . .   5 7 1 . . . . .   5 8 1 . . . . .   5 9 1 . . . . .

P878122 495 GCTTCTCTc t g t CCTCAGCC CGCGCGCCGC CATCGCCGT C ATGCTGGGCG
P878123 491 GCTTCTCgTC AGCCTCAGCC AGTGCCTGT GGTGCGCGT C ATGCTCGCCG
P878124 473 GCTTCTCTT C AGCCCAGCC AGTGCCTGT GGTGCGCGT C ATGCTCGCCG
      * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * *
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alignment
position    6 0 1 . . . . .   6 1 1 . . . . .   6 2 1 . . . . .   6 3 1 . . . . .   6 4 1 . . . . .

P878122 545 CCGCTCTCCG CCGCTGCGCT GTGGCCGCaa ccacccgggc cgaacctCGA
P878123 541 CTGCCCTCCG TCGCTGTACC GCAGCCGCGG CtGCC - - - - - - - - - - CGA
P878124 523 CTGCCCTCCG TCGCTGTACC GCAGCCGCGG CcGCC - - - - - - - - - - CGA
      * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * *
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alignment position	6 5 1	6 6 1	6 7 1	6 8 1	6 9 1
P878122	595 G G C C T C C T G C	A C T C C G C C C G	G A C C C C C G G C	C C C G C C G t g G	G T A A G G C C C C
P878123	579 G G C C T C C T G C	A C C C C G C C T C	G G C T C C C A G C	C C C G C C G C C G	G T A A G G T C C G
P878124	561 G G C C T T C T G C	A C C C C G T C T C	G G C T C C C A G C	C C C G C t G C C G	G T A A G G C C C G
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	* * * * *	* * * * *	* * * * *	* * * * *	* * * * *
	* * * * *	* * * * *	* * * * *	* * * * *	* * * * *
	* * * * *	* * * * *	* * * * *	* * * * *	* * * * *
	* * * * *	* * * * *	* * * * *	* * * * *	* * * * *
	* * * * *	* * * * *	* * * * *	* * * * *	* * * * *
	* * * * *	* * * * *	* * * * *	* * * * *	* * * * *
alignment position	7 0 1	7 1 1	7 2 1	7 3 1	7 4 1
P878122	645 T G C T T G C C A C	T G C C C G C G C C	C T C G T G T C C T	T G C G G T G A C C	T G G G T C C C C G
P878123	629 C G C C G C C A C	A G C C C T C G C T	C G C G T G T C C T	T G C T G T G A C C	T G G G C T C C C G
P878124	611 C T C C C G C C A C	A G C C C G C G C C	C G C G T G T C C T	T G C T G T G A C C	T G G G C T C C C G
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	* * * * *	* * * * *	* * * * *	* * * * *	* * * * *
	* * * * *	* * * * *	* * * * *	* * * * *	* * * * *
alignment position	7 5 1	7 6 1	7 7 1	7 8 1	7 9 1
P878122	695 C T G C C A C T C C	G G G G C G G G C T	C t c c c - C G G C	C T A G C C C T T G	C C C T a c c c t g
P878123	679 C C G C C A C T C G	A G G G C A G G C T	C C C T G G C G G C	C T A G C C T T T G	C C C T G C g A G C
P878124	661 C C G C C A C T C G	A G G G C A G G C T	C C C T G G C G G C	C T A G C C T T T G	C C C T G C a A G C
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	* * * * *	* * * * *	* * * * *	* * * * *	* * * * *
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	* * * * *	* * * * *	* * * * *	* * * * *	* * * * *
alignment position	8 0 1	8 1 1	8 2 1	8 3 1	8 4 1
P878122	744 g t t a c t - - G A	A C C C G G T G A C	C G C G G G C C G C	C C t g e c C G C C	G C C T C G A G T A
P878123	729 C G G C A T T G G A	G C C C G G T G A C	C G C A G T G C G T	C C g c g - - G C C	G T C T G G A G T C
P878124	711 C G G C A G T G G A	G T C C G G T G A C	C G C A G G g t a t	c c a - - C T G C C	G T C T G G A G T T
	* * * * *	* * * * *	* * * * *	* * * * *	* * * * *
	* * * * *	* * * * *	* * * * *	* * * * *	* * * * *
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	* * * * *	* * * * *	* * * * *	* * * * *	* * * * *
	* * * * *	* * * * *	* * * * *	* * * * *	* * * * *
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	* * * * *	* * * * *	* * * * *	* * * * *	* * * * *
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	* * * * *	* * * * *	* * * * *	* * * * *	* * * * *
alignment position	8 5 1	8 6 1	8 7 1	8 8 1	8 9 1
P878122	792 G T G G A G G A c c	t g a a a g c g c g	c C C C G G G G C	C T C C C C C G C	G C A A C T T C C T
P878123	777 G T G T A G G A G A	CT - - - - -	- C C T C C G G G C	C T C C C T C C C C	G C C A C T T C C T
P878124	759 A T G T G G G A G A	CT - - - - -	- C C C G G G G C	C T C C C T - C C C	G C C A C T T C C T
	* * * * *	* * * * *	* * * * *	* * * * *	* * * * *
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	* * * * *	* * * * *	* * * * *	* * * * *	* * * * *
alignment position	9 0 1	9 1 1	9 2 1	9 3 1	9 4 1
P878122	842 G g c t g t g c c a	C C G C G G A C A G	g t c a g a - T G T	G G A C C T G C T G	T G G G C G C C G A
P878123	818 G A T G C C G a a c	C C G C G G C C A G	T C A G A G T G T G T	G G A C T T G C C G	G G G T C G C C G A
P878124	799 G A T G C C G g a t	a c a C G A C C G G	T C A G A G T G T A T	G G A C C T G C C C	G G G T C G C T A A
	* * * * *	* * * * *	* * * * *	* * * * *	* * * * *
	* * * * *	* * * * *	* * * * *	* * * * *	* * * * *
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alignment position 951 961 971 981 991
P878122 891 GGAGGGGACG CAGCGCTCCC CTTCGGT TCC CGGGCCATGA CCCTGCCCCca
P878123 868 GGAcgag-GCT CAGCACTTCC TTTCAGTCTC TGGGCCGTGA CCGTTCCCTG
P878124 849 CGACAGGGCT CATCACTTCC TTTCAGTCTC TGGGCCGTGA CCGTTCCCTG

alignment position 1001 1011 1021 1031 1041
P878122 941 gcgccGACCC T GCGGCCACC T GACCGAGAG TGGCCG CCGC CGGCC t g c a G
P878123 917 CGCT-GACCC C G C A G C C A C C T G A C C G G A G T G G C C C C G C C G G C C T G C G G
P878124 899 CGCT-GACCC C G C A G C C A C C T G A C C G G A G T G G C T C C C G C C G G C C T A C G G

alignment position 1051 1061 1071 1081 1091
P878122 991 CGCCTCGGC AAGGTGACAT TGAGCCTCCG GGCACGCCGC t t g g g - - -
P878123 966 CATCTTGGC AAGGTGACAT TGAGCCTCCG GGCAGGCCGC CCGCCTCTGC
P878124 948 CGTCTTGGC AAGGTGACAT TGAGCCTCCG GGCAGGCCGC CCGCCTCTGC

alignment position 1101 1111 1121 1131 1141
P878122 1037 - - T C G A G G A C A C A A T A T A C T T C G t a - T G G A C A C A c g a t t a t a c t t t
P878123 1016 G T T T C T A G A A C A C A A T T T G A T T C C C A G T G G A C A C A A T A C C C T T T T A G
P878124 998 G T T T C T A G A A C A C A A T T C G A T T C C C A G T G G A C A C A A T A C C C T T T T A G

alignment position 1151 1161 1171 1181 1191
P878122 1083 t c - - A A T C A G G C A T T T C T C G G T T A G C G A T T - A G T G T G t c - - - - -
P878123 1066 C C C T g A T C A G G C A A T T C T C T G C T G G C A T T T t T G T G T C A C C T T C A - - - -
P878124 1048 T C C T A A T C A G G C A A T T C T C T G C T G G C A T T C - T G T G T C A C C T T C A t a a c g g


```

alignment      1 2 0 1 .
position
P878122 1119 - - - - -
P878123 1110 - - - - -
P878124 1097 g t a c 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.

	P878123 (1109 bp)	P878124 (1101 bp)
P878122 (1118 bp)	0.267 52 %	0.238 52 %
P878123 (1109 bp)		<u>1.000</u> 87 %

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

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

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

DiAlign professional TF Release 3.1 December 2004

Thu May 5 22:14:45 2005

Solution parameters:

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

Aligned Sequences:

No.	Sequence Name	Sequence Description	Length
1	P875606	sym=COX5B loc=Loc1329 taxid=9606 spec=Homo sapiens chr=2 ctg=NT_022171 str=(+) start=328045 end=329345 len=1301 tss=501 comm=cytochrome c oxidase subunit Vb; (NM_001862/524/bronze;)	1301 bp
2	P875607	sym=Cox5b loc=Loc12859 taxid=10090 spec=Mus musculus chr=1 ctg=NT_039170 str=(+) start=14310302 end=14311631 len=1330 tss=501,530 comm=cytochrome c oxidase, subunit Vb; (AK008339/530/gold;NM_009942/501/bronze;)	1330 bp
3	P875608	sym=Cox5b loc=Loc94194 taxid=10116 spec=Rattus norvegicus chr=9 ctg=NW_047814 str=(+) start=1737477 end=1738777 len=1301 tss=501 comm=cytochrome c oxidase subunit Vb; (NM_053586/531/bronze;)	1301 bp

Alignment (DiAlign format):

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

V\$EGRF
V\$NRF1
U\$NRF1
V\$ETSF
V\$NFKB
V\$SPIF
V\$STAT
U\$NRF2
V\$XBBF
V\$SF1F
V\$MYT1
V\$RARE
V\$RORA
V\$EREF
U\$EREF

```

alignment
position      1 . . . . . 1 1 . . . . . 2 1 . . . . . 3 1 . . . . . 4 1 . . . . .
P875606      1 c g a a a c t g - - - - - - - - - - - - - - - - - - - - G G C C A G G A C
P875607      1 t t a a a a a c a a a c a a A A C A G A G T G G A G G a - - G G G A A T T G A G G C T A A G A C
P875608      1 - - - - - - - - - - - - - - - A A G A G A G T G G A G G c g c G G G A T T G A G G C T A A G A C
    
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alignment position	5 1	6 1	7 1	8 1	9 1						
P875606	18 TGCAGGTAG-	- - - - -	GTCCCGTCCAA	TGCgacacgctc	gcgacggccc						
P875607	49 TGTGtg t g t g	gggggggt	GTACTGTCAATTT	CTGACggAGT	GGGCCATTC						
P875608	35 TGTGGGGAG-	- - - - -	GTCCCTGTCAA	TTCTGACccAGT	GGGCCATTC						
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alignment position	1 0 1	1 1 1	1 2 1	1 3 1	1 4 1						
P875606	60 acgcactgc-	- - - - -	- - - - -	- - - - -	- CAGAACCA	AGCCCTGCCACT					
P875607	99 ACAATTTGG	TAACA	ACTAAAGCT-	- GTCTGCAGTCT	CGAACCCGTGGCT						
P875608	77 ACAAGTTGG	TAATG	GCTAAAGCTc	tGTCTGCAGAC	CACGAACCTGCAGCT						
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alignment position	1 5 1	1 6 1	1 7 1	1 8 1	1 9 1						
P875606	88 AACCAAGCCTA	GTA	Aggaa	cgcatCTTTAGGAG	CCACTTCTAAATT						
P875607	147 AACAGGCATA	ACA	AAcAA	CAGG--	- CTTCCGTAGCTCA	CGCCCAAGGT					
P875608	127 CACAGGCATA	ACA	AAcAA	CAGT--	- CTTCCCGAGCTCA	CGCCCAAGGT					
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alignment position	2 0 1	2 1 1	2 2 1	2 3 1	2 4 1						
P875606	138 CAAATCATT	TGGGGT	TCAgt	aagtcctctc	acagacgggg	acctaatagc					
P875607	194 TGTATGATT	CGTGGT	ggaag	cccttgactg	cggga-AC	TTCGGCTTCCAC					
P875608	174 TGTACCATT	CGTGCT	TCAaa	tccctaac	tgaagaggACT	TTCGGCTTCCAC					
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alignment position	2 5 1	2 6 1	2 7 1	2 8 1	2 9 1						
P875606	188 tttccattagc	agcctccacg	tttgc	tgaacacgactac	gggcccagac	CC					
P875607	243 AGCACCTCCA	- - - - -	- - - - -	- - - - -	- - - - -	CT					
P875608	224 AGCACCTCCA	- - - - -	- - - - -	- - - - -	- - - - -	CT					
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alignment position	3 0 1	3 1 1	3 2 1	3 3 1	3 4 1						
P875606	238 ACAGGA	ACTCA	ATGTGG	TTCAGCCGCT	caactccaggga	ccaaaagac					
P875607	255 ACAAGA	ACTCA	CTATGTGG	CTGGGACACT	GGGCACAAC	ACCAAGCGGAc					
P875608	236 AC-	- - - - -	- TAAGTGG	CTTCGACTCT	GGGCGGAGCA	GC AAGCGGAa					
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alignment position	3 5 1	3 6 1	3 7 1	3 8 1	3 9 1						
P875606	288 tttccc	acctccc	agcgtta	ttaaaggca	aa	ccc-	- - - - -	- - - - -	CGCC		
P875607	305 aggtc	atgaa	ccCGAAAG	CCGCTAGCTG	TACAGGGT	GACTGAC	GCCACGCC				
P875608	277 cagtc	aa-	- - - - -	CGATAG	CCACAAG	GTAAC	CGGTAACTG	ACGCTACGCC			
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alignment position	4 0 1	4 1 1	4 2 1	4 3 1	4 4 1
P875606	325 C C C A A G e c t c	a g c c a - - C T A	C G C G G T G C A G	A A A G A G G C A G	A G C T G G G C A T
P875607	355 C C g g A G G C G	G C G G A G T C T G	C G C G G C C C A C	G A A G A G G C A G	A A C T G C G C A T
P875608	321 C C C A A G G C G	G C G G A G T C T G	C G C G A C C G G C	G A A G A G T C A G	A G C T G C G C A T
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alignment position	4 5 1	4 6 1	4 7 1	4 8 1	4 9 1
P875606	373 G C G C A A t t t c	c g c c c c g c c	a c a g t c t t g g	g a g t g g g c g g	g c t c g a g g g c
P875607	405 G T G C G G C G T C	T A C T T T T A G C	G C T G C T T C G G	C T G G t c - G G -	- - - - -
P875608	371 G T G C A A C A T C	T A C C T T T A G C	G C T T C T T C G G	C T G G c c g G G -	- - - - -
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alignment position	5 0 1	5 1 1	5 2 1	5 3 1	5 4 1
P875606	423 t G G G A G G A A G	C C G A A A G C T G	A C C G A G A G g a	g a a A G A A G C C	C G C C C C G G A
P875607	443 - G G C A G G A A G	C C G A A G A C T G	A C C G G G C G T T	G T T A G A C T C C	C A C C A A C G G A
P875608	410 - G G C A G G A A G	C C G A A A G C T G	A C T G G G C G T T	G T T A G A C a C C	T A C C A A C G G A
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alignment position	5 5 1	5 6 1	5 7 1	5 8 1	5 9 1
P875606	473 A G T C C C T C C T	G T C T C t g - C A	G C T T G T T C C C	G G A A G T T T T G	C T G C T A G T C G
P875607	492 A G T C C C G C C C	A T C T T G C T C A	G C C T G T T C C C	G G A A G T G C A T	C T G C T T G T C T
P875608	459 A G T C C C G C C T	G T C T T G C T C t	g t C T G T T C C C	G G A A G T G C A T	C T G C T T G T C T
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alignment position	6 0 1	6 1 1	6 2 1	6 3 1	6 4 1
P875606	522 C G G A C G c a A T	G G C T T C A A G G	T T A C T T C G	C G G A G c t g g a a c	g c T G G C C G C G
P875607	542 C G G G C G A G A T	G G C T T C A A G G	T T A C T T C G	C G G A G T G G G C G C	T T T G G C G G C G
P875608	509 C G A G C G A G A T	G G C T T C A A G G	T T A C T T C G	C G G A G T A G G C G C	T T T G G C G G C T
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alignment position	6 5 1	6 6 1	6 7 1	6 8 1	6 9 1
P875606	572 C A G G C C C T G A	G G G C T C G C G G	C C C C a G T G G C	G C G G C C G C G A	T G C G C T C C A T


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P875607 592 C A G G C C C T G A G G G C C C A C G G C C C C C G T G G C G C G G C C G T G A C C C G C T C C A T
P875608 559 C A G G C C C T G A G G G C C C A C G G A C C C C G T G G C G T G G C C G C T A C C C G C T C C A T
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alignment position 7 0 1 7 1 1 7 2 1 7 3 1 7 4 1

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P875606 622 G G C A T C T G G A G G T A C t c g g g t c t C C G G G C G T G C C A G G g a c c a g a g t g t t g
P875607 642 G G C T T C T G G A G G T A C G T G A C C A G C T G G G C G G G A C A G G C - - - - -
P875608 609 G G C T T C T G G A G G T A G G T G A C T A G C T G G G T G C G C C A G G T - - - - -
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alignment position 7 5 1 7 6 1 7 7 1 7 8 1 7 9 1

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P875606 672 c c c t c c c a g g g t g g t c c c a g g g c g g c a a a g c g g c g c g g c t c g t g c a g c t t
P875607 680 - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
P875608 647 - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -

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

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P875606 722 c t c g a g g t c c c a g t g g c c g c t t t a C G G T C C C C A G T G C C T C A G G C t c t g c a
P875607 680 - - - - - - - - - - - - - - - - - - - - C G G T G T C C A T G G C C T C C G G C T G G T T
P875608 647 - - - - - - - - - - - - - - - - - - - - C G G T G T C C T T G G C C T C C G A C G T G G T T
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alignment position 8 5 1 8 6 1 8 7 1 8 8 1 8 9 1

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P875606 772 g g c a - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
P875607 706 G G T g A T G G G C G G T C G A G C G G G G T C G G C C A T T A G c g t t c t C T C G A G C C C T G
P875608 673 G G T a A T G G G C G G T C G A G C G G G G T C G G C C A T T A G a g c t c c C T C G A G C C C T G
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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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P875606 776 - - - - - - - - - - - - - - - - - - - - - - - - - - - T C T C C C T G T A A
P875607 756 C T G A C C A C C T T A G G C T C C G G A G A C C G G C G c t c t g t C C G G T C T T G C T G T A A
P875608 723 C T G A C C A C C T T A G T C T C C G G A G A C C G G C G c c c g c C C G G T C T T G C T G T A A
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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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P875606 787 T T c t g g a c c g c t g c t c C T G C C G C T C C C C G A A C T C A C T C C G C T G C G A A A G T

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P875608 1060 T G T C A C C T T T C C C G T G T T G A T C T T T T T A G C G C G T A T T C A T C T T G G T C A T A
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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

P875606 881 - - - - -

P875607 1142 T C A a t t g c c g t a g c T C A T T T T T C T T C T T C T A G G T G G T G T C C C c A C T G A T G

P875608 1110 T C A g g t c c c a t a a t T C A T T T T T C T T C T T C T A G G T G G T G T C C C t A C T G A T G
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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

P875606 881 - - - - - G C C A C C G G G A T G G G G A G G G t c c g g c c t c c c t t c a a a c c t g c

P875607 1192 A G G A G C A G G C T A C T G G G C T G G A G A G G A G A T C A T G A T A G C A G C A C A G A A G

P875608 1160 A G G A G C A G G C T A C C G G G C T G G A G A G G A G A T C A T G A T A G C A G C A C A G A G 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

P875606 923 g c c c a c c t c a a g c a g a g t g g g t t c t a c a t g c t t t t a g a c a a a t g t c g a c a

P875607 1242 G G A C T G G T A A - - - - -

P875608 1210 G G A C T G G T G 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

P875606 973 a a t t t g c c t c g g t g g t t g g a g a a a g a a a a g c t c a t a g g c c g g g c g c g g t g

P875607 1252 - - - - -

P875608 1220 - - - - -

alignment position

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

P875606 1023 g c t c a c a a c t g t a a t c c c a g c a c t t t g g g a g g c c g a g g c G G A C A G A T C C C

P875607 1252 - - - - - G G A G A A A T G C T

P875608 1220 - - - - - G A A G c t - - - C T
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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

P875606 1073 C T G A G G T C A G G A G C T C a a g a c c a g c c t g g c c a a c a t g g t a a a c c c c g t t

P875607 1263 G T G T C C T C T G G A G C C C T G G G G C T T G G A T G G G A T T A - - - - -

P875608 1228 G T G T C C T C T G G A G A C C T T G G G C T G G A T G G G A T C A - - - - -
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alignment position

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

P875606 1123 t c t a c t a a a a a t a c a a a a t t a g c c g g g c g t g g t g g c g c g c g c c t g t a g t

P875607 1298 - - - - -

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P875608 1263 - - - - -
alignment
position      1 6 5 1 . . . . . 1 6 6 1 . . . . . 1 6 7 1 . . . . . 1 6 8 1 . . . . . 1 6 9 1 . . . . .
P875606 1173 c c c a g c t a c t c g g g a g g c t g a g g c a g g a g a a t c g c t t a a a c c c g g g a g GC
P875607 1298 - - - - - GA
P875608 1263 - - - - - GA
                                         *
                                         *
                                         *
                                         *

alignment
position      1 7 0 1 . . . . . 1 7 1 1 . . . . . 1 7 2 1 . . . . . 1 7 3 1 . . . . . 1 7 4 1 . . . . .
P875606 1223 G G A G G T T C C C G T G A G C C A A C A T C G C G C C A T T G C A c t c c a g c c t g g g c a a c
P875607 1300 G g a - G T T C C T G T C A G C C A G C G T C T G G T C C T G A - - - - -
P875608 1265 G G A G T C T C C T T T C A G C C A G C T T T T G G T C C T G A C A a c t - - - - -
      * * * * * * * * * * * * * * * * * * * * * * * * * * * *
      *           * * * * * * * * * * * * * * * * * * * * * *
      *
      *

alignment
position      1 7 5 1 . . . . . 1 7 6 1 . . . . . 1 7 7 1 . . . . .
P875606 1273 a a g a g c a a a a c t c c g t c t c a a a a a g a a a
P875607 1331 - - - - -
P875608 1302 - - - - -
    
```

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.

	P875607 (1330 bp)	P875608 (1301 bp)
P875606 (1301 bp)	0.148 29 %	0.142 27 %
P875607 (1330 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

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

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

DiAlign professional TF Release 3.1 December 2004

Thu May 5 23:50:03 2005

Solution parameters:

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

Aligned Sequences:

No.	Sequence Name	Sequence Description	Length
1	P879022	sym=COX6A2 loc=Loc1339 taxid=9606 spec=Homo sapiens chr=16 ctg=NT_010393 str=(-) start=22752500 end=22753300 len=801 tss=501 comm=cytochrome c oxidase subunit VIa polypeptide 2; (NM_005205/501/bronze;)	801 bp
2	P879023	sym=Cox6a2 loc=Loc12862 taxid=10090 spec=Mus musculus chr=7 ctg=NT_039433 str=(-) start=46288613 end=46289449 len=837 tss=501,537 comm=cytochrome c oxidase, subunit VI a, polypeptide 2; (AK002506/556/gold;NM_009943/520/bronze;)	837 bp
3	P879024	sym=Cox6a2 loc=Loc25278 taxid=10116 spec=Rattus norvegicus chr=1 ctg=NW_047562 str=(-) start=30145948 end=30146748 len=801 tss=501 comm=cytochrome c oxidase, subunit VIa, polypeptide 2; (NM_012812/584/bronze;)	801 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\$MYOD V\$AP4R V\$MEF2 V\$AREB V\$COMP V\$ECAT V\$PCAT V\$MZF1 V\$SETF V\$NKXH

```

alignment position 1 . . . . . 11 . . . . . 21 . . . . . 31 . . . . . 41 . . . . .
P879022      1 t g c c a a a a t c c a g g t t g a c a c a t t c c t a c c t t a c a t a a a c t t c a t a a a a
P879023      1 g c c c a g g a t a g c t t t g a c c t t g g t a c g t a g t c c a a g a t g g c c t t g a a c t c
P879024      1 - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
    
```

```

alignment position 51 . . . . . 61 . . . . . 71 . . . . . 81 . . . . . 91 . . . . .
P879022      51 t g a t g t a a g g g c c g t g t a g t g g c t c a t g c c t g t a a t c c c a g c a c t g t g g g
P879023      51 c t g a c c c t t c t g c c t c c a t g t c c c a a g t g c t g g c t g g c a t t a t a a a t a a g
P879024      1 - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
    
```

```

alignment position 101 . . . . . 111 . . . . . 121 . . . . . 131 . . . . . 141 . . . . .
P879022     101 a g g c t g a g g c g g g a g g a t c a c g t g a g c t c a a g a g t t c c a c a c c a g c c t g g
P879023     101 t g c a C C - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
P879024      1 - - - - - C C - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
                * *
                * *
                * *
                * *
    
```

```

alignment position 151 . . . . . 161 . . . . . 171 . . . . . 181 . . . . . 191 . . . . .
P879022     151 a c a a t a t a g t g a g a t c c c c g t c t c c a g t a t t t a a a a a a t c t t t t a a g g t a
P879023     107 - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
P879024      3 - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
    
```

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alignment position 201 . . . . . 211 . . . . . 221 . . . . . 231 . . . . . 241 . . . . .
P879022     201 c g a a t t a t t a t a c a t t t t a c a g c t g a a a A C A C T G A G A c t c a a a a a - - - -
P879023     107 - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
P879024      3 - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
                * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * *
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                * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * *
                * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * *
    
```

```

alignment position 251 . . . . . 261 . . . . . 271 . . . . . 281 . . . . . 291 . . . . .
P879022     246 - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
P879023     129 G G G A A A G A A C T C A G G a C A T T A T G G G T A C T T G G T A G G C A G A C A C T G C A G G C
P879024     25 G G G A A A G A A C T C A G G g C A T T A T G G G T A C T A A G T A G G C A G A C A C T C C A G G C
                * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * *
                * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * *
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                * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * *
    
```

```

alignment position 301 . . . . . 311 . . . . . 321 . . . . . 331 . . . . . 341 . . . . .
P879022     246 - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
P879023     179 A g t c T A C C A A C T G A G C T A C A C T C C C A C C C C A C C C C A C C C C C a c t g t - - A A
P879024     75 A t t T A C C A A C C G A A C T A C A C T C C C A C C C G A C C C C A C C C C A T T T T A A A
                * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * *
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alignment position 351 . . . . . 361 . . . . . 371 . . . . . 381 . . . . . 391 . . . . .
P879022     266 A A T A T T T A T T A A A G C C C A a c t g t g t g c c a g c c a c c a g g c a t a g a a t a g g g
P879023     227 A A T T T G T T T A A A G A C A A G A T C T T A G G T A G T T C A A G C T G T G A T C A A A C T C
P879024     125 A T T T T G T T T A A A G A T G G G A T C T T A G G T T G T T C A A G C T G C G C T C A A C T T C
                * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * *
                * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * *
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                * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * *
    
```

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alignment position 401 . . . . . 411 . . . . . 421 . . . . . 431 . . . . . 441 . . . . .
P879022     316 a a c a a a a t a g t t t c c c t g c a a c t a t a t a a a a a g a a t g g c a t a t t g t a c - -
P879023     277 A T T A A G T T G A T A A C A G T G G C C T T G A A C T C T G A T C C T C C A G C T T A C A T A T T
P879024     175 A C T A A C T T G A C C A C A G T G G C C T T G A A C T C T G A T C T T C C T G C C T A C C T G T T
                * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * *
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```

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alignment position 451 . . . . . 461 . . . . . 471 . . . . . 481 . . . . . 491 . . . . .
P879022     364 - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
P879023     327 T C A A G T t t g t a - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
    
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P879024 225 TCAAGTg ccg ggccgacagg cttgtatggc caagccagg gcg t at t TCA
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alignment position 501 511 521 531 541

P879022 364 - - TAAATGC CTCCTTGCCA AAATAAGAGG CACA **AGGACAA** **CAGCTGTCTG**
P879023 341 CTTAAATCT TCt CTGCCA AAATAAAGG CACA **TTGCAT** **CAGCTGCCTG**
P879024 275 CTTAAATGT TCCCTTGCCA AAATAAAGG CACA **TTGCAT** **CAGTGCCAG**

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alignment position 551 561 571 581 591

P879022 412 **G**AGATGACCT CAAGCCAGTC AGGCCCATT T TAAATATA **G** **AAA - CCCTA**
P879023 391 **A**AGAGGATCT CCTGCCAGTC AAGACCCACT T TAGATAGAG **AAAGCCCTA**
P879024 325 **A**AGAGGATCT CCTTCCAGTC AAGACCCACT T TAGt c AGAG **AAAGTCCCTA**

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alignment position 601 611 621 631 641

P879022 461 **AGAATAGCCg** **ccagtgctcc** aga **CTCAACA** **GGTGATTGGC** **CCAAGAGGG**
P879023 441 **AAAATAGCCA** **TCCATGTGCg** GG- **CTCAACA** **GGTGATTGGC** **TCTGAGAGGG**
P879024 375 **AAAATAGCCA** **TCCATGTGCc** GG- **CTCAACA** **GGTGATTGGC** **TGCAGAGTGG**

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alignment position 651 661 671 681 691

P879022 511 **G**AGGTGACC Cag g c c c c a g g a a a g g g a g c g - - - - AGGA CAGCGCTGGT
P879023 490 **G**AGGAGAGCC t c t c GACTGG GTGAAGGAGA CAGA GAA GGA CAGTGC CAT T
P879024 424 **G**AGGAGATCC Cc t a GACTGA GTGAAGGAGA CAGA GAA GGA CAGTGC CAT T

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alignment position 701 711 721 731 741

P879022 556 TCCCGGC TCC CCGCACCA t c ATGGCTTTGC CTCT GAGGC C CCTGACCCGG
P879023 540 CCTAGCC TCC CTTTGACA - - ATGGCTCTGC CTCT AAAGGT CCTGAGCCGG
P879024 474 CCTAGCC TCC CTTCAACA - - ATGGCTCTGC CTCT TAAAGT CCTCAGTCGG

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alignment position 751 761 771 781 791
P879022 606 GGC TTGG CCA g c g c t GCCAA AGGAGGCCAC G GA **GGAGCAG** **GAGGTGAGT G**
P879023 588 AGC ATGG CCA GCGCAGCCAA AGGAGACCAT G GA **GGGGCAG** **GAGGTAA GT G**
P879024 522 AGC ATGG CCA GCGCATCCAA AGGAGACCAC G GA **GGCGCAG** **GAGGTAA GT G**

alignment position 801 811 821 831 841
P879022 656 **GGGa** a c g g g c g g a t c c g g g - - - - - - - - - -
P879023 638 **GGGC** CAG GCC TGAc t c t GAT TTAGT AGCCT AGCC GAT CT G TTCTCT TTGC
P879024 572 **GGGC** CAG GCC TGAg g g a GAT TTAGT AGCCT AGCC CAT TT G TTT TCT TGGC

alignment position 851 861 871 881 891
P879022 675 - - - - - - - - - - - - - - - - GGC T CCC CT ACC C TGc c c - - - -
P879023 688 CCg - GCT TCC CCCTCCTTCT GTCTCCTGGC T CCT CTCTCC TGATCT ACC A
P879024 622 CCc t GCC TTC CCCTCCCTCC CTTTCCTGGC T CCC CTCTCC TGATCT ACC A

alignment position 901 911 921 931 941
P879022 693 - A
P879023 737 GGC ACTG ATC TTT CAGACCT CTAGGCCAG G GAT AGT TTT T TGC CTATGAA
P879024 672 GGC ACCG ATC TTT CAGACCT CTAGGCCAG T GAT AAC TTT T TAC CTGTGAA

alignment position 951 961 971 981 991
P879022 694 CCT GTTC ACA GGC CCGCC g c c c c a g g a c c g c c g c g c t c a c c c c g c t c c g t
P879023 787 TCT ACTC ACA C- CCCACCTT TGCTCCTCCA GCCAAC- - - - -
P879024 722 TCT GCTC TCA CTCCACCTT TGCTCTCCA GCCAAC- - - - -

alignment position 1001 1011 1021 1031 1041
P879022 744 c c g c a g c t c g t ACCTGGCGT CTGCT GACCT T CGT GCT GGC GCT GCC CAGC
P879023 822 - - - - - - - - - - ACCTGGCGC CTCCT GA- - - - -
P879024 758 - - - - - - - - - - ACTTGGCGC CTCCT GACCT T TGT GCT GGC TCT CCC CAGC


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alignment position 1 0 5 1 . . . .
P879022      794 GT g g c c c t
P879023      838 - - - - -
P879024      797 GT a 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.

	P879023 (837 bp)	P879024 (801 bp)
P879022 (801 bp)	0.214 30 %	0.229 34 %
P879023 (837 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

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 6 22:06:49 2005

Solution parameters:

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

- ALL user_defined.lib (0.75/Optimized)
- ALL vertebrates.lib (0.75/Optimized)

Selected groups
(core/matrix sim):

Aligned Sequences:

No.	Sequence Name	Sequence Description	Length
1	P911188	sym=COX6C loc=Loc1345 taxid=9606 spec=Homo sapiens chr=8 ctg=NT_008046 str=(-) start=14123568 end=14126068 len=2501 tss=2001 comm=cytochrome c oxidase subunit VIc; (NM_004374/508/bronze;)	2501 bp
2	P911190	sym=Cox6c loc=Loc12864 taxid=10090 spec=Mus musculus chr=15 ctg=NT_039618 str=(-) start=27052693 end=27055194 len=2502 tss=2001,2002 comm=cytochrome c oxidase, subunit VIc; (AK013459/502/gold;NM_053071/501/bronze;)	2502 bp
3	P911192	sym=Cox6c loc=Loc54322 taxid=10116 spec=Rattus norvegicus chr=7 ctg=NW_047778 str=(-) start=3775762 end=3778262 len=2501 tss=2001 comm=cytochrome oxidase subunit VIc; (NM_019360/501/bronze;)	2501 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\\$TBPF](#) [V\\$LHXF](#) [V\\$NRFI](#) [V\\$NRFI](#) [V\\$IRFF](#) [V\\$SETF](#) [V\\$EREF](#) [V\\$USERF](#) [V\\$RORA](#) [V\\$SFIF](#)

```

alignment position 1 . . . . . 11 . . . . . 21 . . . . . 31 . . . . . 41 . . . . .
P911188          1 a a a t c a c a c t a t g c c c g g c t a a g t t t t a a g t t t t t a t g - - - - -
P911190          1 g a a c t c a a a t t a a c t a a c a g g c c a g t a c c t a g c a t c a g t t t c c a g a t t a c
P911192          1 c a t c c a - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -

```

```

alignment position 51 . . . . . 61 . . . . . 71 . . . . . 81 . . . . . 91 . . . . .

```

```

P911188      41 - - - - -
P911190      51 a c t c a a c a a c a a g a t c t t c c a c t a a c a c c a g t t t c c a g g t t c c t g c c c c t
P911192      7 - - - - -

alignment position 1 0 1 . . . . . 1 1 1 . . . . . 1 2 1 . . . . . 1 3 1 . . . . . 1 4 1 . . . . .
P911188      41 - - - - -
P911190     101 g a c a c t t c a c t t c c t a a c a a c c a c t g a t c c g g a g g a a a g c a g a a g t t a c g
P911192      7 - - - - -

alignment position 1 5 1 . . . . . 1 6 1 . . . . . 1 7 1 . . . . . 1 8 1 . . . . . 1 9 1 . . . . .
P911188      41 - - - - -
P911190     151 t t t g t g g t t t g g c t c t g a a c a a t t a t g t t a a a g g c c a t a a t g g c c c c c t a
P911192      7 - - - - -

alignment position 2 0 1 . . . . . 2 1 1 . . . . . 2 2 1 . . . . . 2 3 1 . . . . . 2 4 1 . . . . .
P911188      41 - - - - -
P911190     201 g c c a g g t g t g t a c c a a g c t a g a t a a a c c c c c c c c t t t t g c c t c t a t a a a
P911192      7 - - - - -

alignment position 2 5 1 . . . . . 2 6 1 . . . . . 2 7 1 . . . . . 2 8 1 . . . . . 2 9 1 . . . . .
P911188      41 - - - - -
P911190     251 t g c t t g c c t g a a a c t g g g c t t t g g g c c c c c t c c c a t t c t c c t g c a t c a G A
P911192      7 - - - - -
                                                                * *

alignment position 3 0 1 . . . . . 3 1 1 . . . . . 3 2 1 . . . . . 3 3 1 . . . . . 3 4 1 . . . . .
P911188      43 G A T G G T G G T C T A T G T T G C T C A G G T T g g t c t c c a a c a c c t g g g c t c a a g t a
P911190     301 G A A G G T G G T A T G T A T A G C C C A A G C T c a a g c t t g a a t a a a g g g a c c t t a a t
P911192      7 - - - - -
                                                                * * * * *

alignment position 3 5 1 . . . . . 3 6 1 . . . . . 3 7 1 . . . . . 3 8 1 . . . . . 3 9 1 . . . . .
P911188      93 a t c t g c c t t c c t t g g c c t c c c a a a g t g c t - - - - -
P911190     351 g t a a t t g c a t c g g a a t c a g c t c c t t g g t g g t c t t t t g g g g g t t c a t g a a t
P911192      7 - - - - -

alignment position 4 0 1 . . . . . 4 1 1 . . . . . 4 2 1 . . . . . 4 3 1 . . . . . 4 4 1 . . . . .
P911188     122 - - - - -
P911190     401 g a t t c c t g g c a c a g c a g a a c c t t a c c t t c a t t g t t a G G G A C T A A A G G T G T
P911192      7 - - - - -
                                                                * * * * *

alignment position 4 5 1 . . . . . 4 6 1 . . . . . 4 7 1 . . . . . 4 8 1 . . . . . 4 9 1 . . . . .
P911188     136 g a g c c a c c a c a c c c a g t - - - - -
P911190     451 t c a c t a a g g g c g a g t c t g t t t t t t c c a g c c a a a t c a t a c t g t a a t c t a g
P911192      7 - - - - -

alignment position 5 0 1 . . . . . 5 1 1 . . . . . 5 2 1 . . . . . 5 3 1 . . . . . 5 4 1 . . . . .
P911188     153 - - - - -
P911190     501 g g t g t c t a c a t t t g g c t g g a t c a t a t a c g t c t c a g t c t c c t t g t t g C T G G
P911192      7 - - - - -
                                                                * * * *

alignment position 5 5 1 . . . . . 5 6 1 . . . . . 5 7 1 . . . . . 5 8 1 . . . . . 5 9 1 . . . . .
P911188     157 A A T A A G A T T t g a c t g t t g t a g a a t c a c a t g g c t a g a a g t g a t g a a g g a t t
P911190     551 A T T A A A A T T c c c c t a c a t - - - - -
P911192      7 - - - - -
                                                                * * * * *

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

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P911188 207 g a t t a a g c a c t g c t a c t a a a a g a a a g a t t g a a g g a a t g c a g g a c a g g c a a
P911190 569 - - - - -
P911192 7 - - - - -

alignment position 651 . . . . . 661 . . . . . 671 . . . . . 681 . . . . . 691 . . . . .
P911188 257 a a g a a c a c a g g g a g g a a t g c a t a t t c a g a a t g t c t g t t t g t c a a g c a c t g
P911190 569 - - - - -
P911192 7 - - - - -

alignment position 701 . . . . . 711 . . . . . 721 . . . . . 731 . . . . . 741 . . . . .
P911188 307 t a t a g g t t g a a c a c c c t t a a t c t g a a a a t c c a a a a t c c a a a a c g c t c c a a
P911190 569 - - - - -
P911192 7 - - - - -

alignment position 751 . . . . . 761 . . . . . 771 . . . . . 781 . . . . . 791 . . . . .
P911188 357 a a t c c a a a a c t t t t t g a g c a c t g a t g t g a t g c t c a a g g a a a t g c t c a g t g
P911190 569 - - - - -
P911192 7 - - - - -

alignment position 801 . . . . . 811 . . . . . 821 . . . . . 831 . . . . . 841 . . . . .
P911188 407 g a g c a t t t t g g a t t t c a g a t t t t c a g a t t g g g a t g c t c a a c t g g c a t g t a
P911190 569 - - - - -
P911192 7 - - - - -

alignment position 851 . . . . . 861 . . . . . 871 . . . . . 881 . . . . . 891 . . . . .
P911188 457 t t c t g c a a a t a c t c a a a a a t c t g a a a a a a t c c a a a a t c t g a a a c a c t t c t
P911190 569 - - - - -
P911192 7 - - - - -

alignment position 901 . . . . . 911 . . . . . 921 . . . . . 931 . . . . . 941 . . . . .
P911188 507 g g t c t c a a a t a t t t c a g a t a a g g g a t a c t c a a g c t g c a t a t a c a t t a t c c
P911190 569 - - - - -
P911192 7 - - - - -

alignment position 951 . . . . . 961 . . . . . 971 . . . . . 981 . . . . . 991 . . . . .
P911188 557 c a t t t a a t t t a c a t c a c a a c c c a a c a a a a t g g g t a c t a t t t t t a g a g g a g
P911190 569 - - - - -
P911192 7 - - - - -

alignment position 1001 . . . . . 1011 . . . . . 1021 . . . . . 1031 . . . . . 1041 . . . . .
P911188 607 a a a g c a g a c t t a g a a a g a t g a a g a a a t t t g c c g c t a c a a g t t g a t g a g c t
P911190 569 - - - - -
P911192 7 - - - - -

alignment position 1051 . . . . . 1061 . . . . . 1071 . . . . . 1081 . . . . . 1091 . . . . .
P911188 657 g g g a c t c a a a t c c a g g t c t g t t c g g c t c t a g a a c a g a a c c t a t a t g t a a c
P911190 569 - - - - -
P911192 7 - - - - -

alignment position 1101 . . . . . 1111 . . . . . 1121 . . . . . 1131 . . . . . 1141 . . . . .
P911188 707 a T G T C T C T C T T C A T C T A T C G C T C A G g t t t t a t t c a c g t g t c a c c c t c a g t
P911190 569 - T G T A T C A G T T C A A A G A A C G C T C A G a c t g t t c a c t g t c a t a t a a a a t c t g
P911192 7 - - - - -
          * * * * * * * * * * * * * * * * * * * *

alignment position 1151 . . . . . 1161 . . . . . 1171 . . . . . 1181 . . . . . 1191 . . . . .
P911188 757 c a t t c a c t a t g g t t c a c t - - - - -
  
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P911190    618 c t t g a a g g c t a a a g t t g t a t t c t a a g t t t a a a t t a c t g g g c t t a a g a g a t
P911192    7  - - - - -
alignment position 1 2 0 1 . . . . . 1 2 1 1 . . . . . 1 2 2 1 . . . . . 1 2 3 1 . . . . . 1 2 4 1 . . . . .
P911188    775 - - - - -
P911190    668 c t a t c a a t c a a a c a t g c c t c t a a c c t g t a a g c c t c a c t t g c c c a a g g g c a
P911192    7  - - - - -
alignment position 1 2 5 1 . . . . . 1 2 6 1 . . . . . 1 2 7 1 . . . . . 1 2 8 1 . . . . . 1 2 9 1 . . . . .
P911188    775 - - - - -
P911190    718 g a t a a t c t c t g g a g t g c t g g g g g c t g t t a c t t a t g t a a g a t a g t g a a c t a
P911192    7  - - - - -
alignment position 1 3 0 1 . . . . . 1 3 1 1 . . . . . 1 3 2 1 . . . . . 1 3 3 1 . . . . . 1 3 4 1 . . . . .
P911188    775 - - - - -
P911190    768 t g g t g t t t t c t c t t c t g t a a a c a a c c t c a c t t g c c c c a a c t t t a c a g g a t
P911192    7  - - - - -
alignment position 1 3 5 1 . . . . . 1 3 6 1 . . . . . 1 3 7 1 . . . . . 1 3 8 1 . . . . . 1 3 9 1 . . . . .
P911188    775 - - - - -
P911190    818 a a g c t t g a t c a c a c a c a g g t g g a g g t a g g c t g g a g g t t c a t a a g g a a a t a
P911192    7  - - - - -
alignment position 1 4 0 1 . . . . . 1 4 1 1 . . . . . 1 4 2 1 . . . . . 1 4 3 1 . . . . . 1 4 4 1 . . . . .
P911188    775 - - - - -
P911190    868 c a t t g g g a t c t a a g c g t g c c c c t g a t t g g a c g a a g g t g g g a a g t a c t g a c
P911192    7  - - - - -
alignment position 1 4 5 1 . . . . . 1 4 6 1 . . . . . 1 4 7 1 . . . . . 1 4 8 1 . . . . . 1 4 9 1 . . . . .
P911188    775 - - - - -
P911190    918 c c t t t g g g g g t t g c c t t t a t a a g c c t c t g a c t g a g t t g t a a t g t g g c g a t
P911192    7  - - - - -
alignment position 1 5 0 1 . . . . . 1 5 1 1 . . . . . 1 5 2 1 . . . . . 1 5 3 1 . . . . . 1 5 4 1 . . . . .
P911188    775 - - - - - GG ATAGCT AGGG AAGCACAGAA CAa a c a - - - - -
P911190    968 g t a t t t t g GG ATTCCT AGGT ATGCACCT GA CA g t g t c c a c t g a a c t g g c c
P911192    7  - - - - -
                        * * * * *
alignment position 1 5 5 1 . . . . . 1 5 6 1 . . . . . 1 5 7 1 . . . . . 1 5 8 1 . . . . . 1 5 9 1 . . . . .
P911188    803 - - - - -
P911190   1018 a a t g c t t a a t a a a g c t t g t t t t a a a t t t g g t t c a a a a c t t a c a g t a g c c g
P911192    7  - - - - -
alignment position 1 6 0 1 . . . . . 1 6 1 1 . . . . . 1 6 2 1 . . . . . 1 6 3 1 . . . . . 1 6 4 1 . . . . .
P911188    803 - - - - -
P911190   1068 t t t t c a c t a t t c t c a c c g g g t g g g a t t a a c c g TAGCC CTG GTACTCT GAT
P911192    7  - - - - -
                        TAGCC CTG GTACTCT GAT
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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 . . . . .
P911188    803 - - - - -
P911190   1118 CCC g - TGAAC CTTTCTTTGT AACCATGGGt t c a g t t c a g - - - - -
P911192    25 CCC c a TGAAC CTTTCTTTCT AATCATAGGg t g g t c c a g CT CAGTAGC TCA
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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
P911188	815	CTCAGgtcag	gctctgtgcc	ctgagtggtgc	ctgtcttttgc	catgttctcc
P911190	1156	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -
P911192	75	CTC AG - - - - -	- - - - -	- - - - -	- - - - -	- - - - -
		* * * * *				
alignment	position	1 7 5 1	1 7 6 1	1 7 7 1	1 7 8 1	1 7 9 1
P911188	865	cagccaatgt	tttctctcca	atftctccag	ttttccaggc	tttccat tag
P911190	1156	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -
P911192	80	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -
alignment	position	1 8 0 1	1 8 1 1	1 8 2 1	1 8 3 1	1 8 4 1
P911188	915	actgaaactc	agctctgctt	ccatctcttc	cacgtattgt	ctgaagcttt
P911190	1156	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -
P911192	80	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -
alignment	position	1 8 5 1	1 8 6 1	1 8 7 1	1 8 8 1	1 8 9 1
P911188	965	ccctgaTGGT	TTCACAtaca	ctaatccctg	tgaactctta	agttcaccac
P911190	1156	- - - - -TGGT	TTCACAacct	cagtt a- - - -	- - - - -	- - - - -
P911192	80	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -
		* * * *	* * * * * *			
alignment	position	1 9 0 1	1 9 1 1	1 9 2 1	1 9 3 1	1 9 4 1
P911188	1015	ttcttctctg	ggggtgggga	tggaaagaga	atagaaacaa	attactctct
P911190	1176	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -
P911192	80	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -
alignment	position	1 9 5 1	1 9 6 1	1 9 7 1	1 9 8 1	1 9 9 1
P911188	1065	ggacaaattc	catgcaagga	ttttcagctg	ggtagaccct	tgataagagg
P911190	1176	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -
P911192	80	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -
alignment	position	2 0 0 1	2 0 1 1	2 0 2 1	2 0 3 1	2 0 4 1
P911188	1115	cctgaaaaac	gttggtaaag	tccaaaaccta	cttttgaacc	tcaattgagc
P911190	1176	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -
P911192	80	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -
alignment	position	2 0 5 1	2 0 6 1	2 0 7 1	2 0 8 1	2 0 9 1
P911188	1165	acctttcttt	gtggccaggt	TTCACCCTCC	AGAGTGT TGG	TTAATAG GTt
P911190	1176	- - - - -	- - - - -	TTCTCCAT AT	AGTGT GATGG	TGCATGT GTc
P911192	80	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -
				* * * * * *	* * * * * *	* * * * * *
alignment	position	2 1 0 1	2 1 1 1	2 1 2 1	2 1 3 1	2 1 4 1
P911188	1215	gaggacaaag	actccctgat	cagaatgaga	ctcccgaag	atctgtcctc
P911190	1206	actgctcaag	cagggttcct	aagccctctc	aaaccctgca	tatatataaa
P911192	80	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -
alignment	position	2 1 5 1	2 1 6 1	2 1 7 1	2 1 8 1	2 1 9 1
P911188	1265	ttgttttagca	gaatctggca	catagtaggt	actcagtgta	tatatcgact
P911190	1256	gta- - - - -	- - - - -	- - - - -	- - - - -	- - - - -
P911192	80	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -
alignment	position	2 2 0 1	2 2 1 1	2 2 2 1	2 2 3 1	2 2 4 1
P911188	1315	caatatcatg	catctgttgt	gtcccagcta	ccttccacag	GGCTTGA TGG
P911190	1259	- - - - -	- - - - -	- - - - -	- - - - -	GGCTTAC TCA
P911192	80	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -
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alignment	position	2 2 5 1	2 2 6 1	2 2 7 1	2 2 8 1	2 2 9 1

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P911188 1365 GTTGACTTAA ATAATGCTTT TAAAa t t c a g g t t a t t t c a a t a c a a a c a g c
P911190 1269 GCTGACTTAA GTAACA CCTG TGAATCTAGT TGATGTC Act gAAGTAA GAT
P911192 80 - - TGATTTAA GTAGCC CCTG TGAATCTAGT TGATGTC At t a AAGTAA GAC
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alignment position 2 3 0 1 . . . . . 2 3 1 1 . . . . . 2 3 2 1 . . . . . 2 3 3 1 . . . . . 2 3 4 1 . . . . .
P911188 1415 c t g g c a t c a t t a a g g c a c a a g a g c c t c a c c c t t c t a c a c c a C T T T C C A C G
P911190 1319 A A A C G T C C C A A G G C A c g a a a a g t c a T C T T T A G T C G G - - - - C T T T C C A A A
P911192 128 A A G C G T C C C A A G G C A a a a g t c a t t t T C T T T A G T C A G - - - - C T T A C C C A A
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alignment position 2 3 5 1 . . . . . 2 3 6 1 . . . . . 2 3 7 1 . . . . . 2 3 8 1 . . . . . 2 3 9 1 . . . . .
P911188 1465 A A C T T C C a g t t g c c t t c c - T T C A A A A T C C T T G T T T T C T T A A G A A A C C C A C
P911190 1364 A A C A T C C C T G T T G T T C C C g T T C A C A C G T T A T T T T T A T T A A G A A C C C G A C
P911192 173 A A C A T C C C T G T T G T T C C C a T T C A G A A G T T A T C T C T T A T T A A G A A C C C A G C
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alignment position 2 4 0 1 . . . . . 2 4 1 1 . . . . . 2 4 2 1 . . . . . 2 4 3 1 . . . . . 2 4 4 1 . . . . .
P911188 1514 A A A A A T A C C g c c c c t c t a t c a a a a c g T C C T C A G C T T T G C C A G G T A G A G A A
P911190 1414 A C A A A T A C C c a t t a c g a - - - - - - - - - - - - - - - T T T G T T A A G C A G A T C A
P911192 223 A C A A A C A C C t a a t a g g a t t - - - - - - - - - T G C T C A T G T T T G T T A A G C A G A T T A
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alignment position 2 4 5 1 . . . . . 2 4 6 1 . . . . . 2 4 7 1 . . . . . 2 4 8 1 . . . . . 2 4 9 1 . . . . .
P911188 1564 T T G C T T C T G C A G T A G c t - - - - G G G C C A C G T C T C T g t g g t a g t g c C C A C T
P911190 1447 T T G A G T c - - T G G C A G T G G A G T G G G A T C A C A T C T C T A G T T T G T T - - C C A C A
P911192 266 T T G G G T T T G T G G C A G T G G A G T G G G G T C A C A T C T C T A G T T T G T T - - C C A C g
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alignment position 2 5 0 1 . . . . . 2 5 1 1 . . . . . 2 5 2 1 . . . . . 2 5 3 1 . . . . . 2 5 4 1 . . . . .
P911188 1609 G C A T G G G A T C G G T A T T A A T C T - - G T T T G T C T T T t t c a t c t t c t g g g c t g t
P911190 1493 G C A T C G G T T C T A A A A T T A C A T - - G T T A A A C T C T G A A A T T G G C C t t t c t c g
P911192 314 G C A T G T G T A C T A A A A T T A C A T t g G T T A A G C T C T A A A A T T G G C C a t t t c c c
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alignment position 2 5 5 1 . . . . . 2 5 6 1 . . . . . 2 5 7 1 . . . . . 2 5 8 1 . . . . . 2 5 9 1 . . . . .
P911188 1657 g a g c t c c t a g a a g t c a g c t t t t C A C T T T T A C C C A A G C C A A A C G G T T A T T
P911190 1541 - - - - - - - - - - - - - - - - - - - - - C T C T T T G C C A A A A A C C A A G C G T T T A T T
P911192 364 t c - - - - - - - - - - - - - - - - - - - - - T T T A C C A A A A C C A G G C A T T T A T T
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alignment position 2 6 0 1 . . . . . 2 6 1 1 . . . . . 2 6 2 1 . . . . . 2 6 3 1 . . . . . 2 6 4 1 . . . . .
P911188 1707 C G C G T A A G G T T G G T t a T A A T T A A A A T G t c g g t T T G T G C A C A T G G T T T G G G
P911190 1568 G T G C C G A G G T A G T T G - T A A T G A A A A T G C - - - - T T A T T C A T G T G G T T T G G G
P911192 389 G T G C C A A G G T A G C T G - T A A T A A A A A T G C - - - - T T G T G C A T G T G G T T T G G G
    
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alignment position 2 6 5 1 . . . . . 2 6 6 1 . . . . . 2 6 7 1 . . . . . 2 6 8 1 . . . . . 2 6 9 1 . . . . .
P911188      1757 a c t c t g t g t a - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
P911190      1613 C A A T C C T T T G A C a c a a a t g t c a t g t c c c c c A A G A T A T G C C T T T T C T C A A G
P911192      434 C A A T C C T T T G A C g t g a g g c c c c t - - - - - - - A A A A T A T G C C T T T T C A C A A G
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alignment position 2 7 0 1 . . . . . 2 7 1 1 . . . . . 2 7 2 1 . . . . . 2 7 3 1 . . . . . 2 7 4 1 . . . . .
P911188      1767 - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
P911190      1663 G T T G G G C A T T T A G A A A A A A a a a g c t c t c a g a t g a t g t a g t g c c - - - - -
P911192      477 G T T G G G C A T T T A G A A A A A A g c c c t c a g a c t t a a a g t t c c t g c t c g c t a a a
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alignment position 2 7 5 1 . . . . . 2 7 6 1 . . . . . 2 7 7 1 . . . . . 2 7 8 1 . . . . . 2 7 9 1 . . . . .
P911188      1767 - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
P911190      1706 - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
P911192      527 a g g a a c c a t t c t c t t t t t c t c t g g c a a a a g g g a a g t g t a g c t c t t t t g t t

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alignment position 2 8 0 1 . . . . . 2 8 1 1 . . . . . 2 8 2 1 . . . . . 2 8 3 1 . . . . . 2 8 4 1 . . . . .
P911188      1767 - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
P911190      1706 - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
P911192      577 a a c a t a t t a c t g t g c t g c c t a t t a g c g t g t t g g a g t c g a g g t t c a g g t c g

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alignment position 2 8 5 1 . . . . . 2 8 6 1 . . . . . 2 8 7 1 . . . . . 2 8 8 1 . . . . . 2 8 9 1 . . . . .
P911188      1767 - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
P911190      1706 - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
P911192      627 a t t a c c a g c t t c t a g g c c t c c t t g c t c t a g c t c c t a g g c t g c t t t t c t c c

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alignment position 2 9 0 1 . . . . . 2 9 1 1 . . . . . 2 9 2 1 . . . . . 2 9 3 1 . . . . . 2 9 4 1 . . . . .
P911188      1767 - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
P911190      1706 - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
P911192      677 c a a t a c a t t t g a c c c a g g c t a a c c a c c t c a c c a c c a a t c c c c t a c a c a g

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alignment position 2 9 5 1 . . . . . 2 9 6 1 . . . . . 2 9 7 1 . . . . . 2 9 8 1 . . . . . 2 9 9 1 . . . . .
P911188      1767 - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
P911190      1706 - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
P911192      727 c t t c t c t c t g c t t t c c c a g t a g a c a g c c t t g a c a c t t t g g a a c t t t c c c c

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alignment position 3 0 0 1 . . . . . 3 0 1 1 . . . . . 3 0 2 1 . . . . . 3 0 3 1 . . . . . 3 0 4 1 . . . . .
P911188      1767 - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
P911190      1706 - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
P911192      777 t t t t c a c c c a c g c a g a g g c t a a t t t g g t t t c t t t a c t g t g c c t a t t t t t t

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alignment position 3 0 5 1 . . . . . 3 0 6 1 . . . . . 3 0 7 1 . . . . . 3 0 8 1 . . . . . 3 0 9 1 . . . . .
P911188      1767 - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
P911190      1706 - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
P911192      827 c a t t g a g t a t a t t a t t a t a c t T T T A T A G A G T A T A T T A T T T T T t c c c c a C A

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alignment position 3 1 0 1 . . . . . 3 1 1 1 . . . . . 3 1 2 1 . . . . . 3 1 3 1 . . . . . 3 1 4 1 . . . . .
P911188 1767 - - - - - - - - - - - - - - - - - - - - - - - - - T GAGTACG ACT
P911190 1735 TGT GAAAT AT ATACGAATTC CT TAATAAGT TCACAAC Acc gga CAAGATT
P911192 874 TGT GAAAT AT ATATGAATTC CT TAATAAGT CCTCAAC At T GGGCAAGATT
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alignment position 3 1 5 1 . . . . . 3 1 6 1 . . . . . 3 1 7 1 . . . . . 3 1 8 1 . . . . . 3 1 9 1 . . . . .
P911188 1778 AAT ATCTT CA ATTTACTA Ag a a g a t a a a g a g g t c g a t a a a t a AGGAGGTC
P911190 1785 AAT ATTTGTA ATTTACTGAA GAAACCTTGT T- - - - - - - - - - AGGTAGTC
P911192 924 AAT ATTTGTA ATTTATTTAA GGAATCTTGT T- - - - - - - - - - AGGTAGTC
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alignment position 3 2 0 1 . . . . . 3 2 1 1 . . . . . 3 2 2 1 . . . . . 3 2 3 1 . . . . . 3 2 4 1 . . . . .
P911188 1828 AAGCCCGT TT TGCAAGGT CA CACAG- - - - - - - - - - G AAAGAAg c a g
P911190 1824 AGGACTCGTT TTCAAGGT Cc t g t t a g g g a a a a a a a a A AAAAAAA GAC
P911192 963 AGA ACTCGTT TTCAAGGT TC CACTT - - - - - - - - - - A GAAGAAA AGC
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alignment position 3 2 5 1 . . . . . 3 2 6 1 . . . . . 3 2 7 1 . . . . . 3 2 8 1 . . . . . 3 2 9 1 . . . . .
P911188 1864 a c c a c g a a - - - - ATGAAC TT CGGCTGTC ACCTGCGGTG GGC GCAC TAG
P911190 1874 ATAGTGT AAC TGGCAT AAAT TT CAGCTGTG ACCGGCTGGA TGC GCGC TTG
P911192 999 ATAGTCCAGC TAATAT Ag g T TT CAGTTGTG ACCAACTGGA TGC GCGT TTG
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alignment position 3 3 0 1 . . . . . 3 3 1 1 . . . . . 3 3 2 1 . . . . . 3 3 3 1 . . . . . 3 3 4 1 . . . . .
P911188 1908 Ag g t C T T T T G AACTCCTT CG GCTACCGT CG CCGCGTT CTC g c t g t g c a c t
P911190 1924 AAT ACTTT T GACTCCTT AG GCCACCGT CG CCGGGTCTC CATCGAC TCt
P911192 1049 TAT ACTTT T GACTCCTT AG GCCACCGT CG CCGATTC CTC CATCGAC TC-
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alignment position 3 3 5 1 . . . . . 3 3 6 1 . . . . . 3 3 7 1 . . . . . 3 3 8 1 . . . . . 3 3 9 1 . . . . .
P911188 1958 c t t a t CTGC GCCTGCGCGC GGCTA CAGCA CGGTT CGTTT TTCCt t agt
P911190 1974 - - - - - T GC GCATGCGTGC TGCT GGAAAG CTCTC CGTTT CTCCGAG AAc
P911192 1098 - - - - - CTGC GCATGCGTGC TGCT AGAAAG CTCTC CGTTT CTCCGAG AAc
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alignment position 3 4 0 1 . . . . . 3 4 1 1 . . . . . 3 4 2 1 . . . . . 3 4 3 1 . . . . . 3 4 4 1 . . . . .
P911188      2008 c a G G A A G G A C G T T G G T G T T G A G G T G A G t c c g g t c c c t t t t g c a t c c c t a c
P911190      2017 C G G G A A G G A C G T T G G T G T A G A G G T G A G A A T G G T G G A G - - - A G A G A G A G G
P911192      1142 C G G G A A G G A C G T T G G T A T A G A G G T G A G A A T G G T G G A G a g a g A G A G A G A G G
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alignment position 3 4 5 1 . . . . . 3 4 6 1 . . . . . 3 4 7 1 . . . . . 3 4 8 1 . . . . . 3 4 9 1 . . . . .
P911188      2058 c c c g a c - - - - - - - - - - AC T G C G G G T T g t c a c a a c g g c a c c c t c c c g c t
P911190      2063 A G A T T C T G G G G T T T G A C A A C T G C G G G T T T C t c G G C T T C T C G T g G G G G C G G
P911192      1192 A G A T C C T G G G G T T T G A C A A C T G T G G T T T T C - - G G C T T C T C G T - G G G G C G G
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alignment position 3 5 0 1 . . . . . 3 5 1 1 . . . . . 3 5 2 1 . . . . . 3 5 3 1 . . . . . 3 5 4 1 . . . . .
P911188      2096 t t c t c t c t g c c t c g g a t t t a g t c g t g a c t g t g t g t c t c c g c c g t g G T G C A
P911190      2113 C G A A C T A G G A T G T C T T G C A C G T C A C A G C C c A - - - - - - - - - - - - - - G T G G A
P911192      1239 C G A A C T A G G A T T T G T T C C A T G T C C C A G C C t A - - - - - - - - - - - - - - G T G G A
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alignment position 3 5 5 1 . . . . . 3 5 6 1 . . . . . 3 5 7 1 . . . . . 3 5 8 1 . . . . . 3 5 9 1 . . . . .
P911188      2146 G C T T C A G G C C T c t c c c g c a t c t a c t c t c t c a c g e t t c e g c t g - - - - - - -
P911190      2149 G C C T C G G G C C T G C C T T C C T C G T G G G C G C G - T T G C C C C G C C G C G T C C T C A
P911192      1275 G C C G C G G G C C T A C C T T C C T C G T G G C C G C G c T T G T C C C T C C G G G T C C T C A
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alignment position 3 6 0 1 . . . . . 3 6 1 1 . . . . . 3 6 2 1 . . . . . 3 6 3 1 . . . . . 3 6 4 1 . . . . .
P911188      2188 - - - - - - - - - - - - - - - - C G G C C T - - G A G G G A G G G C G G C g g g c g g a c c a c
P911190      2198 G G A G G C T G C G G G C C T G a c C G G C C T - - G A A C T C G G G C G G C C C G C C A T C T C
P911192      1325 G G A G G C T G C G G G C C T G g t g g g c c t g a G A G C T C G G G C G G C C C G C T G T T A
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alignment position 3 6 5 1 . . . . . 3 6 6 1 . . . . . 3 6 7 1 . . . . . 3 6 8 1 . . . . . 3 6 9 1 . . . . .
P911188      2218 g g a c c g g g g t g g g t t g c g a c g g c c c c a c c g a a g c c g g g t g g g c t g c g g g a
P911190      2246 C C C G C G T G C G C T c t t a g g g c t c c G G A G G A G C T C T G C G G A G C C T C A G G G T C
P911192      1375 C C C G A G T G C G C T a t c g g g g c c t t G G A G G A G C T C T G C G G A G C C T C T G G G C C
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alignment position 3 7 0 1 . . . . . 3 7 1 1 . . . . . 3 7 2 1 . . . . . 3 7 3 1 . . . . . 3 7 4 1 . . . . .
P911188      2268 c c c t c g a g a a c c c a g c t g g c t t c g g a g t g a g c t g G C C C G G G G C T G G T A C C
P911190      2296 T C G C T G g T G G C C - - - - - - - - - - - - - - - - - - - - - G G C C G G G C C G T T T C C
P911192      1425 T C G C T G a T G G C C - - - - - - - - - - - - - - - - - - - - - G G C C G G G C C G T T A C C

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alignment	position	4 1 5 1	4 1 6 1	4 1 7 1	4 1 8 1	4 1 9 1
P911188	2483	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -
P911190	2503	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -
P911192	1849	g a g a g a a g c g	g a a c c g g c a a	a g a t g a a g c t	g c c t a a g t c a	c t g a a a c c t t
alignment	position	4 2 0 1	4 2 1 1	4 2 2 1	4 2 3 1	4 2 4 1
P911188	2483	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -
P911190	2503	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -
P911192	1899	g c a g a a g t c a	g t c c g c a g t t	a c t a a a a t a c	g a t g t g c a c g	t a g a g t t c a t
alignment	position	4 2 5 1	4 2 6 1	4 2 7 1	4 2 8 1	4 2 9 1
P911188	2483	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -
P911190	2503	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -
P911192	1949	t c a a t c a c t t	a c c c c a t t c t	c a g g c t t t t t	t g t t t g t t t g	t t t g t t t t a c
alignment	position	4 3 0 1	4 3 1 1	4 3 2 1	4 3 3 1	4 3 4 1
P911188	2483	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -
P911190	2503	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -
P911192	1999	t t g c a a a g g a	c a t t g g c t a c	c a t g a g t t c c	g g t g c t c t g t	t g c c g a a a c c
alignment	position	4 3 5 1	4 3 6 1	4 3 7 1	4 3 8 1	4 3 9 1
P911188	2483	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -
P911190	2503	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -
P911192	2049	a c a g a t g c g t	g g t c t t c t g g	c c a a g c g t c t	g c g g g t t c a t	a t t g t t g g c g
alignment	position	4 4 0 1	4 4 1 1	4 4 2 1	4 4 3 1	4 4 4 1
P911188	2483	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -
P911190	2503	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -
P911192	2099	c a t t c g t t g t	g g c c c t a g g a	g t t g c t g c t g	c c t a t a a g g t	a t g t g c t t g c
alignment	position	4 4 5 1	4 4 6 1	4 4 7 1	4 4 8 1	4 4 9 1
P911188	2483	- - - - -	- - - - -	- - - - -	- - - - -	AGCGTTT TAA
P911190	2503	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -
P911192	2149	t t g t g t g t g c	t t t a g g t t a c	a a g g t t t a a a	c c t a g t t a a g	AGCTTTT TAA

alignment	position	4 5 0 1	4 5 1 1	4 5 2 1	4 5 3 1	4 5 4 1
P911188	2493	ATT AG Ag c t -	- - - - -	- - - - -	- - - - -	- - - - -
P911190	2503	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -
P911192	2199	AAA AG Aa a c t	c c c a t c t t t a	a g a t a t t c c c	c t c t t t a a c c	t t c c a t a a g c

alignment	position	4 5 5 1	4 5 6 1	4 5 7 1	4 5 8 1	4 5 9 1
P911188	2502	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -
P911190	2503	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -
P911192	2249	t t c a g c g t g c	c a g g a g c c c a	t g t a g t t g a c	c c t a t c t a c a	a a t g a a g c t g
alignment	position	4 6 0 1	4 6 1 1	4 6 2 1	4 6 3 1	4 6 4 1
P911188	2502	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -
P911190	2503	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -
P911192	2299	t g t t t g c t a t	a t c a a a g a a c	c a g g c c g a g t	g g t t t a a a t g	c a g a a a t t t g
alignment	position	4 6 5 1	4 6 6 1	4 6 7 1	4 6 8 1	4 6 9 1
P911188	2502	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -
P911190	2503	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -
P911192	2349	c t t t c t t a c a	g g g c t g t t t t	t g a g a t a g g t	c t t a c t a t a t	a a c c c t g c c t

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alignment position 4 7 0 1 . . . . . 4 7 1 1 . . . . . 4 7 2 1 . . . . . 4 7 3 1 . . . . . 4 7 4 1 . . . . .
P911188      2502 - - - - -
P911190      2503 - - - - -
P911192      2399 a g g c a a g g c t g g c c a g g a g c t c a t g t g a t t t g c c t g c c t c t a c c c c a c a a

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alignment position 4 7 5 1 . . . . . 4 7 6 1 . . . . . 4 7 7 1 . . . . . 4 7 8 1 . . . . . 4 7 9 1 . . . . .
P911188      2502 - - - - -
P911190      2503 - - - - -
P911192      2449 t g c t g g g a t c a a a a g a t g t g c a c c a c c a t a c t c c c a g t t t t t a a g a t c a a

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alignment position 4 8 0 1
P911188      2502 - - -
P911190      2503 - - -
P911192      2499 g g 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.

	P911190 (2502 bp)	P911192 (2501 bp)
P911188 (2501 bp)	0.087 19 %	0.076 12 %
P911190 (2502 bp)		<u>1.000</u> <u>40 %</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

GEMS Launcher Task: *DiAlign TF*: Multiple alignment plus TF sites working on C4-COX6B2-HMR (3 seq.)

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

DiAlign professional TF Release 3.1 December 2004

Fri May 6 01:19:06 2005

Solution parameters:

Sequence file: [C4-COX6B2-HMR](#) (3 seq.)
Type of sequences: nucleotide sequences
Threshold T: 0.00
'*' signs below alignment denote: diagonal similarity (max. similarity is represented by 10 '*' signs)
 complete alignment is shown
Alignment output: # 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
1	P984975	P984975 sym=COX6B2 loc=Loc125965 taxid=9606 spec=Homo sapiens chr=19 ctg=NT_011109 str=(-) start=28133854 end=28134769 len=916 tss=501,516 comm=cytochrome c oxidase subunit VIb polypeptide 2 (testis); (AK057427/501/gold;NM_144613/516/silver;)
2	mCOX6B2	mCOX6B2 mm6_dna range=chr7:3998838-3999737 5'pad=0 3'pad=0 revComp=TRUE strand=? repeatMasking=none
3	rn3_dna	rn3_dna range=chr1:67888264-67889158 5'pad=0 3'pad=0 revComp=FALSE strand=? repeatMasking=none

Alignment (DiAlign format):

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

[V\\$NFKB](#)
[V\\$TBPF](#)
[V\\$ZBPF](#)
[V\\$SEGRF](#)
[V\\$SPIF](#)
[V\\$MAZF](#)
[V\\$PAX2](#)
[V\\$ECAT](#)
[V\\$PCAT](#)
[V\\$NF1F](#)
[V\\$AP2F](#)
[V\\$HNF4](#)
[V\\$SETF](#)
[V\\$VMYB](#)
[V\\$CMYB](#)

alignment position 1 1 1 2 1 3 1 4 1
P984975 1 a g g g g g g c g a g g g a - - - - - GG AGG GT G G GG GGG Gc g g g t a a c g g a g g g
mCOX6B2 1 G A G A A C A C C G A G T G T G G T C G C G G A G G G T G G A G G G G G A T - - - - -
rn3_dna 1 G A G A A C A C C G A G T G T G G T C G C G G A G G G - G G A G G G A G A T - - - - -

alignment position	51	61	71	81	91
P984975	44 g g a g g a c g a	g g g g g c g g g	g g g g t t c c c a	g g a g c c c g g a	c c c c a c c g c t
mCOX6B2	39 - - - - -	- - - - -	- - - - -	- - - - -	- - - - -
rn3_dna	38 - - - - -	- - - - -	- - - - -	- - - - -	- - - - -
alignment position	101	111	121	131	141
P984975	94 g c t c t t t c c t	c t t a a c c c c a	c a g g c c c c g a	g g g t t c t g t g	c g c a c c g a c t
mCOX6B2	39 - - - - -	- - - - -	- - - - -	- - - - -	- - - - -
rn3_dna	38 - - - - -	- - - - -	- - - - -	- - - - -	- - - - -
alignment position	151	161	171	181	191
P984975	144 g t a g g a a g c g	g a a t g t t g a a	a g c c g c t t g g	g GGGATTTC	CCCCTCTGGT
mCOX6B2	39 - - - - -	- - - - -	- - - - -	- GGGATCCTC	CTTCTCCCAT
rn3_dna	38 - - - - -	- - - - -	- - - - -	- GGGATCCTC	CTCCTCCCAT
				*****	*****
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alignment position	201	211	221	231	241
P984975	194 AGATAC CAGA	ACTAt gga t a	t g c c t t TATA	TATTGGGGGG	CGGGGGGGGG
mCOX6B2	58 AGAGAC CAGA	GCTA GATATA	AG- - - TTTA	T- - - - TGGT	GAGGATGGGG
rn3_dna	57 AGAGAC CAGA	GCTA GATATA	AA- - - TTTA	TC TTA CTGGG	GAGGATGGGG
	*****	*****	*****	*****	*****
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alignment position	251	261	271	281	291
P984975	244 CGGGGGCGAG	c c c g t - GGAG	CCG CCAACT	TCGCAGAGAT	TAAAgc t t g -
mCOX6B2	99 CGGGGCAGAG	- - - - - GGAG	AAGCTCAACT	TTGTAGGGAT	TAAAAGTCCT
rn3_dna	103 CGGGGCTGAt	g g t c a a GGAG	AAGCTCAATT	TTGTAGGGAT	TAAAAGTCCT
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	*****	*****	*****	*****	*****
alignment position	301	311	321	331	341
P984975	292 AGCCTGAGAC	TCAg c g a g t c	g c a c c t c g g t	g c c t g t g t g c	a c - - - - -
mCOX6B2	143 AGTCTGAGAC	TCAAAGCCCT	GTCTTCGTGC	TGGTAAGTGT	ACGCGc TCTT
rn3_dna	153 AGTCCGAGAC	TCAAAGCCCT	GTCTTCGTGC	TGGTAAGTGT	AAGCGt TCTT
	*****	*****	*****	*****	*****
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	*****	*****	*****	*****	*****
	*****	*****	*****	*****	*****
alignment position	351	361	371	381	391
P984975	334 - - GC GC AGGC	CCCCGAGGGG	Gc g t c g g g g -	- - GAGCAAGG	GGTGGGGTGG
mCOX6B2	193 GTGC GC GGTT	CTCA CAAGGG	GACTGCCTAC	AA GAACCAAG	GGGGAGGGGC
rn3_dna	203 GTGC GC GGGT	CCCC CCAGGG	GACTGCCTAC	AA GAACt a - -	GGGGGAGGGC
	*****	*****	*****	*****	*****
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	*****	*****	*****	*****	*****
	*****	*****	*****	*****	*****
alignment position	401	411	421	431	441
P984975	379 GGGC GC CCCT	ACCAGCCCCG	CGGTGC Ac GA	CG GCTCCAT	TGGCTGGGGC

mCOX6B2	243	CGCCAC TGAT	CCCACCCCCG	CATTAC A-	G A CA	GCTCC TAT	TGGCTGGGAC
rn3_dna	251	CTCCAC TGAT	CCCACCCCCG	CATTAC A-	G A CG	GCTCC TAT	TGGCTGGAAC
		* * * * *	* * * * *	* * * * *	* * * * *	* * * * *	* * * * *
		* * * * *	* * * * *	* * * * *	* * * * *	* * * * *	* * * * *
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		* * * * *	* * * * *	* * * * *	* * * * *	* * * * *	* * * * *
alignment position		4 5 1	4 6 1	4 7 1	4 8 1	4 9 1	
P984975	429	T Cg g g c	gt c c	t - AGCCAATC	CGGCCGCGGG	GT g c g - - - T	T T C T C C t g a c
mCOX6B2	292	TCCCTG	GGa G	CCAGCCAATC	CGGCCTGAGG	GT CGT AT T T T	T T C T C C c - - G
rn3_dna	300	TCCCTG	GGg G	CCAGCCAATC	AGGCCTGGGG	GT CGT AT T T T	T T T T C t c g t G
		* * * * *	* * * * *	* * * * *	* * * * *	* * * * *	* * * * *
		* * * * *	* * * * *	* * * * *	* * * * *	* * * * *	* * * * *
		* * * * *	* * * * *	* * * * *	* * * * *	* * * * *	* * * * *
		* * * * *	* * * * *	* * * * *	* * * * *	* * * * *	* * * * *
		* * * * *	* * * * *	* * * * *	* * * * *	* * * * *	* * * * *
alignment position		5 0 1	5 1 1	5 2 1	5 3 1	5 4 1	
P984975	474	c c g g g t g g g a	c c g c a c c c c g	c g g a c t c a g a	a g c g a g c g g c	a c c c c	G G G A C
mCOX6B2	340	T G C T C T T - - -	- - - - -	- - - - -	- - - - -	- - - - -	G G G A C
rn3_dna	350	T G C T C T T - - -	- - - - -	- - - - -	- - - - -	- - - - -	G G G A C
		* * * * *	* * * * *	* * * * *	* * * * *	* * * * *	* * * * *
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		* * * * *	* * * * *	* * * * *	* * * * *	* * * * *	* * * * *
alignment position		5 5 1	5 6 1	5 7 1	5 8 1	5 9 1	
P984975	524	C A T C C C A C A g	c a g a t c c a g t	g g c c g c - - - -	- - - - -	- - - - -	- - - - -
mCOX6B2	352	C A G C C C T C A T	T C T C A A A C T A	A A G G C A C g G G	T G G A T T C C G C	A G C C C T G G T G	
rn3_dna	362	C A G C C C T C A T	T C T A A A G C T A	A A G G C A C t G G	T G G A C T C C G C	A A C T G T G G T G	
		* * * * *	* * * * *	* * * * *	* * * * *	* * * * *	* * * * *
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alignment position		6 0 1	6 1 1	6 2 1	6 3 1	6 4 1	
P984975	550	- - - - -	- - - - - C A A C	G T C A G G C T G G	T G A G G G C A C G	A C G G G T G G G G	
mCOX6B2	402	T T C C A G C T A C	T T T G G c t C A C	T T C A G T C T G G	T A A G G A C A G G	G T G G G T G G T G	
rn3_dna	412	T T C C A G C T A C	G T T G G t C C A C	T T C A G T C T G G	T G A G G A C G G G	G T G G G T G G T G	
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alignment position		6 5 1	6 6 1	6 7 1	6 8 1	6 9 1	
P984975	584	T T C A G G G g c g	g G G G T C A G G A	T G G G G A G A C G	G g t c g g a g c g	a G G G C G C C C C	
mCOX6B2	452	T T T A G A G t - - -	- G G G A C A G G A	G C T G G G G A A G	G T G G A A G C A C	G A G G C G C C C T	
rn3_dna	462	T T T A G A G t - - -	- G G G T T A G G A	G C T G G G G A A G	G T G G A A G C A C	G G G G C G G C C C	
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alignment position		7 0 1	7 1 1	7 2 1	7 3 1	7 4 1	
P984975	634	C T C G G C C C C A	C G G A G T C C c c	g t c c c g t C C C	G T C T C G C A G G	A G T T G c c t c C	
mCOX6B2	499	C T A G G C C C C A	C G G A G C C C T G	C A C - - - C C C	T T C C T G C A G G	A A T T G - - - C	
rn3_dna	509	C T A G T C T C C A	C G G A G C T C T G	C A C - - - C C T	T T C T T G C A G G	A A T T T - - - C	


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alignment position

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

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P984975
mCOX6B2
rn3_dna

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684 T T C G T G G A T G T T G G A T G T G G A A G C C C A G G A G C C C C c a a g g g g a a a t g g t
541 T A C t T G G A T G T T G G G T G T T C A A G C C C A G A A G C C C C T C C G G G C C A A T G G A
551 T A C C T G G A T G T T G G G T G T T C A A G C C C A G A T G C C T G C T C C A G G C C A A T G G A
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alignment position

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

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P984975
mCOX6B2
rn3_dna

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734 c g A C G C C G C C C T T C G A C C C G C G C T T C C C C A G C C A G A A C C A G A t c C G T A A C
591 C A A C G C C G C C C T T T G A T C C G C G C T T C C C T A A C C A G A A C C A G A C G C G T A A C
601 C A A C G C C G C C C T T C G A C C C G C G C T T C C C T A A C C A A A A C C A G A C G C G T A A C
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alignment position

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

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P984975
mCOX6B2
rn3_dna

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784 T G C T A C C A G A A C T T C C T G G G T G A G A C C t G C T C A G C C A G G T T A T G G G A G G A
641 T G C T A C C A G A A T T T T C T G G G T G A G A C C G G T T G A G C C A A A T T A G A G G G G A G
651 T G C T A C C A G A A T T T T C T G G G T G A G A C C G G T T G G G C C A A A T T A G A G G G G A G
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alignment position

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

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P984975
mCOX6B2
rn3_dna

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834 G C a g g g t g t g a c a a g g g a c g g c a g g g a g g g g c a c t C C C A C C C T A A G T C C C
691 G C C - - - - - - - - - - - - - - - - - - - - C C C A C C T G G A G a C C G
701 G C C - - - - - - - - - - - - - - - - - - - - C C C A C C T G G A G G C C G
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alignment position

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

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P984975
mCOX6B2
rn3_dna

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884 G C G G A G A C C G T T A G G G T G G G A G G C C G G G C g g g g - - - - - - - - - -
709 T A G G A G A C C G T T G G A A T G G G A G G C T G G G C C G C G G C T G G A G G G G T G G G G C
719 T C G G A G A C C G T T G G A A T G G G A G G C T G c a C C G T G G C T A G A G G G G T G G 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 . . . . .
P984975      917 - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
mCOX6B2     759 C T G T A C C A A a g t g g g T G G G G C T G A G C C A T G G A G G G G C G G G G C C T G G A A T G
rn3_dna     769 C T G C A C A A A g c g g a - T G G G G C T G A A C C A T G G A G G G A C C G A C C C T G G A A 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 . . . . .
P984975      917 - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
mCOX6B2     809 G A G G G A G G C A G C T G G T C T G A A G G G A T T A A G T T T G C C G C G T T G G a g t g a a a
rn3_dna     818 G A G G G A G G C A G C T G G T C T G G A G G A A T A A G A T T G C C A C G T T G G g - - - - -
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          * * * * * * * * * * * * * * * * * * * * * * * * * * * *
alignment
position      1 1 0 1 . . . . . 1 1 1 1 . . . . . 1 1 2 1 . . . . . 1 1 3 1 . . . . . 1 1 4 1
P984975      917 - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
mCOX6B2     859 t g t A T T G A G C C A G A A G G G A T G G A G C C T T G T C T G T A A A g g c a
rn3_dna     862 - - - A T T G A G C C A G A A A G G A T G G A G C C T T G T C T G T A A A - - - - -
          * * * * * * * * * * * * * * * * * * * * * * * * * * * *
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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.

	mCOX6B2 (900 bp)	rn3_dna (895 bp)
P984975 (916 bp)	<u>0.205</u> 40 %	<u>0.189</u> 42 %
mCOX6B2 (900 bp)		<u>1.000</u> <u>88 %</u>

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

Extract alignment region

Positions in alignment	from: <input style="width: 50px;" type="text"/> to: <input style="width: 50px;" type="text"/>
Output file	<input style="width: 90%;" type="text" value="dialign.seq"/>

Extract aligned sequences

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

GEMS Launcher Task: *DiAlign TF*: Multiple alignment plus TF sites working on C4-COX6A1 (3 seq.)

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

DiAlign professional TF Release 3.1 December 2004

Wed Aug 10 18:02:04 2005

Solution parameters:

Sequence file: [C4-COX6A1](#) (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 vertebrates.lib (0.75/Optimized)

Aligned Sequences:

No.	Sequence Name	Sequence Description	Length
1	hCOX6A1	hCOX6A1 sym=hCOX6A1 spec=Homo sapiens chr=12 str=(+) start=119338137 end=119339250 len=1114 tss=493	1114 bp
2	mCOX6A1	mCOX6A1 sym=mCOX6A1 spec=Mus musculus chr=5 str=(-) start=114458935 end=114460045 len=1111 tss=522	1111 bp
3	rCOX6A1	rCOX6A1 sym=rCOX6A1 spec=Rattus norvegicus chr=12 str=(+) start=42392988 end=42394045 len=1058 tss=532	1058 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\\$PLZF](#)
[V\\$NRF1](#)
[V\\$SP1F](#)
[V\\$ZBPF](#)
[V\\$EGRF](#)
[V\\$SETF](#)
[V\\$YY1F](#)
[V\\$CP2F](#)
[V\\$HESF](#)
[V\\$CHRE](#)
[V\\$VMB](#)

```

alignment position 1 . . . . . 1 1 . . . . . 2 1 . . . . . 3 1 . . . . . 4 1 . . . . .
hCOX6A1      1 a c t c t t g g t a t c a c a - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
mCOX6A1      1 t g c c a t g a a a G A T T T C G G G T A A C T C T C G G G A T G C A G C G C T G G C A A A A a T C
rCOX6A1      1 - - - - - - - - - - G A T T T C G G G T A A C T C T G G G A A T G C A G C G C T G G C A A A A - T C
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alignment position 5 1 . . . . . 6 1 . . . . . 7 1 . . . . . 8 1 . . . . . 9 1 . . . . .
hCOX6A1      16 - - - - - - - - - - - G A C T T T A T A T T C T A G T G G G G G A G A C A G A C A A A A T A A T A A
mCOX6A1      51 T A A G C A C T G C G G A C T T T A C A G T C T A T G T A G G G C A C A A C G G A A G A G A A T A A
    
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rCOX6A1	40	TAAGCAC	CAC	GGACTTTACA	G	GTC	CAT	AT	AG	GGCGT	CAC	AG	AAG	AGA	AATAA
		*****	*****	*****	*****	*****	*****	*****	*****	*****	*****	*****	*****	*****	*****
		*****	*****	*****	*****	*****	*****	*****	*****	*****	*****	*****	*****	*****	*****
		*****	*****	*****	*****	*****	*****	*****	*****	*****	*****	*****	*****	*****	*****
alignment position		101	...	111	...	121	...	131	...	141	...	151	...	161	...
hCOX6A1	55	t	-	-	-	-	-	-	-	AT	AAC	GAC	g	a	agg
mCOX6A1	101	CAACGGT	CTT	T	AAGAGCGAT	a	g	g	a	c	a	a	t	g	AT
rCOX6A1	90	CAACGGT	CTT	T	AAGAGTGAT	g	a	c	a	a	g	g	-	-	-
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		*****	*****	*****	*****	*****	*****	*****	*****	*****	*****	*****	*****	*****	*****
alignment position		151	...	161	...	171	...	181	...	191	...	201	...	211	...
hCOX6A1	76	t	t	a	t	g	t	g	c	t	a	t	g	a	a
mCOX6A1	151	GTCGAGG	GCC	T	GGGAAATCG	C	G	A	A	T	A	G	A	G	A
rCOX6A1	119	GTCGGGT	GCC	T	TGGAAATCG	C	G	A	A	T	A	G	A	G	A
		*****	*****	*****	*****	*****	*****	*****	*****	*****	*****	*****	*****	*****	*****
		*****	*****	*****	*****	*****	*****	*****	*****	*****	*****	*****	*****	*****	*****
alignment position		201	...	211	...	221	...	231	...	241	...	251	...	261	...
hCOX6A1	120	GAACGGA	ATT	T	AGATAGGG	C	G	T	C	T	G	G	A	T	C
mCOX6A1	201	GAATGGC	GCC	T	CCGCTAACG	T	G	A	C	T	T	G	T	C	T
rCOX6A1	166	GAATGGC	GCT	T	CCGATAACG	T	C	A	T	T	G	T	C	T	C
		*****	*****	*****	*****	*****	*****	*****	*****	*****	*****	*****	*****	*****	*****
		*****	*****	*****	*****	*****	*****	*****	*****	*****	*****	*****	*****	*****	*****
alignment position		251	...	261	...	271	...	281	...	291	...	301	...	311	...
hCOX6A1	170	TCCATGG	ACT	C	CAACGAAGG	G	A	G	C	G	A	T	T	c	c
mCOX6A1	249	TCCAGGG	ACT	C	CAAAGAAGG	G	A	G	C	G	A	T	T	A	A
rCOX6A1	214	TCCAGGG	ACT	C	CAAAGAAGG	T	A	G	C	A	g	T	T	A	A
		*****	*****	*****	*****	*****	*****	*****	*****	*****	*****	*****	*****	*****	*****
		*****	*****	*****	*****	*****	*****	*****	*****	*****	*****	*****	*****	*****	*****
alignment position		301	...	311	...	321	...	331	...	341	...	351	...	361	...
hCOX6A1	220	c	a	-	-	-	-	A	A	C	C	T	C	T	T
mCOX6A1	291	TCGCAAA	AGT	T	CAGTTCCGC	G	G	A	C	A	T	C	C	T	C
rCOX6A1	264	TCACAGA	AGC	T	CTATTCAGC	G	A	A	C	A	T	C	C	T	C
		*****	*****	*****	*****	*****	*****	*****	*****	*****	*****	*****	*****	*****	*****
		*****	*****	*****	*****	*****	*****	*****	*****	*****	*****	*****	*****	*****	*****
alignment position		351	...	361	...	371	...	381	...	391	...	401	...	411	...
hCOX6A1	249	-	-	A	G	G	T	G	G	G	a	c	g	t	a
mCOX6A1	341	GGAGATG	GGG	C	A	C	-	-	-	-	-	-	-	-	-
rCOX6A1	311	GGAGGTG	GGG	C	A	C	-	-	-	-	-	-	-	-	-
		*****	*****	*****	*****	*****	*****	*****	*****	*****	*****	*****	*****	*****	*****
alignment position		401	...	411	...	421	...	431	...	441	...	451	...	461	...
hCOX6A1	297	a	a	a	c	g	t	a	a	a	g	c	c	t	g
mCOX6A1	354	-	-	-	-	-	-	-	-	-	-	-	-	-	-
rCOX6A1	324	-	-	-	-	-	-	-	-	-	-	-	-	-	-
		*****	*****	*****	*****	*****	*****	*****	*****	*****	*****	*****	*****	*****	*****
		*****	*****	*****	*****	*****	*****	*****	*****	*****	*****	*****	*****	*****	*****
alignment position		451	...	461	...	471	...	481	...	491	...	501	...	511	...
hCOX6A1	347	A	G	a	t	g	-	-	C	C	G	A	G	G	A
mCOX6A1	384	AGCCGCC	CCa	g	-	-	-	-	-	-	-	-	-	-	-
		*****	*****	*****	*****	*****	*****	*****	*****	*****	*****	*****	*****	*****	*****


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* * * * *
alignment position 1 1 0 1 . . . . . 1 1 1 1 . . . . . 1 1 2 1 . . . . . 1 1 3 1 . . . . . 1 1 4 1 . . . . .
hCOX6A1 950 g t t a t g t g t g c c t t a g t g c a a g t t c t t c a t t c t c t g a a g g c a t g g g t g c c
mCOX6A1 981 G T T G T C C A C T C C C C T G G C C C A G C C C T t g g g g g a g t t t T A G G A T C T T G G -
rCOX6A1 935 G T T G T C C A C T C C C C A G T C C C A G C C C T t g g t g c g c - - T A G G A T 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 . . . . .
hCOX6A1 1000 a g g c g t g t a C A G C T T G T T T A T C C T C A C A A A C A G A A A A T G T A T T T T C T T C -
mCOX6A1 1029 - - - - - - - C T G C C T G T C C G T C C G T G C A G A T A G A A T A T T T T A T T T A C T C T
rCOX6A1 980 - - - - - - - C T G C C T G T C T A T C C G C G C A G A C T G A A C A T T T T A T T T A C T C T
* * * * *
* * * * *
* * * * *
alignment position 1 2 0 1 . . . . . 1 2 1 1 . . . . . 1 2 2 1 . . . . . 1 2 3 1 . . . . . 1 2 4 1 . . . . .
hCOX6A1 1049 - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
mCOX6A1 1070 t C G T T T G A C G G A A G G G A A G C C A G T T T G T A G G T C G T G G C T c g g - - - - -
rCOX6A1 1021 - C G T T T A C A T G A G G G A A G C C A G T T T G T G G G T C G C G G C T - - - - -
* * * * *
* * * * *
* * * * *
alignment position 1 2 5 1 . . . . . 1 2 6 1 . . . . . 1 2 7 1 . . . . . 1 2 8 1 . . . . .
hCOX6A1 1079 a t t a c g t c t c a a t t c t c t t c t t c a a g g t c a t a c a a t
mCOX6A1 1112 - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
rCOX6A1 1059 - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -

```

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.

	mCOX6A1 (1111 bp)	rCOX6A1 (1058 bp)
hCOX6A1 (1114 bp)	0.293 37 %	0.371 47 %
mCOX6A1 (1111 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 style="width: 50px;" type="text"/> to: <input style="width: 50px;" type="text"/>
Output file	<input style="width: 90%; height: 20px;" type="text" value="dialign.seq"/>

[licensed users only](#) **Extract aligned sequences**

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


```

alignment position 51 . . . . . 61 . . . . . 71 . . . . . 81 . . . . . 91 . . . . .
P875609      14 TAT AAAATGC At at at at - - - - - - - - - - - - - - - - - - - - - - -
P875610      51 TCT TCACTGC AATAAAACAC AAAC TAAGAT TGTCTATCCC GA AAA CCCAA
rCOX6B1      25 TCT TCA CAGC AATAAAACAC AAAC TAAGAT ACCTTATCTC GA AAA TCCAA
      * * * * *
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      * * * * *
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      * * * * *
alignment position 101 . . . . . 111 . . . . . 121 . . . . . 131 . . . . . 141 . . . . .
P875609      32 - - - - - - - - - - - - - - - ATCC A GGAGTAGCGG TGC GC ATCTG
P875610     101 ATA AAt AA AT AT AAATAACT TT CGAATCAA GGCACAGGGG TAAAC GCTTG
rCOX6B1      75 ATA AAc AA AC AT AAATAACT TT TGAATCAA AGCATAGGGG TAAAAGCTTG
      * * * * *
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      * * * * *
      * * * * *
alignment position 151 . . . . . 161 . . . . . 171 . . . . . 181 . . . . . 191 . . . . .
P875609      57 TAATCC CAGC TACT cgg g ag g a t g a g g c g g g a g a a t c g c t t g a a c c c a g g
P875610     151 TTATCC TAAC ACCT - - - - - - - - - - - - - - - - - - - - - - -
rCOX6B1      125 TTATCC TAGC ACTC - - - - - - - - - - - - - - - - - - - - - - -
      * * * * *
      * * * * *
      * * * * *
alignment position 201 . . . . . 211 . . . . . 221 . . . . . 231 . . . . . 241 . . . . .
P875609     107 a g g c g g a g g t t g c A GTGAGC TGAGATCg c g c t a c t g c a c t CC AGC CTGGG
P875610     165 - - - - - - - - - - - - A GTAA TC TGTGATCAA At - TTCGAGG CC AGT CTGAG
rCOX6B1      139 - - - - - - - - - - - - A GGAATC TGTGATCAA Aa g TTCGAGG CC AGT CTGTG
      * * * * *
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      * * * * *
      * * * * *
alignment position 251 . . . . . 261 . . . . . 271 . . . . . 281 . . . . . 291 . . . . .
P875609     157 CCATAG AGTA AGAC CCTGTC TCAAAAa t t a a a a a a a g a a a a a a a a t
P875610     201 ATATAC AGCG AAGT CCTATT TCAAAAa c A GATTAT - - - - - - - - - - -
rCOX6B1      176 CTGTAT AGCA AAGT CCTGTC TCAAAA- - CA GATTAT - - - - - - - - - - -
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      * * * * *
alignment position 301 . . . . . 311 . . . . . 321 . . . . . 331 . . . . . 341 . . . . .
P875609     207 t t a a a g a a a a g a a a t a c c t g a c a c a g a a a a g c g t t c a a t a a a t a t t t c t
P875610     237 - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
rCOX6B1      210 - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
alignment position 351 . . . . . 361 . . . . . 371 . . . . . 381 . . . . . 391 . . . . .
P875609     257 t g c a t g a a t a a a a g t a c t t t c g CT GGGAC A TTTTCTCCA CACCT ACCCT
P875610     237 - - - - - - - - - - - - - - - - - - CT GTGAC A CTTTTC - - CA TT CCC ACTCT
rCOX6B1      210 - - - - - - - - - - - - - - - - - - CT Gg t - - A TATTTTCCCA TT CCC ACTCT
      * * * * *
      * * * * *
      * * * * *
alignment position 401 . . . . . 411 . . . . . 421 . . . . . 431 . . . . . 441 . . . . .
P875609     307 CCA GCC AGCC CC g g g a t c t a t a a c a c t c t c t c c g a g t g AA GA CAC AGAGG
P875610     263 GAA GAC AGTC Tt a t g - - - C TTTT CCCTC T GGGA- - - - AG GA CAG GCAGG
rCOX6B1      236 GCA GAC AGCC TC a c t c t g t c TTTT TCATC T GGGA- - - - AG GA C T G G C A G G

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alignment position 7 5 1 7 6 1 7 7 1 7 8 1 7 9 1
P875609 652 **GTGAGTGTGG** AGGGTtCTGT AACC TGGGAC - CCCAGTCTA GC GGGCTGAG
P875610 602 **GTGAGTGTGA** AGGGT- CGGG AT CC TGGGGG - AACCTTGT C G T T G C A G A G
rCOX6B1 579 **GTGAGTGTAA** AGGGT- CA GG AT CC TGGGGG g AACCTTGT C T G T G G T A G A G
* * * * *
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alignment position 8 0 1 8 1 1 8 2 1 8 3 1 8 4 1
P875609 701 GAGCcggacc ccaGCTTCCC TGAGAACGGG **TTGAGGCTTC** **CGGCTGGC**g_g
P875610 650 AAGCGCCCG GG- GCTTCCC TGACGCCAAG **CAGAACTTC** **CGGCGGC**CAC
rCOX6B1 628 AAGCGCCCG GG- GCTTCCC TGAAGCCGGG **AAGAACTTC** **CGGCTAC**CCT
* * * * *
* * * * *
* * * * *
* * * * *

alignment position 8 5 1 8 6 1 8 7 1 8 8 1 8 9 1
P875609 751 cgtccg g c c t c c c t g g a c c c CGGGGCCCT G t t c t g t t c a t c g t a a GAGCT
P875610 699 GGGTc - - - - - - - - - - CGGTGTCCT G - - - - - - - - - - GAGCT
rCOX6B1 677 GGGCg - - - - - - - - - - CGGGTTCCT G - - - - - - - - - - GAGCT
* * * * *
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* * * * *

alignment position 9 0 1 9 1 1 9 2 1 9 3 1 9 4 1
P875609 801 AAC AAT GATA CGGT TCTTCC TTGATGC- - - CAGGCAACA TC C- CAAACA
P875610 719 AAC CAT TATA GCCGCCTTTC TT CATGAt g g c TAGGTCGCT Tt c t AAGCAG
rCOX6B1 697 CAC CAT TATA TCCGCCTTCA T- GATGT- - - TAGGTCGCT TGA- AAGCAG
* * * * *
* * * * *
* * * * *

alignment position 9 5 1 9 6 1 9 7 1 9 8 1 9 9 1
P875609 846 ACT TTA ATTA ATTTATTt a a c t c t c c c a C C AGCCCTATGA GATAGGCCT
P875610 769 TCc c - TATTA CTCCATCCT- - - - - - - - - - TC AGCCCTAc a a g - - - - -
rCOX6B1 741 TCTCTTATTA CTCCATTC T- - - - - - - - - - C C AGCCCTATGA AC TAGGACCT
* * * * *
* * * * *
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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
P875609 896 GCGATT -
P875610 800 - - - - - TCC CCTT TGAT AG CGTT GGGGC T GGAGTGTGAA GC GCC TT a c c
rCOX6B1 782 GCCATT a TCC CCTT TAAC AG AGCT GGGGC T GGAGTGTGAA GC GCC TT 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

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P875609 902 - - - - -
P875610 843 c g t G G C T A T A A G G C A A T T C G G A T T T A G A C C C A G T A A A T T G G A C T G T G G A G
rCOX6B1 832 a g c G G C T G T A T G G C A A T T A G G A T T T G G A C C C A G T A A A T T G A A C T G T G G T G
      * * * * *
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      * * * * *
alignment position 1 1 0 1 . . . . . 1 1 1 1 . . . . . 1 1 2 1 . . . . . 1 1 3 1 . . . . . 1 1 4 1 . . . . .
P875609 902 - - - - -
P875610 893 C T T T T A G T T G C G A G T T C A C A G G C G T G G C C A C C C g c g t t c c A A G G C C G A A G
rCOX6B1 882 C T T T T G G T C G C G G G C T C A C A G G C G T G G C C A C C C g - - - - - A A G G C C G A A G
      * * * * *
      * * * * *
      * * * * *
      * * * * *
alignment position 1 1 5 1 . . . . . 1 1 6 1 . . . . . 1 1 7 1 .
P875609 902 - - - - -
P875610 943 C C T G T C G C C T T G A C T C G T g t c t t t c
rCOX6B1 926 T C T G T C G C C T T G A C T C 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.

	P875610 (967 bp)	rCOX6B1 (943 bp)
P875609 (901 bp)	0.126 37 %	0.167 36 %
P875610 (967 bp)		<u>1.000</u> <u>82 %</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

GEMS Launcher Task: *DiAlign TF*: Multiple alignment plus TF sites working on C4-COX7C (3 seq.)

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

DiAlign professional TF Release 3.1 December 2004

Wed May 11 16:45:21 2005

Solution parameters:

Sequence file: [C4-COX7C](#) (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
1	P985294	P985294 sym=COX7C loc=Loc1350 taxid=9606 spec=Homo sapiens chr=5 ctg=NT_006713 str=(+) start=36507518 end=36508642 len=1125 tss=601,625 comm=cytochrome c oxidase subunit VIIc; (AK026505/501/gold;NM_001867/525/bronze;)
2	P985295	P985295 sym=Cox7c loc=Loc12867 taxid=10090 spec=Mus musculus chr=13 ctg=NT_039589 str=(-) start=9490489 end=9491609 len=1121 tss=601,606,621 comm=cytochrome oxidase, subunit VIIc; (AK002494/526/gold;AK027989/531/gold;NM_007749/546/bronze;)
3	rCOX7C	rCOX7C rn3_dna range=chr2:15175947-15176956 5'pad=0 3'pad=0 revComp=TRUE strand=? repeatMasking=non

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\\$MYOF](#) [V\\$STAT](#) [V\\$RBPF](#) [V\\$STAF](#) [V\\$GKLF](#) [V\\$RORA](#) [V\\$ETSE](#) [V\\$PLAG](#)

```

alignment position 1 . . . . . 1 1 . . . . . 2 1 . . . . . 3 1 . . . . . 4 1 . . . . .
P985294      1 t t c a t c a g g c g g a c a c c a g t t c c t a g t c c a g g c t a g c t c c a g g t G T C A G A
P985295      1 a a - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
rCOX7C       1 - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
                                                                * * * * *
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                                                                * * * * *
    
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alignment position 51 . . . . . 61 . . . . . 71 . . . . . 81 . . . . . 91 . . . . .
P985294 51 GGCCACTTTT CCCTTCTACT CCTCACACAT GCTGt a c t c a t a c c a g a c t t
P985295 9 AGGT TCTTGT GTCTTCTCCA ACCTAATCAT GCTGc g c a t a g g a g t t t c T A
rCOX7C 7 AGGT ACTCAT CTCTTCCATA ATCTAATCAT GCTt c a c a t a t c g t t - - TA
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alignment position 101 . . . . . 111 . . . . . 121 . . . . . 131 . . . . . 141 . . . . .
P985294 101 g a g t t t t c c c t g c c c t t t g t t c t t c c t T C T T T T T A T T C G A T T C C C A T T A
P985295 59 T C - - - - - - - - - - - - - - - - - - - - - T G T A T G T C C T C T T A T A T C C A A T T
rCOX7C 54 T C - - - - - - - - - - - - - - - - - - - - - T G T A T G T T C T T A A A T A T C C A T T T
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alignment position 151 . . . . . 161 . . . . . 171 . . . . . 181 . . . . . 191 . . . . .
P985294 151 T C T T T A G T g - - - - - A T C A T T C C C T T A G C A T T T C A G T t t t c t c t c t g a
P985295 84 T C T A T A C C T T C A A a a a a - C C A G G T C T T A G C A C T T C A G T C C A G T T T T C A C
rCOX7C 79 T C T G T A T T T T C A A a a a c A T C C A G C T C T T G C C A C T T C A G T C C A G T T T T C A C
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alignment position 201 . . . . . 211 . . . . . 221 . . . . . 231 . . . . . 241 . . . . .
P985294 193 a g - - - - T C C T T T G T G C T G C A C G T T G T T T G A T T A C T T G t g t t t a t g c T T T
P985295 133 T A C G G C A T C C T T T G T G C T A C A T A C T G T T T G A T C A G T T G C T - - - - - T G T
rCOX7C 129 C A T G G C A T C c - T T G T G C T A C A T A C T G T T T G A T T A G T T G C C - - - - - T G T
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alignment position 251 . . . . . 261 . . . . . 271 . . . . . 281 . . . . . 291 . . . . .
P985294 238 G T T T C T T C A G C T A G G A T C A T T A g c a C A T A T C T C T C A G C A T T G G C A A A A g t
P985295 176 G T T C C C T C A G A C A G G A C T A T A A T G - C A C A T C T T T C A A C C T T G G C A A A G A A
rCOX7C 171 G T T C C C c t c - - - - G G A A T A G A A T G - C A C A T C T T T C A A T G T T G G C A A A A A
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alignment position 301 . . . . . 311 . . . . . 321 . . . . . 331 . . . . . 341 . . . . .
P985294 288 c c - - - T C G A A A T C A T T G A C A C C T - - - - - A G C A T A T A C T T T A T T T T T a a
P985295 225 C C A T A A T C A A A A T G A C T G A T A t a c t c a c a a G A A A A T A A T T T T A T T T C T T G
rCOX7C 216 T C A T A A T C A A A A T G A G T G A T A C A T - - - - - G A A A A T A A T T T T A T T T C T T G
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alignment position 351 . . . . . 361 . . . . . 371 . . . . . 381 . . . . . 391 . . . . .
P985294 328 a a a a g a a g a a a a g a a g a g a a a a g g g a t g g g t t t a t t g t c c t t T T C A A C A G
P985295 275 - - - - - - - - - - - - - - - - - - - - - - - - - - - T T C C A T T A
rCOX7C 260 - - - - - - - - - - - - - - - - - - - - - - - - - - - T T C C A T A A
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alignment position 401 . . . . . 411 . . . . . 421 . . . . . 431 . . . . . 441 . . . . .
P985294 378 A C T A G A G T A T A C G G G G T G A A A C T G C T T C A C T T G A T T C A A T a A A A T C G T T T
P985295 283 A C T T G A A C A C A C A T G T T A A A G C A G C T T T A G T T T C T T C A A T - A A A T T G T T T
rCOX7C 268 A C T T G A A C A C A C A C G G T T A A A C A A C T T T A G T T A C C T C A A T - A A G T T G A T T

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alignment position 45 1 . . . . . 46 1 . . . . . 47 1 . . . . . 48 1 . . . . . 49 1 . . . . .
P985294    428 CCGGTAACA G GCCCCAAGGA A TCCTAGACC T a a g c - - - - -
P985295    332 CTGGAACA A ATCCCAAGGA A TCCTAGATC T GA ACTC AT AG GACAGCTC AG
rCOX7C    317 ACGGAAACA A ATCCCAAGGA A TCCGAGATC T GA ACTC AG AA AACAGCTC AG
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alignment position 50 1 . . . . . 51 1 . . . . . 52 1 . . . . . 53 1 . . . . . 54 1 . . . . .
P985294    462 - - - - -
P985295    382 GT c c c a t t g a a t c a c t a a a g g t a AGT TAT C AC TTGGT GCT GGTGCGCGCT
rCOX7C    367 GT t c t a a a c a c a g a t g a t a a g c t AGC TAT C AC TTGGT GGG GGAGCGCGCT
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alignment position 55 1 . . . . . 56 1 . . . . . 57 1 . . . . . 58 1 . . . . . 59 1 . . . . .
P985294    462 - - - CTGGC G CGAAAC TACA TTTCCACAA TCCTTCGG g g g c t g a t a a g g
P985295    432 CA TT CTAGAG CCAGAC TACA TTTCCACAA TCCATCGGAG CC GATATGGc
rCOX7C    417 CA TT - - - - - CAGAC TACA TTTCCAAA TCACCGGAA CC GATATGGg
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alignment position 60 1 . . . . . 61 1 . . . . . 62 1 . . . . . 63 1 . . . . . 64 1 . . . . .
P985294    508 c t CC GCAAT G GTCTGA ACT A CAATTCC CAC AA TCCa g g g c g a t t t c c g c t
P985295    482 GC CC GGTAT T ATCTAA ACT A CAAAGC CAC AA ACCT CAGA GC CCGCCGGT
rCOX7C    460 GC CA GGTAT T ATCTAA ACT A CAAATC CAC AA TCCT CGGA GC CCGCCAGT
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alignment position 65 1 . . . . . 66 1 . . . . . 67 1 . . . . . 68 1 . . . . . 69 1 . . . . .
P985294    558 t t g t c g CGT T TCCTCAAGGC TCCGCC CC AT TTCCCATCTT TCTTTTCAGT
P985295    532 TG AG TACGT T TCAGGAAGT T CCTGTT GT AA CTCCCATCTT CCCTTTCGGT
rCOX7C    510 TG AT TGCGT c - CAGGAAGT C CGTGCT GT AG TTCCCATCTT CCCTTTCGGT
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alignment position 70 1 . . . . . 71 1 . . . . . 72 1 . . . . . 73 1 . . . . . 74 1 . . . . .
P985294    608 CC TT GCGCA C CGG GGAACA GGTCGT GAA AA Aa a g t c t TG GT GAGGTG
P985295    582 CT T C GCGCT C TGC CGAGCA GGTCGT GTA AA AGGG GAG- Tt AGGTGGTA
rCOX7C    559 CT T C TCGTT C CGG ATAGCA GGTCGT GAA AA AGTAGG G- TGAGGTGGTA
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alignment position 75 1 . . . . . 76 1 . . . . . 77 1 . . . . . 78 1 . . . . . 79 1 . . . . .

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alignment position 1051 . . . . . 1061 . . . . . 1071 . . . . . 1081 . . . . . 1091 . . . . .
P985294 958 CCTAGCGCGT AGCCGCTaaa ggaatgggca ggtagatc c g ga AGCCCTGC
P985295 899 CACGCGCC T AGCCGCTGC C TC- - - - - - - - - - - - - - - CACGCCGC
rCOX7C 870 CACAGCGCC T AGCTGCTGC C TC- - - - - - - - - - - - - - - AGCACTGC
    * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * *
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alignment position 1101 . . . . . 1111 . . . . . 1121 . . . . . 1131 . . . . . 1141 . . . . .
P985294 1008 CTc c a t c a g c c a c c t g a c g C C C C T C C C C C G C C C C G C A G A A A G C C T G A G
P985295 929 CT g t c a g c c g - - - - - - - - - - - - - - - C A G A G C G A G G C C T G G A
rCOX7C 900 CT - - - - - - - - - - - - - - - G C C T G C C A C C T C T T C C C A G A G C C A G G C C T G G A
    * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * *
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alignment position 1151 . . . . . 1161 . . . . . 1171 . . . . . 1181 . . . . . 1191 . . . . .
P985294 1058 ATGg c t c c g g g a g g c c a c g g c t g t a g g t g t g t t g g t t a a a t c c g a g c T G G
P985295 955 AGGTTCGGT G GGAGCTGGGC GGCGt c g g a g a t - - - - - - - - - - - - - - - T G A
rCOX7C 934 AGGT TAGGT T GGACCTGGGC GGCGt c a g a g a t g a g c - - - - - - - - - - - - - - - G A
    * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * *
    * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * *
    * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * *
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alignment position 1201 . . . . . 1211 . . . . . 1221 . . . . . 1231 . . . . . 1241 . . . . .
P985294 1108 A G G T C A T C G G A C C C G A A A - - - - - - - - - - - - - - - - - - - - - - -
P985295 990 A G G T C A T T G G A A A C A A A A G A A G A G G G C C T G T G G C T G g t t a t t a g c g c t t t
rCOX7C 972 A G G T C A T T G G A A A C A A A A G A A A A G G G C T T G A G G C T G t g g - - - - - - - - - -
    * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * *
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    * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * *
    * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * *

alignment position 1251 . . . . . 1261 . . . . . 1271 . . . . . 1281 . . . . . 1291 . . . . .
P985294 1126 - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
P985295 1040 a a a c c a g c a a g c c a c g t t t g a a g c g g c g a t c c t c g g t t a g g c c c g g t t a
rCOX7C 1011 - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -

alignment position 1301 . . . . . 1311 . . . . . 1321 . . . . . 1331
P985294 1126 - - - - - - - - - - - - - - - - - - - - - - -
P985295 1090 g c c c c a g t g t a a g t a a a c g g a g t a c t t a g t g
rCOX7C 1011 - - - - - - - - - - - - - - - - - - - - - - -
    
```

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.

	P985295 (1121 bp)	rCOX7C (1010 bp)
P985294 (1125 bp)	0.272 45 %	0.246 43 %
P985295 (1121 bp)		<u>1.000</u> <u>77 %</u>

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

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

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

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GEMS Launcher 4.1.1

GEMS Launcher Task: *DiAlign TF*: Multiple alignment plus TF sites working on C4-COX7B (3 seq.)

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

DiAlign professional TF Release 3.1 December 2004

Sat May 7 01:36:43 2005

Solution parameters:

Sequence file: [C4-COX7B](#) (3 seq.)
Type of sequences: nucleotide sequences
Threshold T: 0.00
'*' signs below alignment denote: diagonal similarity (max. similarity is represented by 10 '*' signs)
 complete alignment is shown
Alignment output: # 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
1	P985229	P985229 sym=COX7B loc=Loc1349 taxid=9606 spec=Homo sapiens chr=X ctg=NT_011651 str=(+) start=450269 end=452269 len=2001 tss=1001 comm=cytochrome c oxidase subunit VIIb; (NM_001866/501/bronze;)
2	P985231	P985231 sym=Cox7b loc=Loc66142 taxid=10090 spec=Mus musculus chr=X ctg=NT_039711 str=(+) start=11047340 end=11049343 len=2004 tss=1001,1004 comm=cytochrome oxidase subunit VIIb; (AK002593/514/gold;NM_025379/511/bronze;)
3	rCOX7B	rCOX7B rn3_dna range=chrX:94210088-94212438 5'pad=0 3'pad=0 revComp=FALSE strand=? repeatMasking=nc

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\\$RBP](#) [V\\$IKRS](#) [V\\$OCT1](#) [V\\$CLOX](#) [V\\$E2FF](#) [V\\$SF1F](#) [V\\$GATA](#) [V\\$STAT](#) [V\\$LEFF](#) [V\\$TCFF](#)

```

alignment position 1 . . . . . 1 1 . . . . . 2 1 . . . . . 3 1 . . . . . 4 1 . . . . .
P985229      1 g c g a t t c t g c c g c c t c a g t c t a c a g a g t a g c t g g g a t t a c a g g c a c a t g c
P985231      1 a c T A T T A C T G A A T G G G A c a T G C T A A G A T C C T A T A C C T T T T G A T A G G A T G C
rCOX7B       1 a t T A T T A C T G A A T G G G A - - T G C T A A G G T C C T A T A C C T T C T G A T A G G A T G C
    
```



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          * * * * * * * * *
          *
          *
alignment position 451 . . . . . 461 . . . . . 471 . . . . . 481 . . . . . 491 . . . . .
P985229      424 g t c t c g a a c t c c g a c c t c g t g a t c c g c c c a c c t t g g c c t c t c a a a g t g c t
P985231      231 - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
rCOX7B      218 - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -

alignment position 501 . . . . . 511 . . . . . 521 . . . . . 531 . . . . . 541 . . . . .
P985229      474 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 g g c c a a t a g e t t t c c A A A G T T A
P985231      231 - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - A T T
rCOX7B      218 - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - A A A C A T T
                                                                    * * * * * * *

alignment position 551 . . . . . 561 . . . . . 571 . . . . . 581 . . . . . 591 . . . . .
P985229      524 T T T T A T C A C G T A T T T A T C T A c - - A T A T T A C A G A A G T T T T A C T G T T C T T G
P985231      234 A T T T A T T A T A T g t a a g t a c a c t g t a g e t g t c t t c a g a c a c a c c a g a a g a g
rCOX7B      225 T T T T A T T A T A T A T T T C T T A t t t A C A T T T C A A A G G T T A T T A C C C T T C C T G
          * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * *

alignment position 601 . . . . . 611 . . . . . 621 . . . . . 631 . . . . . 641 . . . . .
P985229      572 c a a c t t t t c t c t a a a c t t g a c g t t a t t t g a a a - - - - - - - - - - - - - - - - - -
P985231      284 g g c a t c a g a t c t c a t t a a g g a t g g t t g t g a g c c a c c a t g t g g t t g c t g g g
rCOX7B      275 g t t t c c t g t c c a t a a g c c c c a t c c c c t c c c c c t c c c t c a t a t g g g t a t t

alignment position 651 . . . . . 661 . . . . . 671 . . . . . 681 . . . . . 691 . . . . .
P985229      604 - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
P985231      334 a t t t g a a c t c t g g a c c t t t g g a a g a g c a g t c g g g t g c t c t t a c c c a c t g a
rCOX7B      325 c c c c c t a c t g c c c c c c c c c c a t a t t c c c t t g c a c t g g g g g g t c c a a c c

alignment position 701 . . . . . 711 . . . . . 721 . . . . . 731 . . . . . 741 . . . . .
P985229      604 - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
P985231      384 g c c a t c t c a c c a g - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
rCOX7B      375 t t g g c a a g a c c t a g g g c t t t c c c t t c c a c t g g t g c c c c a a c a a a g c t a t t

alignment position 751 . . . . . 761 . . . . . 771 . . . . . 781 . . . . . 791 . . . . .
P985229      604 - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
P985231      397 - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - C C C T A C A C A G A G T T T c
rCOX7B      425 c t c t g c t a c a t a t g c a g t t g g a g c C C T T A C A C A G A G T T T a a g a a g a t a c a
          * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * *

alignment position 801 . . . . . 811 . . . . . 821 . . . . . 831 . . . . . 841 . . . . .
P985229      604 - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
P985231      413 - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
rCOX7B      475 t t t g n n n n n n n n n n n n n n n n n n n n n n n n n n n n n n n n n n n n n n n n n n n n n n n n n n

alignment position 851 . . . . . 861 . . . . . 871 . . . . . 881 . . . . . 891 . . . . .
P985229      604 - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
P985231      413 - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
rCOX7B      525 n n n n a t a t c t g a a g c a t g t g a a g a t g t c a c c t a c a t g c c c a g g c g t t c a c

alignment position 901 . . . . . 911 . . . . . 921 . . . . . 931 . . . . . 941 . . . . .
P985229      604 - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
P985231      413 - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
rCOX7B      575 a c a g a t g c c t c t g g g a a g a a a a c t t c a g g c a a t a c a a a t c g c a a g a c a g g

alignment position 951 . . . . . 961 . . . . . 971 . . . . . 981 . . . . . 991 . . . . .
P985229      604 - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
P985231      413 - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -

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rCOX7B      625  a g t g a a g c t t  a a a c a c a g c t  g t c t g c t t a g  c c t t g g c t g a t c a g t c a g g a
alignment position 1 0 0 1 . . . . . 1 0 1 1 . . . . . 1 0 2 1 . . . . . 1 0 3 1 . . . . . 1 0 4 1 . . . . .
P985229    604  - - - - -
P985231    413  - - - - -
rCOX7B      675  c a g c a g g a c a  c t g c t t c c c t  c t a g g c a a a t  a c t a a a c t g a a c c c a c a g t t
alignment position 1 0 5 1 . . . . . 1 0 6 1 . . . . . 1 0 7 1 . . . . . 1 0 8 1 . . . . . 1 0 9 1 . . . . .
P985229    604  - - - - -
P985231    413  - - - - -
rCOX7B      725  t g t t c c g t c t  g c t c t a a c c a  a g a g t a g g a a  a g a g a t g a g a a a a g c a c c t a
alignment position 1 1 0 1 . . . . . 1 1 1 1 . . . . . 1 1 2 1 . . . . . 1 1 3 1 . . . . . 1 1 4 1 . . . . .
P985229    604  - - - - -
P985231    413  - - - - -
rCOX7B      775  g a g a t t c c t a  t t t g g a a a a g  a g a a g c c a a a  t g c a c a t g a a t a c t t t t a c a
alignment position 1 1 5 1 . . . . . 1 1 6 1 . . . . . 1 1 7 1 . . . . . 1 1 8 1 . . . . . 1 1 9 1 . . . . .
P985229    604  - - - - -
P985231    413  - - - - -
rCOX7B      825  t t t c a a a g g t  t a t t a c c c t t  c c t g g t t t c c  t g t c c a t a a g c c c c c a t c c c
alignment position 1 2 0 1 . . . . . 1 2 1 1 . . . . . 1 2 2 1 . . . . . 1 2 3 1 . . . . . 1 2 4 1 . . . . .
P985229    604  - - - - -
P985231    413  - - - - -
rCOX7B      875  c t c c c c t c c  c t c a t a t g g g  t a t t c c c c c t  t a c t g c c c c c c c c c c c a t a t
alignment position 1 2 5 1 . . . . . 1 2 6 1 . . . . . 1 2 7 1 . . . . . 1 2 8 1 . . . . . 1 2 9 1 . . . . .
P985229    604  - - - - -
P985231    413  - - - - -
rCOX7B      925  t c c c t t g c a c  t g g g g g g t c c  a a c c t t g g c a  a g a c c t a g g g c t t t c c c 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 . . . . .
P985229    604  - - - - -
P985231    413  - - - - -
rCOX7B      975  c a c t g g t g c c  c c a a c a a a g c  t a t t c t c t g c  t a c a t a t g c a g t t g g a g c c c
alignment position 1 3 5 1 . . . . . 1 3 6 1 . . . . . 1 3 7 1 . . . . . 1 3 8 1 . . . . . 1 3 9 1 . . . . .
P985229    604  - - - - -
P985231    413  - - - - - T T A A G A A G A  T A C A - - -  T A T A T A G T A T T C  T T G C C A G A T G
rCOX7B    1025 t t a c a c a g a g  t T T A A G A A G A  T A C A t t t g  T A T A T A G T A T C A  T T G C C A G A T G
      * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * *
alignment position 1 4 0 1 . . . . . 1 4 1 1 . . . . . 1 4 2 1 . . . . . 1 4 3 1 . . . . . 1 4 4 1 . . . . .
P985229    604  - - - - -
P985231    448  C A C A T g a a c -  - - T G G A A T C  C T T A G G G A A  A A A g t c - A A T T G A T C T C C C
rCOX7B    1075 T A C A T a c a c t  g a a T G G A A T C  C C T A G G G A A A  A A A a g a c t A A T T G A T C T C C C
      * * * * *
      * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * *
alignment position 1 4 5 1 . . . . . 1 4 6 1 . . . . . 1 4 7 1 . . . . . 1 4 8 1 . . . . . 1 4 9 1 . . . . .
P985229    604  - - - - -
P985231    493  A G c a c t t g g g  a g g c a a a g g c  a g g a c t t t t t  c t g t g a g t t c c a g g c c a g c t
rCOX7B    1125 A G - - - - -
      * *
alignment position 1 5 0 1 . . . . . 1 5 1 1 . . . . . 1 5 2 1 . . . . . 1 5 3 1 . . . . . 1 5 4 1 . . . . .
P985229    604  - - - - -

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P985231	543	t g g t c t a c a t a g a g a g t t c c t g g t c a g c c a g g a c t a a a t a g a g a g g c c g t				
rCOX7B	1127	-----				
alignment position	155 1	156 1	157 1	158 1	159 1	
P985229	604	-----	-----	-----	-----	AC T AAAAGCTAA
P985231	593	g t c t c a a c t c c c c a c a a a a t t c c a a a a a a a a a c c A A T A A A G G T A A A				
rCOX7B	1127	-----	-----	-----	-----	-----
						* * * * * *
alignment position	160 1	161 1	162 1	163 1	164 1	
P985229	616	G C C A A T T A G T A T A G T a G T A A T A G C A G A C A A A A a a a a T G A G A G A A G T A A G				
P985231	643	A C C A A T T A A T G T A G - - G T A A T A G G A G A C A G A A t g - - T G A A A A A T T T G A A G				
rCOX7B	1127	-----	-----	-----	-----	-----
		* * * * * *	* * * * *	* * * * *	* * * * *	* * * * * *
alignment position	165 1	166 1	167 1	168 1	169 1	
P985229	666	G A A G T T T T G G G G G A A C A G A A A G A a g a a a g a g c t a g t g t g g a g a t a c t a a a				
P985231	689	G G A C T G T A A T T G G A A G T G A G A C A c t a g a t c c a a t - - - - -				
rCOX7B	1127	-----	-----	-----	-----	-----
		* * * * * *	* * * * * *	* * * * *		
alignment position	170 1	171 1	172 1	173 1	174 1	
P985229	716	c c g a a g C T T G T G G A A C T T G A A C G C C A T T T T G A A G C T A G T T C C T T A g a c g a				
P985231	723	- - - - - C C T C T G G A G T T T T A G C A C C A T T T T G A T G C T G G T G C C T T A T G T - -				
rCOX7B	1127	-----	-----	-----	-----	-----
		* * * * *	* * * * *	* * * * *	* * * * *	* * * * *
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alignment position	175 1	176 1	177 1	178 1	179 1	
P985229	766	t t c g g t c g A A G A T C T G T C T C T C G G C T G C C C T C T A T A G A G C T C T A A A C C T G				
P985231	765	- - - - - - - A A G G T C G G T G T C T C A G C T C T C C T T T G T A G A G T C C G A A A C C T T				
rCOX7B	1151	- - - - - - - A A G G T T G G T G T C T C A G a T C T C C T T T G T A G A G T C C T A A A C C T T				
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alignment position	180 1	181 1	182 1	183 1	184 1	
P985229	816	G C T T C A A G G A G T T C T - T T C a t t c t t c a t t a g a t a c c a c c c a c c a t a c g t c				
P985231	807	T G T C C A A A G A G T T A a c C T C C C T G C T T A G T A A A T A C T A C T T T A T G G a A G C C				
rCOX7B	1193	T G T C C A A A G A G T T A T - C T C C C T G T T T A G T A A A T A C T A G T C A A T G G c A G C C				
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				* * * * *	* * * * *	* * * * *
alignment position	185 1	186 1	187 1	188 1	189 1	
P985229	865	a t t t A T A A A G C C G G A A A C T A C A T T T C C C A A A a g g c c t t t a T T - - - T T T				
P985231	857	- - - - - A T C A A G C T T G A A A C T A C A T T T C C C A A A G A C C - - - - - T T c c t a T T T				
rCOX7B	1242	- - - - - A T C A A G T T T G A A A C T A C A T T T C C C A A A G G C C - - - - - T T - - - T T T				
		* * * * * *	* * * * * *	* * * * *	* * * * *	* * * * *
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				* * * * *	* * * * *	* * * * *
alignment position	190 1	191 1	192 1	193 1	194 1	

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P985229 911 CCT CGC GGA A AAG GAT TG CAATTACTAT AGGT t t t a c a g g - - - - TAT
P985231 897 CCT CGC AGGA A CT A G G A T GA CAATTTCTAT AGGT CAAc - - CCCTAAATCT
rCOX7B 1278 TCT CGC AGGA A AT A G G A T TA CAATTTCTAT AGGT CAAt t t CCCCAAATCT
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alignment position 1951 . . . . . 1961 . . . . . 1971 . . . . . 1981 . . . . . 1991 . . . . .
P985229 956 CGC GAGATTT C GT CAAATCT CATTACGGAT CC CG GCTGAA AGCCATTTTG
P985231 945 CGC GACATCT C ACCAATCT CATTTGGCT CC CT GCTGAA AGCCATTTTG
rCOX7B 1328 CGC GATATGT T AC CAAATCT CATTAGGAAT CG CC GcA GAA AGCCATTTTG
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alignment position 2001 . . . . . 2011 . . . . . 2021 . . . . . 2031 . . . . . 2041 . . . . .
P985229 1006 TTT TTC AGCT C AC - - TT CAA GGGTACCT GA AG CG AATTGG CACCAAAGCA
P985231 995 TTT TTC AGGA C g c t t TG CAA GGGTAGCT GG GG TGAATTGG CACCAAAGCA
rCOX7B 1378 TTT TTC AGGA C TC - - TG CAA GGGTAGCT GG GG TGAATTGG CACCCAGGTA
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alignment position 2051 . . . . . 2061 . . . . . 2071 . . . . . 2081 . . . . . 2091 . . . . .
P985229 1054 GCAGCT GTAt t - GC CGC AGT TCTAGCTT CA CCTT CACGAT GTTTCCTTG
P985231 1045 GCAGCa - TAG T CGC CGC AGT TCCATCTT CG TCTC CGCGAT GTTGCCCTTA
rCOX7B 1426 GCAGCT GTAG T CAC CGC AGT TCCATCCT TG TCTC CGCGAT GTTGCCCTTG
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alignment position 2101 . . . . . 2111 . . . . . 2121 . . . . . 2131 . . . . . 2141 . . . . .
P985229 1103 GTC AAA AGCG C ACT AAA TCG TCTCCAAGGT GAGC Aaaa a t t a t g a c a a a t
P985231 1094 GCC AAA AACG C ACT AAG CCG TCTCCAAGGT GAGC AGATAA TGTGGGCGAG
rCOX7B 1476 GCC AAA AACG C ACT AAG TCG TCTCCAAGGT GAGC AGATAA TGTGGGCGAG
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alignment position 2151 . . . . . 2161 . . . . . 2171 . . . . . 2181 . . . . . 2191 . . . . .

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P985229 1153 c a - TTT ACAA C AAC Ct t at A TCAATGTGTC CT CGCGGCCCT Ct cgt g t g c t
P985231 1144 TTC TTT ACAA C ACC CGG G- A TCCg g c t g t C CT CGTGCTCT TCTGCCCTCT
rCOX7B 1526 CCC TTT ACAA C ACC CGG G- A TCCATCTGCC CT CGTGCTCT CATGCCTTTT
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alignment position 2 2 0 1 . . . . . 2 2 1 1 . . . . . 2 2 2 1 . . . . . 2 2 3 1 . . . . . 2 2 4 1 . . . . .
P985229 1202 t t c c t t t t a c g a a c a t c t c g g c c t t c t a a t c t t g a a t g c t g t c t GTCTCC
P985231 1193 TCC TCC GCCC C AAATCC T Gc g g GTTTTA AT TCTAGGTGCA TG- - GTCCCC
rCOX7B 1575 TCC TCT GCCC T AAA GCC T Gc a - GTTTTA AT TCTAGGTGCA CG- - GTt CCC
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alignment position 2 2 5 1 . . . . . 2 2 6 1 . . . . . 2 2 7 1 . . . . . 2 2 8 1 . . . . . 2 2 9 1 . . . . .
P985229 1252 CAT CTC GTCC C AAGTCATTG GGATGATg t c c t t a g - - - - -
P985231 1241 TGC GTGTCT C CAGTCACTG GGAAGg g a a g c t a g c c a t a a c a g a GGTAGC
rCOX7B 1622 TGC GTGTCT C CAGTCACTG GGAAGATa g c a a t g a c a g t - - - - GGTAGC
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alignment position 2 3 0 1 . . . . . 2 3 1 1 . . . . . 2 3 2 1 . . . . . 2 3 3 1 . . . . . 2 3 4 1 . . . . .
P985229 1287 - - - - CATTG GCTTTATCAC CCAGTATTTC TGT T t e g g t t t c c a g c t c t c
P985231 1291 TGT GAC AGTG GCTTTATCAT CCTGTCCTTG TGT T CCTAAC CTCGTT - - - -
rCOX7B 1667 TGT GAC AGTG GCTTTATCAT CCTGTCCTTG TGT T CCTAGC CTAGTT - - - -
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alignment position 2 3 5 1 . . . . . 2 3 6 1 . . . . . 2 3 7 1 . . . . . 2 3 8 1 . . . . . 2 3 9 1 . . . . .
P985229 1332 t t t c t g t t a t c g g a g t g a t a g t c t a g c c CT GC TT TTTAAT TCTTCAGTAA
P985231 1337 - - - - - - - - - - - - - - - - - - - - AT GC AT TCTCTT TCTTCAGAGA
rCOX7B 1713 - - - - - - - - - - - - - - - - - - - - CT GC AT TCTCTT TCTTCAGAGA
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alignment position 2 4 0 1 . . . . . 2 4 1 1 . . . . . 2 4 2 1 . . . . . 2 4 3 1 . . . . . 2 4 4 1 . . . . .
P985229 1382 CCT TTGATTT CAGG GAA Gg a c a t t c t t g g t a GAC ACCTCG TTCCTT AAGT
P985231 1359 CCT ATGATTT C CAG GAA GAA CGCTTTGGCG - GAC ACCTTG CTCTTT TAGC
rCOX7B 1735 CCT ATCATTT C CAG GAA GAC CGTTTTGGCG - GGC ACCTTG CTCTTT TAGC
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alignment position 2 4 5 1 . . . . . 2 4 6 1 . . . . . 2 4 7 1 . . . . . 2 4 8 1 . . . . . 2 4 9 1 . . . . .
P985229 1432 GAT GTC CTAC ATTT TAGCTT TGGg g a t a t g t t t a c t c c t a a c c c t GTATA
P985231 1408 GAT GAT CTAA ATTT TAGCTC TGGGAGTGT A T T T A c - - - - - GTAGA
rCOX7B 1784 CAT GTT CTAA ATTGTAGCTT TGGGACTGTA T T T A t a t - - - - -

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alignment position 2501 . . . . . 2511 . . . . . 2521 . . . . . 2531 . . . . . 2541 . . . . .
P985229 1482 GAA AAA TATC T TCT CCA ATt c c t a t t a c t g t a a t a g a c g g a a a c t g t a a a
P985231 1448 AGA ACT GATC T CCT ACA ATa a - - - C G G T G G T A G G A A A C T A A A T C T A - - - -
rCOX7B 1821 AGA ACT GATC T CCT At g g t g g t a g C G G T G G T A G G A A A C T A A A T C T A - - - -
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alignment position 2551 . . . . . 2561 . . . . . 2571 . . . . . 2581 . . . . . 2591 . . . . .
P985229 1532 t c t a g c t C T T C A C C T G G T T T A A T T G C A G G G A A A C A A C C C A A A t g g t a t c g
P985231 1491 - - - - - C C G C A T C T G G A T T C A T A G C A A G G g g t t g a a a a c c t t a a g c C T G
rCOX7B 1867 - - - - - C C T C A C C T G C A T T C A T A G C G A G G G G G A A A G C A A A a t t - - C T G
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alignment position 2601 . . . . . 2611 . . . . . 2621 . . . . . 2631 . . . . . 2641 . . . . .
P985229 1582 a t G C A G C T T T G A A G t t a t t t g t g g a t t a a c a a t g t t a g c t g g c c a g g c g c
P985231 1534 - - G C A G C T T T G A A G A A G T C A T C T G T A G A T T A T T A A C G G - - - - - - - - - -
rCOX7B 1908 - - G C A G C T T T G A A G A A G T C G T C T G T A G A T T A T T A A C G G - - - - - - - - - -
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alignment position 2651 . . . . . 2661 . . . . . 2671 . . . . . 2681 . . . . . 2691 . . . . .
P985229 1632 g g t g g c t c a c a c t t g t a a t c c c a g c a c t t t g g g a g g c c a a g g c g g g c g g a
P985231 1570 - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
rCOX7B 1944 - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -

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alignment position 2701 . . . . . 2711 . . . . . 2721 . . . . . 2731 . . . . . 2741 . . . . .
P985229 1682 t c c c c t g a g g t c a g g a g t t c g a g a c c a g c c t g g c c a a c a t a g t g a a a c g c
P985231 1570 - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
rCOX7B 1944 - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -

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alignment position 2751 . . . . . 2761 . . . . . 2771 . . . . . 2781 . . . . . 2791 . . . . .
P985229 1732 c g t c c c t a c t a a a a t a c a a a a a t t a g c c g g g c g t g g t g g t g g g c g c c t g
P985231 1570 - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
rCOX7B 1944 - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -

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alignment position 2801 . . . . . 2811 . . . . . 2821 . . . . . 2831 . . . . . 2841 . . . . .
P985229 1782 t a a t c c c a g c t a c t t g g g a g g c t g a g g c a a g a g a a t c g c t t g t a c c c g g g
P985231 1570 - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
rCOX7B 1944 - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -

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alignment position 2851 . . . . . 2861 . . . . . 2871 . . . . . 2881 . . . . . 2891 . . . . .
P985229 1832 a g g c g g a g g t t g c a g t g a g c c a a g a c t g c t a c t g c a c t c c a g c c t g g g c a
P985231 1570 - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
rCOX7B 1944 - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -

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alignment position 2901 . . . . . 2911 . . . . . 2921 . . . . . 2931 . . . . . 2941 . . . . .

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**
alignment position 3 2 5 1 . . . . . 3 2 6 1 . . . . . 3 2 7 1 . . . . . 3 2 8 1 . . . . . 3 2 9 1 . . . . .
P985229 2002 - - - - -
P985231 1873 AAG CCC AACT G AT C T T T CAT CT GCT ACA AG CT GT GTT t a t t a T T T C T T T C
rCOX7B 2241 GAG CCC AAT G AT G T T T CAT CT GCC ACA GG CT GT GTT c - - - T T T C T T T C
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alignment position 3 3 0 1 . . . . . 3 3 1 1 . . . . . 3 3 2 1 . . . . . 3 3 3 1 . . . . . 3 3 4 1 . . . . .
P985229 2002 - - - - -
P985231 1923 ACT T T G GACA A AT G AT T T AG CG T T A T A A A c T T GT T T T T GT A A A A C A G A G G
rCOX7B 2287 ACT T T G GACA A AT G AT T T AG C T T T A T A A A t T T GT T T T T GT A A A A C A A A G G
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**
alignment position 3 3 5 1 . . . . . 3 3 6 1 . . . . . 3 3 7 1 . . . . . 3 3 8 1
P985229 2002 - - - - -
P985231 1973 T T A G T A A G T A A T A C C t a t g t c a a a g a c c a t t a
rCOX7B 2337 T T A G T A A G T A A T A C 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.

	P985231 (2004 bp)	rCOX7B (2351 bp)
P985229 (2001 bp)	0.175 28 %	0.171 26 %
P985231 (2004 bp)		<u>1.000</u> <u>65 %</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

- All rights reserved.

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 6 23:46:47 2005

Solution parameters:

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

Aligned Sequences:

No.	Sequence Name	Sequence Description	Length
1	P871935	sym=COX7A2 loc=Loc1347 taxid=9606 spec=Homo sapiens chr=6 ctg=NT_007299 str=(-) start=13773297 end=13774697 len=1401 tss=1001 comm=cytochrome c oxidase subunit VIIa polypeptide 2 (liver); (NM_001865/501/bronze;)	1401 bp
2	P871938	sym=Cox7a2 loc=Loc12866 taxid=10090 spec=Mus musculus chr=9 ctg=NT_039474 str=(-) start=26236564 end=26237987 len=1424 tss=1001,1017,1024 comm=cytochrome c oxidase, subunit VIIa 2; (AK019210/530/gold;AK011269/523/gold;NM_009945/507/silver;)	1424 bp
3	P871940	sym=Cox7a3 loc=Loc29507 taxid=10116 spec=Rattus norvegicus chr=8 ctg=NW_047800 str=(-) start=1094113 end=1095513 len=1401 tss=1001 comm=cytochrome c oxidase, subunit 7a 3; (NM_022503/529/bronze;)	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\\$OCTI](#) [V\\$SETSF](#) [V\\$SCMYB](#) [V\\$SAPIF](#) [V\\$SFIF](#) [V\\$RORA](#)

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alignment position 1 . . . . . 1 1 . . . . . 2 1 . . . . . 3 1 . . . . . 4 1 . . . . .
P871935      1 t g g g c c c a t t   g a c a t a C A G T   A G A T T G T G A A   G A A G A A A a c -   C C C A A G G A T T
P871938      1 - - - - - - - - - - - - - - - C A G T   A G G T T A T G A A   G A A A A A A G T A   C C C C A A G A T T
P871940      1 - - - - - - - - - - - - - - - - - - - - - - - - - - - A A A A G T A   C C C C A A G A G T
    
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alignment position 5 1 . . . . . 6 1 . . . . . 7 1 . . . . . 8 1 . . . . . 9 1 . . . . .
P871935    50 ATAAG GAA T a g t t t t a a t AT TACTA AT TTT TATc c t t t g c t g a a a c t a t g
P871938    35 TGAAG GAA TT A AGC - - - - AT TACCAGT TTT T A TTCACGC A ACAC TGTGGA
P871940    18 TGAAG GAA TT A GGC - - - - AT TACCAGT t t c t c TTCACTC A GCAC TGTTGA
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alignment position 1 0 1 . . . . . 1 1 1 . . . . . 1 2 1 . . . . . 1 3 1 . . . . . 1 4 1 . . . . .
P871935    100 g g t t t c - - - - - - - - - - T TATTT GAAAT GGCAATCAA TAAT TTGTAA
P871938    81 ACCCGTTT AT C ATT AGC TTT TACCT GAAAT GGCAATGAA TCGT TTCTGA
P871940    64 ACCCGTTT AT C ATT AGC TCT TA c - T GAGAT GGCAATGAG TCGT TTCTAA
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alignment position 1 5 1 . . . . . 1 6 1 . . . . . 1 7 1 . . . . . 1 8 1 . . . . . 1 9 1 . . . . .
P871935    137 Ga g t t t g t a g a a a GTGGAAA GA - - - TT ATT GT AATACAGG GTAG A- TATT
P871938    131 GTTTG CAAA A GG- GTGGAAA GA - - - C ATTT GT ATTGTTGA GTAG ATTATT
P871940    113 GTTTA CAAA A GG- GTGGAAA GA a a t TT GTT GT AGTGT TGA GTAG ATTATT
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alignment position 2 0 1 . . . . . 2 1 1 . . . . . 2 2 1 . . . . . 2 3 1 . . . . . 2 4 1 . . . . .
P871935    183 TGCAT TTGTA C ATACTT GAG GGTAAGT ACA AGAAa t a a a - CACT TGTAAT
P871938    177 TTTAC TTGTA C ATt a - - - - - GTGT GC AGA AGAATAAAGG CAGT TGTAAG
P871940    162 TTTAATTGCA C ATACAT TAG GGTGT GC AGA AGAATAAAGG CAGT TGTAAG
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alignment position 2 5 1 . . . . . 2 6 1 . . . . . 2 7 1 . . . . . 2 8 1 . . . . . 2 9 1 . . . . .
P871935    232 GGGGATTACT T AAGCAA AAT GGATG - - - A CACCGACAGC CTTT CTGTAC
P871938    221 GAGGA ATAGT T ATGCAA GAC TGATGCA AAA TGCTAACAGC CTAT CTGTAA
P871940    212 GAGGA ATAGT T AAGCAAGAC TGATGCA AAA CACAAACAT C CTAT CTGTAA
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alignment position 3 0 1 . . . . . 3 1 1 . . . . . 3 2 1 . . . . . 3 3 1 . . . . . 3 4 1 . . . . .
P871935    278 AACAA a t a a t t g c t g t g c t t c t C T A C T C C A G T A A T G A A T G T A G T G C C T G
P871938    271 AATAC GCGCA C TTC TGA - - - - - CAGCT CCA TC CAGGAGT G AAAT GTGCT G
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P871940    262 AATAC GCGCA C CTCTGA - - - - CAACTCCA TC AAGGAGT G AAAT GTACAG
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alignment position 351 . . . . . 361 . . . . . 371 . . . . . 381 . . . . . 391 . . . . .
P871935    328 CTGGA TCT GG GACAGCAAGA Ct t t t g a g t c c a g a t t c g c c a t c c a t t t c
P871938    316 C- GGA TCT GA GAAAGCA CGA CACAGTCGAT AT TTGTGTTG AACg t g g a t T
P871940    307 CT- GA TCT GA GAAAGCA CGA CGCAGTCGTT AT TTGTGTTG AACa t g g a - T
          * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * *
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alignment position 401 . . . . . 411 . . . . . 421 . . . . . 431 . . . . . 441 . . . . .
P871935    378 t t g t t c c c t - - - - - - - - - - AA CGT T T C C T C A G A a g c g a g c g a g c c t
P871938    365 TAAAA AT G T A T T C C C C T C T T T C A G C G T T T T C C A G A C T C A A T A A C G A A G
P871940    355 TAAAA AT G T A T T C C C C T C T T T C A G C G T T T T C C A G A C T C A A T A A C G A A G
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alignment position 451 . . . . . 461 . . . . . 471 . . . . . 481 . . . . . 491 . . . . .
P871935    414 c t t c c a - - - - CAATTTGGG GACAC t g t GG AA GA A C T T C T T G C T T G G G G A
P871938    415 TCAGC CAG T T C C A G T C T G G G G A C A C A - - G G AA G A G C T T C C A G C A A G G A
P871940    405 CCAGC CAG T T C C A G T C T G G G G A C A C A - - G G A C G A G C T T C C A G C A A G A G
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alignment position 501 . . . . . 511 . . . . . 521 . . . . . 531 . . . . . 541 . . . . .
P871935    459 GTTCT GCAGC A G T c g a a g g t a c a g a a t a t a a a a a c t g g t a t c t c g a c a c
P871938    463 GTTTA GCAGA A G a t c c a c a g g t t g g c A T A C C T G T G G A T G C C A C A T C G G T
P871940    453 GTTTA GCAGA A G g t g c t a g - - - - - ATAC CT GTGGATGC CAAC ACCGGT
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alignment position 551 . . . . . 561 . . . . . 571 . . . . . 581 . . . . . 591 . . . . .
P871935    509 a g c t c t t a c a g c a t a t T C T C A A C A C A A G G A a c a g t a a t g t g c c g c a g C A A
P871938    513 Cg TTCCTATA T GA - - T C T C A G C A C A A A G A C T A A C G C C T C C - - - - - C A C
P871940    496 Ct TTCCTATA T GA - - T C T C A G C A C A A A G A C T A A C G C C T C C - - - - - C A G
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alignment position 601 . . . . . 611 . . . . . 621 . . . . . 631 . . . . . 641 . . . . .
P871935    559 TTCCT TCGGT G G A A A A A A c t - - - - - - - - - G A C T G T A T C C G c g - T A A G A
P871938    554 TTTCA TCT GT G G A A G A C A A A C C C T A A A A C T G G A C T C T A T C C G T A T T A A G A
P871940    537 TTTCA TCT GT G G A A A A C A A A C C C C A A A C T G A A C T C T A T C C G T G T T A A G A

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alignment position 651 661 671 681 691
P871935 597 GGAGT AAT TC T TTT TTGAAT TT TAT GA GGC TT c a g a g c t g t a t t t c g g c c
P871938 604 GGAGC TTT TG A AT A TTT AAG CT TGT AC GAC GT AGCTTTGA C- - - - -
P871940 587 GGAGC TTT TG T TT A TTT AAG CT TGC AC GAa GT AGCTTTGA C- - - - -

alignment position 701 711 721 731 741
P871935 647 a ACCC AGT CT T TGT TCAGTT TC TAg c g g c t t c a a g g t t g c c c a g t t t t a c
P871938 645 - ATCC AT T GT T CCT TCAGAC TGTAA AC AAT g g CTCAAAGC CTT- - - - -
P871940 628 - AGCC AT T GT T CCT TCAGAC TGTAA AC AAT g a CTCAAAGC CTT- - - - -

alignment position 751 761 771 781 791
P871935 697 g c c t t c t c g C T CAA AAC AGA CACTA- GTTt t c t t t GATAG CCTG GTCTCA
P871938 687 - - - - - C T CAC AAG ACA AGCTA c T TTC CG- - - GGTAG TCTG GTTGT C
P871940 670 - - - - - C T CAA AAG ACA AGCTA - T TTC CC- - - GATAG TCTG GTTGCC

alignment position 801 811 821 831 841
P871935 746 CAT T GACT TC ATCT AAGCTT AT t a c a t t c g t c t c a t a a a t - - - - -
P871938 725 CACTGACT TC ACCA GAG CGT AT GAAGA GGG CT GCAa GACT TCAC GCc t CT
P871940 707 CACTGACT TC AGCAGA- CGT AC GAAGA GGG CT GCA- GAC A TCAC GC- - CT

alignment position 851 861 871 881 891
P871935 786 - - - - - - - - - - C GTT TGC TT Tt t c c c c a g c c t t a g c t c c a g g g a c c a g
P871938 775 CCATT GCGGG T GGC GTT TGC TT TCC AT TGT GA TTCT g GG T CCGG CCGCAG
P871940 753 CCATT GCGGG C GGC ATT TGC TT TCAGT TGT GA TTCT a GG T CCA CTGCGG

alignment position 901 911 921 931 941
P871935 823 c c t a c t g a a c a t c g a a a a g g t c a g g a a c g a g a t c a c g g g a c t g a g a c g g c
P871938 825 GCGCG GCA GG GCG- -
P871940 803 GTGCC ACA GG GCC- -

alignment position 951 961 971 981 991
P871935 873 GAGCC GGC TA G AGC GGATAG AG CCGT ACTG CC Gc t c t a g t t t t t c t t t t -
P871938 838 GAGCC AAG TG GTAA GGATAG CT TCGGA GGT CC GGAGGCT A GACG GGCCGC
P871940 816 GAGAC AGG AG GTAc a g a t g g a T TCGGA GGT CC GGAGGCT A GACC GGCCGC


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alignment position 1 251 . . . . . 1 261 . . . . . 1 271 . . . . . 1 281 . . . . . 1 291 . . . . .
P871935 1141 GAGGA GGC TG A GGC ACC ACG AC AGA AA ACC CT c a c CTGG G AGGG GTGCCG
P871938 1132 GCGGA GGG TC A GGC ATC CTG AC AGA AA AGC GT G - - CTGG A AATG TGGCAG
P871940 1110 GCCGA GAG TG A GGT ACC TTG AC AAT AA GCC GT G - - CTGG A AATG GGACCG
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alignment position 1 301 . . . . . 1 311 . . . . . 1 321 . . . . . 1 331 . . . . . 1 341 . . . . .
P871935 1191 AAGGC GGC TA A TGA AGT CAC CT TGATT CGT GT CCT TTTT C CCTGACCTTA
P871938 1180 AAGAC AGC AG C CGG AGT CAC CT TG GCC GCG CG TCC TTTT C CCTGACCTT C
P871940 1158 AAGAC AGC A G - CGG AGT CAC CT TG GCC GGG CG TCC TTTT C CCTGACCTT C
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alignment position 1 351 . . . . . 1 361 . . . . . 1 371 . . . . . 1 381 . . . . . 1 391 . . . . .
P871935 1241 Ct t t c c c t t c c g t c t a t TCC T C T C G C C C C A G G C C G T T A C T G G G T A G A T G T
P871938 1230 Cg - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
P871940 1207 Cg a - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
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alignment position 1 401 . . . . . 1 411 . . . . . 1 421 . . . . . 1 431 . . . . . 1 441 . . . . .
P871935 1291 A a g g a g t g g a g a g g c t g g g g a a g t g a c c a g a g a c t c g t g g g t t a g a c c c g
P871938 1265 AGAGG GAA GA G CAG GAT CGC A - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
P871940 1241 AGAGG GAA GA A CAC GAT CAC A - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
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alignment position 1 451 . . . . . 1 461 . . . . . 1 471 . . . . . 1 481 . . . . . 1 491 . . . . .
P871935 1341 t c TTG GGT TC T TAGT C A C C A C C T C T A A C C c t g t c g g t c a t t g a t g a g g t t
P871938 1286 - - TTT GGT TC T TGGT C A C T A C A G C T T A C C G T T G C T T A T g g c t a t g a c t - -
P871940 1262 - - TTT GGT TC C TAGT C A C T A C T G C T T A C T G T T G C T T A T t g a - - - - - - - - -
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alignment position 1 501 . . . . . 1 511 . . . . . 1 521 . . . . . 1 531 . . . . . 1 541 . . . . .
P871935 1391 a GTAG CT C CG A - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
P871938 1332 - GTAG CT C TG A C GT A G G C T C A G T G G G G G g A T C T G G A C A C C T G G A A A C
P871940 1301 - - TAG CT C TG A T G T A G G C T C T A G T G G G G G - A T C T C G A A C A C C T G G A A A C

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GEMS Launcher Task: *DiAlign TF*: Multiple alignment plus TF sites working on C4-COX8A (3 seq.)

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

DiAlign professional TF Release 3.1 December 2004

Wed May 11 23:58:14 2005

Solution parameters:

Sequence file: [C4-COX8A](#) (3 seq.)
Type of sequences: nucleotide sequences
Threshold T: 0.00
'*' signs below alignment denote: diagonal similarity (max. similarity is represented by 10 '*' signs)
 complete alignment is shown
Alignment output: # 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
1	P905108	P905108 sym=COX8A loc=Loc1351 taxid=9606 spec=Homo sapiens chr=11 ctg=NT_033903 str=(+) start=9047274 end=9048374 len=1101 tss=601 comm=cytochrome c oxid subunit 8A (ubiquitous); (NM_004074/501/bronze;)
2	P905109	P905109 sym=Cox8a loc=Loc12868 taxid=10090 spec=Mus musculus chr=19 ctg=NT_082892 str=(-) start=403413 end=404557 len=1145 tss=601,610,641,645 comm=cytoch c oxidase, subunit VIIa; (AK008594/537/gold;AK002524/572/gold;AK002218/528/gold;NM_007750/568/bronze;)
3	rCOX8A	rCOX8A n3_dna range=chr1:210046403-210047502 5'pad=0 3'pad=0 revComp=TRUE strand=? repeatMasking=n

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.

VSSORY
VSPCAT
VSBCL6
VSTCFE
VSETSE
V\$YYIF
VSRORA
VSEREF
USEREF
V\$SFIF
V\$AP2F

alignment position 1 1 1 2 1 3 1 4 1
P905108 1 c t g g - - - - -
P905109 1 g a A C A G T T A C C A G T T A T G T G G A A A C G G G T t T C T G A G A G G A T A A C A G T A A A
rCOX8A 1 g g A C A G T T A A C A G T T A T G T G G A A A C G G G T g T C T G A G A G G A A A A T A G T A A A

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alignment position	5 1	6 1	7 1	8 1	9 1
P905108	5 - - - - -	- - - - -	- - - - -	- - - - -	- - - - -
P905109	51 T G A C A G G A G T	C T C g g G G C T G	G A G A G A G A G C	T C A G C G C T T A	G A A G C A C T c -
rCOX8A	51 T G A C T G G A G T	C T C a - G G C T G	G A G A G A T A G C	T C A G T A G C T A	A A A A C A C T g g
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	* * * * *	* * * * *	* * * * *	* * * * *	* * * * *
alignment position	1 0 1	1 1 1	1 2 1	1 3 1	1 4 1
P905108	5 - - - - -	- - - - -	- - - - -	- - - - -	- - - - CAAGAC
P905109	100 G C T G C T C T T G	C A G A G G T C C A	G T T C A G T T C A	G T T C C C A G C A	t c c a C A A G A T
rCOX8A	100 G C T G C T C T T A	C A G A G G A A C A	G T T C A G T T C A	G T T C C C A G C A	c c t a c a g g t c
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alignment position	1 5 1	1 6 1	1 7 1	1 8 1	1 9 1
P905108	11 T G G T C T C A A A	C T C C T G A C C T	C a g a t g a t c t	a c c g g c c c c g	g c c t c c c a a a
P905109	150 T A C T C A C T A T	T G C C T G A A C T	C c a - G T T C C A	G A G G A T C C A A	C A C C C T C T T T
rCOX8A	150 t - - - A C T A T	T G C T T G t g a t	t c c t G T T C C A	G A G G A T C C A A	C A C C C T C T T T
	* * * * *	* * * * *	* * * * *	* * * * *	* * * * *
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	* * * * *	* * * * *	* * * * *	* * * * *	* * * * *
alignment position	2 0 1	2 1 1	2 2 1	2 3 1	2 4 1
P905108	61 g t g t t g g g a t	t a c a t g c g t g	a g c c a c t g c g	c c c g g c c a a t	t t t t g t a t t t
P905109	199 T G G C C T C T C T	G C G T t e t g c a	t a - - - - -	- C A C A G A T G A	A - - - - -
rCOX8A	196 T G G T C T C T C T	G C G T a c t g c a	t g c a a g t c g t	g C A T A G A T G C	A - - - - -
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	* * * * *	* * * * *	* * * * *	* * * * *	* * * * *
	* * * * *	* * * * *	* * * * *	* * * * *	* * * * *
	* * * * *	* * * * *	* * * * *	* * * * *	* * * * *
alignment position	2 5 1	2 6 1	2 7 1	2 8 1	2 9 1
P905108	111 t t c g t a g a g a	t g g g g t t t c a	c C A T G C T G G C	A A G A C t g g t g	t c a a a c t c c t
P905109	231 - - - - -	- - - - -	- C A T G C T G A C	A A A A C a c t c A	T A A A G T A A A A
rCOX8A	237 - - - - -	- - - - -	- C A T G C A G A C	A A A A C - - - - A	T A A A G T A A A A
	* * * * *	* * * * *	* * * * *	* * * * *	* * * * *
	* * * * *	* * * * *	* * * * *	* * * * *	* * * * *
	* * * * *	* * * * *	* * * * *	* * * * *	* * * * *
	* * * * *	* * * * *	* * * * *	* * * * *	* * * * *
alignment position	3 0 1	3 1 1	3 2 1	3 3 1	3 4 1
P905108	161 g a c c t c a g a t	g a t c t a c c c g	c c c c g g c c t c	c c a a a g t g c t	g g g a t T A G A G
P905109	260 C T A T G T T T T	A A A A C - - - -	- - - - -	- - - - -	- - - - T A G A G
rCOX8A	262 C A A T G T T C T T	A A A A C - - - -	- - - - -	- - - - -	- - - - T A G A G
	* * * * *	* * * * *	* * * * *	* * * * *	* * * * *
	* * * * *	* * * * *	* * * * *	* * * * *	* * * * *
	* * * * *	* * * * *	* * * * *	* * * * *	* * * * *
	* * * * *	* * * * *	* * * * *	* * * * *	* * * * *
alignment position	3 5 1	3 6 1	3 7 1	3 8 1	3 9 1
P905108	211 G C G T g a g c c a	a c g c g c c c a g	c c c g t a c t t t	t t t t t t t t T A	G T A C A G a c g g
P905109	280 G C T T A C T G g t	g g c g A G C T G G	A G T C A C - - - -	- - - - -	T A G T A C A G T G C T

rCOX8A	282	GCGTAC	TGt t	a t g a	AGC TGG	AGT C AC	- - - -	- - - -	- - - -	- - - -	- - - -	TA	GT TGAGT	GC T
		*****			*****	*****							*****	*****
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		*****			*****	*****							*****	*****
alignment position		4 0 1	4 1 1	4 2 1	4 3 1	4 4 1			
P905108	261	c c t	c c c a a a	g t t c t	g a g a t	t a c g g g c g t	g	a g c c a c c a c g	c c c a g c c t	g a				
P905109	318	GGC	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -
rCOX8A	320	GGC	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -

alignment position		4 5 1	4 6 1	4 7 1	4 8 1	4 9 1			
P905108	311	a t A	GAG AGA	G a t t t a a	c a g -	TATGAATGA	A	AGG GAG GAG T	C A A G A A C A G T					
P905109	321	- - A	GAG AGA	G A T C C T A G T T	A A A T G A A T G G	A	AGG GAG GAG C	C A A G G A G T C A						
rCOX8A	323	- - A	GAG AGA	G A T C C T A G T T	A T A T G A A T G G	A	AGG GAG GAG T	T A A G A A C T C A						
		*****	*****	*****	*****	*****	*****	*****	*****	*****	*****	*****	*****	*****
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alignment position		5 0 1	5 1 1	5 2 1	5 3 1	5 4 1			
P905108	359	T T A	G G C T T C T	C G C G T A C A T G	A T T G G G T G G	C	C C C A G A T G T C	A T T C A C A A G T						
P905109	369	A T A	G A C T T G T	A G C T T G T G T G	A T T G G G T G G	C	T A T G C G T G T C	A C T C T C G A a g						
rCOX8A	371	A T A	G A C T T C T	C g g T T G T G T G	A T T G G G T G G	T	T A T A C G T G T C	A C T C T C G A G G						
		*****	*****	*****	*****	*****	*****	*****	*****	*****	*****	*****	*****	*****
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alignment position		5 5 1	5 6 1	5 7 1	5 8 1	5 9 1			
P905108	409	- - A	t a a g c c t	T G G A G G C G G A	A - C A T A A c t c	g a a g a a g a g c	c c c t t t t g t g	c						
P905109	419	a a A	G - - - -	T G G A G G T G G G	A g C A A A G G T G	T C T C A T T T - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -
rCOX8A	421	- - A	G - - - -	T G G A G G C G G G	A - C A A A A G T G	T C T C 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			
P905108	456	T C C	G C C C A T a	g c - G - T A G G A	A G G T G T C a a T	T G	G C T G T T T C	G A G G A A C G C G						
P905109	452	T C C	T C C C A T C	T G T G - T A G G A	T G A T G T C G G T	T G	G T T G T T T C	G A G G A G C G C G						
rCOX8A	451	T C C	T C C C A T C	T G T G g T A G G A	T A A A G T T G G T	T G	G T A G T T T C	A A G G A G C G C G						
		*****	*****	*****	*****	*****	*****	*****	*****	*****	*****	*****	*****	*****
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alignment position		6 5 1	6 6 1	6 7 1	6 8 1	6 9 1			
P905108	504	C C A A A A C T G	C C A A G G g c t g	t g g g a g g	t g -	T G T T C T T G C G	T C A T T T C C G A							

P905109 501 CCA AAA ACAG CC CAGGC GGG CGAGGG g g **CT TGT CCCGACG TCATTTCC GA**
rCOX8A 501 CCA TAA ACAG CC CAGGC GGG CCAGGG a - **CT TGT CCT GACG TCATTTCC GA**
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alignment position 7 0 1 7 1 1 7 2 1 7 3 1 7 4 1

P905108 553 **GAG ACT TCCG CG**Cc g c a g t t t c c c t g c t t c c c CAGC T **CCA GA**ACTTCCGG
P905109 551 **AAT ACT TCCG Gc**t c g - G GCG TCCG GC AACT T - CAGC GC **CG GA**ACTTCCGG
rCOX8A 550 **AAT ACT TCCG GG**Ct g a G GCG TCTAT C AACT T - CAGC G **CCG GA**ACTTCCGG
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alignment position 7 5 1 7 6 1 7 7 1 7 8 1 7 9 1

P905108 603 **CCA GCG CAGC CATTTTGCT TCCTGACCTT GGGCTA**CGGC TGac c g t t t t
P905109 599 **CTG GTT CGGC CATCTTGACT CCCTGACCTT GGa - - - - C TGG**TCCCTCGT
rCOX8A 599 **CTa t t GCGGC CATCTTGACT TCCTGACCTT GGGCTT**CGGC TGGTCCCTGT
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alignment position 8 0 1 8 1 1 8 2 1 8 3 1 8 4 1

P905108 653 t t g t g g t g t A CTCCGTGCCA TCATGT **CCGT CCTGACGCCG CTGCTGCT**Gc
P905109 643 CCGTGGTC- G TTCCGCGCCG TCATGT **CTGT CCTGACGCCA CTGCTGCT**GA
rCOX8A 649 CCTTGGTC- A CTCCGCGCCG TCATGT **CTTC CCTGACGCCG CTGCTGCT**GA
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alignment position 8 5 1 8 6 1 8 7 1 8 8 1 8 9 1

P905108 703 GGGGCTTGAC AGGCTC **GGCC CGGC GGCTC**C CAGTGC CGCG c g c c a a g a TC
P905109 692 GGA GCC TGAC CGGCTC **GGCC CGGC GGCTC**A TGGTGC CGCG GGCTCAGGTC
rCOX8A 698 GGA GCC TGAC CGGCC **GGCC CGGC GGCTT**A TGGTGC CGCG GGCTCAGGTC
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alignment position 9 0 1 9 1 1 9 2 1 9 3 1 9 4 1

P905108	753	CATTCGTTGC	CGCCGGA GGG	GAAGCTTGGG	ATCATGGT - -	GAGGAACGGG
P905109	742	CACTCGAAGC	CGGCGCGGGA	GCAGCTCGGG	GTCCTGGTGA	GC GGGACGGA
rCOX8A	748	CACTCGAAGC	CGCCGCGGGA	GCAGCTCGGG	GTCCTGGTGA	GC GGGACGGA
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alignment position		951	961	971	981	991
P905108	801	CCTGGAAGAG	CGCGGGA GGC	GCCGTGGGCT	g a c c c c t t c t	g c c t a g c t g a
P905109	792	CCGGGAGCGG	GGAGGTGGC	GAACTGTGGT	AGCCTGCGAC	AT - - - - -
rCOX8A	798	GCGGGAGCGG	GGAGGTGGC	GAACTGTGGT	AGCCTGCGAC	AT - - - - -
		*****	*****	*****	*****	*****
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		*****	*****	*****	*****	*****
		*****	*****	*****	*****	*****
alignment position		1001	1011	1021	1031	1041
P905108	851	c c t c a g g t g g	t c c t g a g a a t	g c c t c g c g c c	c c g c a g c g t a	g c g g g g a g c a
P905109	835	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -
rCOX8A	841	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -
		*****	*****	*****	*****	*****
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		*****	*****	*****	*****	*****
alignment position		1051	1061	1071	1081	1091
P905108	901	g c a g t g c c G G	T T T G G G C A T G	T C T G G A G G G C	G C G A A C G A c g	g g g a c a g t g c
P905109	835	- - - - - G G	C T T A G G C C T G	T C C T C A A G G C	A T G G A T G A - -	- - - - -
rCOX8A	841	- - - - - G G	C T T G G G C C T G	T C T G C A A G G C	G T G G A T G A - -	- - - - -
		*****	*****	*****	*****	*****
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alignment position		1101	1111	1121	1131	1141
P905108	951	c c g g g c G A C A	G T C G g g g c t g	t c g - - - - -	G C G T T A G G T C	T T T C C C C A C A
P905109	865	- - - - - G A C A	G T C G c t c g g -	C T G C T C C T A A	G C C C T A G G T A	T T T T T C C C A A
rCOX8A	871	- - - - - G A C A	a g t t g c t c g a	C T G C T C C T A A	A C C C T A G T T A	T T T T T C C C A A
		*****	*****	*****	*****	*****
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alignment position		1151	1161	1171	1181	1191
P905108	994	G C C C A G G A T	C T C G G G T C T G	g t c c t g t c a g	g c c - - - - -	- - - - -
P905109	908	G T T C C T G G A T	G T C A G G T C A G	C C C G C T A G T T	T G T T T A C T - -	C T G T T C G G C C
rCOX8A	915	G T T C C T G G c a	- - - - - C T G	C C A G C C G G T C	A G T T T A C T c g	C T G T T C G G C C
		*****	*****	*****	*****	*****
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		*****	*****	*****	*****	*****
		*****	*****	*****	*****	*****
alignment position		1201	1211	1221	1231	1241
P905108	1027	- - - - -	- - - C T C C C T C	T C C T G T C G C C	T C C T C G C T G C	G C C G C c t c c t
P905109	956	T C T C T A A A C C	C G T C T C T C C T	T C C A T T C C C C	C C C C C C C C C C	A C C G C a g G G G
rCOX8A	958	T C T C T A A A C C	G G T C T C T C T T	T t t a a t t t t t	t t t g c g t - - -	- - - - - G G 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 . . . . .
P905108 1064 g c c g a c t t c t t t a g c c g c t c t g a g c c c a t t t t c t c g t t - - - - -
P905109 1006 A G G G C A T G C C T G G T A A C T G G C A G C g a c g t c a t g g t t g t t a c t g c t a c a t t
rCOX8A   998 A G A A A A T G C C T A G T A A T T G G C A G G g - - - - -
* * * * *

alignment
position  1 3 0 1 . . . . . 1 3 1 1 . . . . . 1 3 2 1 . . . . . 1 3 3 1 . . . . . 1 3 4 1 . . . . .
P905108 1102 - - - - -
P905109 1056 t t a t t a t t a a g g a g g g c T G C A G A G T t - - C A C C A G G T C T a c a - - T T C C C A
rCOX8A  1023 - - - - - T G C A G A G T a c c C A C C A G G T C T t t g g g g T T C C C A
* * * * *

alignment
position  1 3 5 1 . . . . . 1 3 6 1 . . . . . 1 3 7 1 . . . . . 1 3 8 1 . . . . . 1 3 9 1 .
P905108 1102 - - - - -
P905109 1101 G A g A T G T A G G A G C A T T T A G A T A C T A G G A C A A T T T T T A C T T T t a a a
rCOX8A  1056 G A a A T G T A A G A C C A T T T A G A T A T T A G G A C A A T T T T T A C T T T c a a a
* * * * *

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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.

	P905109 (1145 bp)	rCOX8A (1100 bp)
P905108 (1101 bp)	0.184 34 %	0.204 34 %
P905109 (1145 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	

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

GEMS Launcher Task: *DiAlign TF*: Multiple alignment plus TF sites working on C4-COX8C (3 seq.)

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

DiAlign professional TF Release 3.1 December 2004

Thu May 12 17:46:32 2005

Solution parameters:

Sequence file: [C4-COX8C](#) (3 seq.)
Type of sequences: nucleotide sequences
Threshold T: 0.00
'*' signs below alignment denote: diagonal similarity (max. similarity is represented by 10 '*' signs)
 complete alignment is shown
Alignment output: # 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	P304066	P304066 sym=COX8C loc=Loc341947 taxid=9606 spec=Homo sapiens chr=14 ctg=NT_026437 str=(+) start=74812790 end=74813790 len=1001 tss=501 comm=cytochrome c oxidase subunit 8C; (NM_182971/501/bronze;)	1001
2	mCOX8C	mCOX8C m6_dna range=chr12:98345092-98345877 5'pad=0 3'pad=0 revComp=FALSE strand=? repeatMasking=none	786
3	rCOX8C	rCOX8C n3_dna range=chr6:127164794-127165676 5'pad=0 3'pad=0 revComp=FALSE strand=? repeatMasking=none	883

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](#) [U\\$NRF1](#) [V\\$CP2F](#) [V\\$AP4R](#) [V\\$EKL1](#)

```

alignment position 1 . . . . . 1 1 . . . . . 2 1 . . . . . 3 1 . . . . . 4 1 . . . . .
P304066           1 g c c a a t g c c a g g g c a t g t t a a g a g g t a t a t a a a g t a t a g g t a g a g a g g a a
mCOX8C           1 G T A A A A A T G G T A T G A T A T C T G C T A T T G A C T A - - - - -
rCOX8C           1 G T A A A A A T G G T A T G A T A T C T G C T A T T A A C T G - - - - -
                  * * * * *
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alignment position 51 . . . . . 61 . . . . . 71 . . . . . 81 . . . . . 91 . . . . .
P304066      51 g a c AAAGGA A AGGAGTAg g g t g c a a - - - - -
mCOX8C      32 - - - AAAGCA A CGGAATACTG AGCAATAGCT ATAGATGTTG GCAGCCAAT-
rCOX8C      32 - - - AAAt t a g t GGGATACTG AGCAACACCT ATAGATGTTG GCAGCCAATa
          * * * * *
          * * * * *
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alignment position 101 . . . . . 111 . . . . . 121 . . . . . 131 . . . . . 141 . . . . .
P304066      78 - GT CCCTCAC CTTACCc t g c a g a a a g - - - - - AGATA CTTAGTGTGa
mCOX8C      78 GGT CCCTCAC CTTg t g TTAG GAGAAGAAAA TCAGAAAATC CTGAGTGTGG
rCOX8C      79 GGT CCTTCAC CTTACCTTAG GAGAAGAAAA TCAGAAGACC CTGAGTGTGG
          * * * * *
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```

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alignment position 151 . . . . . 161 . . . . . 171 . . . . . 181 . . . . . 191 . . . . .
P304066     119 g g t g g g g T T G G G C T C A G G G G A G G G T G G C A G G A G A G T T T A G G A G G A T A
mCOX8C     128 C - - - - T T T G G g a c t - G A A T A G G T T T G G C A A A G A G T T T G G G A G A G G G C A
rCOX8C     129 C - - - - T T T G G G G C C G A A T A G G T T T G G T A A A G A C T T T G G G A G A G G G C A
          * * * * *
          * * * * *
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alignment position 201 . . . . . 211 . . . . . 221 . . . . . 231 . . . . . 241 . . . . .
P304066     169 G G A c - - - - A C G T G G G T G G A A A G T G A G G T G A A T G A G G g c t g g g a g g t t g c
mCOX8C     171 G G A A G C T G G A C T T G T G A G G A C A T A G G T G G G A A G A A G G T A G - - - - -
rCOX8C     173 G G T A G C T G G A C T T G T G G G G A C A G G G C G G G A A G C A T G T A G - - - - -
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alignment position 251 . . . . . 261 . . . . . 271 . . . . . 281 . . . . . 291 . . . . .
P304066     214 a g g g a g c c c t g a g t g g a a a a g g c g g g g c a g a g c a g g g g g t a c t g a a c t g a
mCOX8C     211 - - - - -
rCOX8C     213 - - - - -
    
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alignment position 301 . . . . . 311 . . . . . 321 . . . . . 331 . . . . . 341 . . . . .
P304066     264 a g a g a g t g g a g c a g a g c a g g g g t g t g c t g g g t g g a a g g g g t g g t g c a g a g
mCOX8C     211 - - - - -
rCOX8C     213 - - - - -
    
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alignment position 351 . . . . . 361 . . . . . 371 . . . . . 381 . . . . . 391 . . . . .
P304066     314 c a a g t g g t g c t a a g c A G A G G G G T G G G C A A A G C A C G G A C T G C T G A G t g g
mCOX8C     211 - - - - - A G A G T G G C A G G G C C A A A C A C A T A C A G C G G A G A A
rCOX8C     213 - - - - - A G T G T G a - T A G G G C G C A G C A T T T A C A G C T G A G G A
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alignment position 401 . . . . . 411 . . . . . 421 . . . . . 431 . . . . . 441 . . . . .
    
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P304066 364 a a a g g g c a g t a c a g a g a a a g g a g t g g t g a g c g GAAGAGGC GGGGCAGAGC
mCOX8C 245 - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - GCAGGGTC GGGTAAGAGC
rCOX8C 246 - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - GCAGGGTG GGGTAAGAGC
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alignment position 451 . . . . . 461 . . . . . 471 . . . . . 481 . . . . . 491 . . . . .
P304066 414 a g g a g g t g c t g g g c a g a a g g g g t g g g g t a g g g g g c g a g g g c a g a g c g c c C
mCOX8C 263 T C A A A T T C C A t g C A A A G G G - - - - - - - - - - - - - - - - - - - - - C
rCOX8C 264 G C A A A T T C C A t t C A A A G G G - - - - - - - - - - - - - - - - - - - - - C
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alignment position 501 . . . . . 511 . . . . . 521 . . . . . 531 . . . . . 541 . . . . .
P304066 464 C C T C G T G G C T G G G G C G C C T G C G C A A A C C A G C T G C C t c a c g a g c a c t g g a g
mCOX8C 283 T T G A G T G G A T G G T G C G C A T G C T C A A A C C A G C T G C C C G C C - - - - -
rCOX8C 284 C C G A G T G G T T G G T G C G C A T G C T C A A A C C A G C T G C T C G C C - - - - -
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alignment position 551 . . . . . 561 . . . . . 571 . . . . . 581 . . . . . 591 . . . . .
P304066 514 c t t g C G T T A C T T G G C C T C A C C T g t g c t - - - - - - - - - - -
mCOX8C 322 - - - - C T T T C C T C G C G C A C A C T T T A C C A A C G G C C T T t g a c t c C G A C A C T G G
rCOX8C 323 - - - - C T C T C C T C G A G C A C A C T T T A C C A A C G G C C T T - - - - - C G A C T C T G G
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alignment position 601 . . . . . 611 . . . . . 621 . . . . . 631 . . . . . 641 . . . . .
P304066 546 - - G T C C A C G C C T G G C T T T G T C T C A C c t g a c g c g a t a t g c - - - - - C
mCOX8C 368 T G G T C T C C G G T T T G C T C T G T C T C A G T G G C C C T T T T C T G A C C T G C G A T G T C
rCOX8C 363 T G G T C T C C C A T T T G C T C T T C C T C g G T G G C C C T T T T C T G A C C T G T G A T G T C
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alignment position 651 . . . . . 661 . . . . . 671 . . . . . 681 . . . . . 691 . . . . .
P304066 584 T C T C C T G C G T G G G C G C T G T C C T G C C G C C G C C A C T A C C G c g c t t g g c c c
mCOX8C 418 T C G C C T G C T G C T A C T C T G C T C T C G C T C C T C G C C A C C G T G C A G T C C T G T
rCOX8C 413 T C G C T T G C T G C A G T T C T G C T C T C C C T C C T C G A C A C C G T G T A G T C C T G T
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alignment position 701 . . . . . 711 . . . . . 721 . . . . . 731 . . . . . 741 . . . . .

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P304066 634 t g c t c g g c c t g c a g c c c g c t c c c c g c t t c G CCC ACTC GGG GCCCC CGCGC
mCOX8C 468 T CT CGAAGC C T- - - - - - - - - - - - - - - - G GCC ACCA G G CC GCCT CAGC
rCOX8C 463 T CT CGAAGC C T- - - - - - - - - - - - - - - - G GCC ACTC AGG CCGCCT CAGC
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alignment position 7 5 1 . . . . . 7 6 1 . . . . . 7 7 1 . . . . . 7 8 1 . . . . . 7 9 1 . . . . .
P304066 684 CA g c g g c c - - - - - - - - - - - - - - - CCT G TCTGCCGC GG TGAGT TGAGG
mCOX8C 500 CAC TCAGAAA GC CCACAAA AAAAA TCCT G TCGCCAC GG TGAGGTAGAA
rCOX8C 495 CAC TCAGAAA GC CCACAAA CCAAGTCCT G ACACCCAC GG TGAGGTAGAg
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alignment position 8 0 1 . . . . . 8 1 1 . . . . . 8 2 1 . . . . . 8 3 1 . . . . . 8 4 1 . . . . .
P304066 716 CCC Ag c c a t c a t g g t g g g c g g g a a g c g c g t g g c c c t g g c g g g g c GCCCCG
mCOX8C 550 CCC Ac t TAAC G- - - - - - - - - - - - - - - - - - - - - - GTCCAA
rCOX8C 545 t c c g c c TAAC G- - - - - - - - - - - - - - - - - - - - - - GTCCAA
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alignment position 8 5 1 . . . . . 8 6 1 . . . . . 8 7 1 . . . . . 8 8 1 . . . . . 8 9 1 . . . . .
P304066 766 ACGGGTGGGG AGAAGGGAGG ACACGGCGT- - - - - - - - - G c a g g c c t c g c
mCOX8C 567 ATGGGTGTGG AGGGGGGAGT GTGTGGTGT- - - - - - - - - G T- - - - - - - - -
rCOX8C 562 GTGGGTGGGG ATTGGGGAGT GTGTGGTGTg t g g t g t g t g G T- - - - - - - - -
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alignment position 9 0 1 . . . . . 9 1 1 . . . . . 9 2 1 . . . . . 9 3 1 . . . . . 9 4 1 . . . . .
P304066 806 GTGGGAGGC T CT TGTGGCTT GGTCGCCGT T GGGGGAGGTt c c t g t g g c - -
mCOX8C 598 GTGTGTGg t t - - - - - - - - - GT GTGTGTGGT T GTGTGTGTTG GCAGCTTCAG
rCOX8C 603 GTGTGTGTT A GGTGTGGCGT GTGTGTTGT A GTGTGTGTTG GCAACTTCAG
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alignment position 9 5 1 . . . . . 9 6 1 . . . . . 9 7 1 . . . . . 9 8 1 . . . . . 9 9 1 . . . . .
P304066 854 - - TTGGTCG CCTTTGGGGG AGGTTCCTGG GAGAGGGTc g c g g t g a g g a t
mCOX8C 640 TTGTGGGg t c ACTTTGGATG GCGGTTCAGG GCGAGGATg a GAGTCCCAAG
rCOX8C 653 TTGTGGGTTT ACTTTGGATG GGGGCTCAGA GTGAGGGT- - GAGTCCAGG
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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 . . . . .
P304066 901 g c c g t c g t c g - - - - - - - - - - - - - - - GGCACAGGGg c g g a a g c c c
mCOX8C 690 TAGGACCTGG CTCTCCATTA TG- - - - - GA GGCACAGGG- - - - - - - - -
rCOX8C 701 TAGGACCTGG CCTCCTTTA TGa g c a t g GA GGTGCAGGA- - - - - - - - -

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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 . . . . .
P304066      931 g g g a c c c t g a g g a a c g c g c g g g g a t t g g g c c TCCTTCGTT GTTACCCTTT
mCOX8C      723 - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
rCOX8C      740 - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
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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 . . . . .
P304066      981 ACC GGCACCT GGCTCGGGG C- - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
mCOX8C      742 T AAT c T ACC T GC CTGGTGGC CAAGACATAG CATTTTCTCT AAAAA- - - - -
rCOX8C      759 T C A T T T A C C T G T C T T G T G G C C G A G C C A T A G C A T T T T C T C T A A A A A a c g a t
          * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * *
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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 . . . . .
P304066      1002 - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
mCOX8C      787 - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
rCOX8C      809 c g g g a c a c t a g a c a t c t t c g a g c t a c c a g a a t c t a g a c g t c a g a a a t t g g

alignment position 1 2 0 1 . . . . . 1 2 1 1 . . . . . 1 2 2 1 .
P304066      1002 - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
mCOX8C      787 - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
rCOX8C      859 c a a c t a t t g a a a g a a a t t g a g t t 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.

	mCOX8C (786 bp)	rCOX8C (883 bp)
P304066 (1001 bp)	0.079 34 %	0.053 27 %
mCOX8C (786 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 style="width: 80px;" type="text"/> to: <input style="width: 80px;" type="text"/>
Output file	<input style="width: 90%; height: 20px;" type="text" value="dialign.seq"/>

Extract aligned sequences

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

- All rights reserved.

GEMS Launcher Task: *DiAlign TF*: Multiple alignment plus TF sites working on promoters.seq (2 seq.)

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

DiAlign professional TF Release 3.1 December 2004

Thu May 12 18:22:09 2005

Solution parameters:

Sequence file: [promoters.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)

- ALL user_defined.lib (0.75/Optimized)
- ALL vertebrates.lib (0.75/Optimized)

Selected groups
(core/matrix sim):

Aligned Sequences:

No.	Sequence Name	Sequence Description	Length
1	P862017	sym=COX10 loc=Loc1352 taxid=9606 spec=Homo sapiens chr=17 ctg=NT_010718 str=(+) start=13569068 end=13570568 len=1501 tss=1001 comm=COX10 homolog, cytochrome c oxidase assembly protein, heme A; (NM_001303/501/silver;)	1501 bp
2	P862018	sym=Cox10 loc=Loc70383 taxid=10090 spec=Mus musculus chr=11 ctg=NT_096135 str=(-) start=29162492 end=29164044 len=1553 tss=1001,1053 comm=COX10 homolog, cytochrome c oxidase assembly protein, heme A; (AK010385/501/gold;NM_178379/553/bronze;)	1553 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\$SETSF
USNRF2
V\$YY1F
V\$NEUR
V\$ZF5F
V\$STAF
V\$SORY
V\$EBOX
V\$RORA
V\$COUP

```

alignment position 1 . . . . . 11 . . . . . 21 . . . . . 31 . . . . . 41 . . . . .
P862017          1 a - - - - -
P862018          1 a a g g g c t a a c t t a t t t a t g a t g a t c a g a g t t c c a g g a a c a g t g g g t c t a a

alignment position 51 . . . . . 61 . . . . . 71 . . . . . 81 . . . . . 91 . . . . .
P862017          2 - - - - -
P862018          51 t t a a c c a a g a t a g c t g t a a a g c a g a a g g c c t c c c t a a g c a g c a c t c a c t

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alignment	position	1 0 1	1 1 1	1 2 1	1 3 1	1 4 1
P862017	2	- - - - -	- - - - -	- - - - -	T C T A C T T	T T T A C T T G T G G A a c c c c a a t
P862018	101	g t t g g t g t g a	t t a g a t c c c a	a a t T G T G C T T	T T C A T T T G T T	G A t t t a a g g -
					*****	*****

alignment	position	1 5 1	1 6 1	1 7 1	1 8 1	1 9 1
P862017	29	c t g a a a g a a	g a t c g a g g g g	t t g g g g g a t g	c t g a g a t c t a	c c c t g g t a a t
P862018	150	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -

alignment	position	2 0 1	2 1 1	2 2 1	2 3 1	2 4 1
P862017	79	c a c a a c a c t t	a t g a t a a c a c	a g g t a a t a a t	c t a t t a g t g c	c t g t a c c t a g
P862018	150	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -

alignment	position	2 5 1	2 6 1	2 7 1	2 8 1	2 9 1
P862017	129	t a g g t g t c t g	g c t a c c c a t g	a a a c a c a t t t	a t c t a a t t c t	c t c a a c c t c t
P862018	150	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -

alignment	position	3 0 1	3 1 1	3 2 1	3 3 1	3 4 1
P862017	179	t a t a a a g a t	g t a c c a t t a c	t a c t c c a t t g	t a t t g c t a g a	t a a c t g a g g t
P862018	150	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -

alignment	position	3 5 1	3 6 1	3 7 1	3 8 1	3 9 1
P862017	229	t c a g a g g a c t	t a g g t a a t t t	g c t c c a a c a a	g g t c a a a a g g	c c a g a a c t a g
P862018	150	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -

alignment	position	4 0 1	4 1 1	4 2 1	4 3 1	4 4 1
P862017	279	a a t a c g g a t t	t c a c t c c a g a	c c a c c a a a t c	t g a a c c t c t a	c a t g c a a t c t
P862018	150	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -

alignment	position	4 5 1	4 6 1	4 7 1	4 8 1	4 9 1
P862017	329	g g a g a t a t c t	g g a t g a t t c a	g t t c c t t t a g	t g t g g c t c a g	a a a c a a g t a a
P862018	150	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -

alignment	position	5 0 1	5 1 1	5 2 1	5 3 1	5 4 1
P862017	379	c c c g g a g t t c	c t c t g g g c t c	c c a t t t g a t a	g a g a c t a c g g	t a a a g t g t a a
P862018	150	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -

alignment	position	5 5 1	5 6 1	5 7 1	5 8 1	5 9 1
P862017	429	t t g a t t a g a c	g t g g a g g t g g	a a g c a t c c c c	a c g a g a a c c a	t t t c c t c a t g
P862018	150	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -

alignment	position	6 0 1	6 1 1	6 2 1	6 3 1	6 4 1
P862017	479	a t g c t c c t g t	c a c c g g g a a g	t g t t c t a a t t	t t a a c t t t a T	T T T T A T T T T A
P862018	150	- - - - -	- - - - -	- - - - -	- - - - -	T T T G T A C T T T G

alignment	position	6 5 1	6 6 1	6 7 1	6 8 1	6 9 1
P862017	529	AAATTTATTT	TTAGAGACAG	GGTCTCActg	tgtcgcccag	actgcaagtgc
P862018	161	TAATATTTCA	CTTAACACAG	CATTTCAaag	tgctcgaaaa	acagtggatt
		*****	*****	*****		

alignment	position	7 0 1	7 1 1	7 2 1	7 3 1	7 4 1
P862017	579	a g t g g c g c a a	t c a c c g c a a c	c t c g a c c t c c	c a g g c t c a a g	c g a t c t C C C
P862018	211	g a a c a g t t g t	t a a c t t t t c a	g t t a t t c a c c	a g a a a - - - -	- - - - - T C C A

alignment	position	7 5 1	7 6 1	7 7 1	7 8 1	7 9 1
P862017	629	G C C T C A G C C T	C C T G A G T a g c	t g a g a c c a c a	g g c a c g c g c c	a c c a c a c c t g

P862018	250	T C C T C T T C T T T C C T T A G T c t a	a g a t t a a t t t	g a t g g g g a c a	a c c a t t a t c c
		* * * * * * * * * * * * * * * * * *			
alignment position	8 0 1	8 1 1	8 2 1	8 3 1	8 4 1
P862017	679	g c t a a t t t t a	c a t t t t t t g t	a g a g g c g g g g	t c t c g c t t t g t t g c c c a g g c
P862018	300	t a g g t c c a c a	g t g a t g a a c t	g t g a t g g g c c	t c a g a a a a t c c c a t t c t c t g
alignment position	8 5 1	8 6 1	8 7 1	8 8 1	8 9 1
P862017	729	t g g t c t c g a g	t t c c c a g g a t	c a a g c g a t c -	- - - - -
P862018	350	c t c t g t c t t c	c t g g t a a a c t	g g a a a a c t c t	c a c a g t t c c t t c t a c t g a g c
alignment position	9 0 1	9 1 1	9 2 1	9 3 1	9 4 1
P862017	758	- - - - -	- - - - -	- - - - -	- - - - -
P862018	400	a g c a a g t t g g	c t c t t c a a a g	c c t t t c t t t a	g c c t a c t t c a c a g a a a t g c t
alignment position	9 5 1	9 6 1	9 7 1	9 8 1	9 9 1
P862017	758	- - - - -	- - - - -	- - - - -	- - - - -
P862018	450	a a c c t c a t t c	c a t a g c g c t t	t c t a c c t t a t	c c c t a t c g g g a t g a c g c t c a
alignment position	1 0 0 1	1 0 1 1	1 0 2 1	1 0 3 1	1 0 4 1
P862017	758	- - - - -	- - - - -	- - - - -	- - - - - C T
P862018	500	c c a t g a c c a g	t t c t t g c t g c	a g a g a c a c a g	t g c g t g c t c t t a c a c a a a C T * *
alignment position	1 0 5 1	1 0 6 1	1 0 7 1	1 0 8 1	1 0 9 1
P862017	760	C C C G C C T C G G	T C T C C C t a a g	c a c t g g g a t t	g c a g g c G T G A G C C A C A G c g c
P862018	550	C C T G T C T C A G	T G G C C C c t g a	t c a g c a c c t g	a g - - - G T G A A C C A C A G a g a * * * * * * * * * * * * * * * * * *
alignment position	1 1 0 1	1 1 1 1	1 1 2 1	1 1 3 1	1 1 4 1
P862017	810	c c g g c c g c t g	t a a c t t t a a a	t t g c c c g g g a	g g a c t c t g c a g c c c a a c c c t
P862018	596	t c t c a c c t c a	t c g c t g a a a g	c a a a c a c a a a	c t g c c c t t g t a a g t c a t g t t
alignment position	1 1 5 1	1 1 6 1	1 1 7 1	1 1 8 1	1 1 9 1
P862017	860	g c c c a c c t c a	c c c g g t c a c c	g g a g g a t g c -	- - - - -
P862018	646	t t g c t c t t t t	a a t g a g t t t c	t t t c t t c c t c	g t t t t t t t a c t t a c c a a a c t
alignment position	1 2 0 1	1 2 1 1	1 2 2 1	1 2 3 1	1 2 4 1
P862017	889	- - - - -	- - - - -	- - - - -	- - - - -
P862018	696	c c a c g a g a a g	c c a a c a g c c t	g c g c a a g a t c	a g c c t g g g t g a c a a c t g 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
P862017	889	- - - - -	- - C T G T C A A C	T T C T G G G A G C	T G C A A G C G C G G G C C G G C C a g
P862018	746	a g g c a t t c a a	t t C T T T C A A G	C T C A G G G A C	T G C C G G C C C G G C C G G A C t c * * * * * * * * * * * * * * * * * *
					* * * * * * * * * * * * * * * * * *
					* * * * * * * * * * * * * * * * * *
alignment position	1 3 0 1	1 3 1 1	1 3 2 1	1 3 3 1	1 3 4 1
P862017	927	t c g t c c g c g c	g c g g c t t t t t	c t t c a g g a c a	g c g g a g g c a c a c c g t g c t t t
P862018	796	- - - - -	- - - - -	- - - - -	- - - - -
alignment position	1 3 5 1	1 3 6 1	1 3 7 1	1 3 8 1	1 3 9 1
P862017	977	g c g g t t c c c g	g a a g t c c t t c	a g g c c t C A G A	C C T G T C A G C C C G C C A C a c t c
P862018	796	- - - - -	- - - - -	- - - - - C A G A	G C C C T A A C C C C G C C A C g a c t * * * * * * * * * * * * * * * * * *
alignment position	1 4 0 1	1 4 1 1	1 4 2 1	1 4 3 1	1 4 4 1
P862017	1027	c a g c c a g t c c	c t t c c g a t c a	c c t c c a g a c a	c c a c g e t e t c c t t t c g g a g c
P862018	820	c g c c t t c c g c	c c g c g g g c t c	c g a c g a t c t g	t c c c t c c c g g g c a g a g a g c t

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

P862017 1077 c c g **c c c - - - -** **- - - - -** **- - - - -** **- - - - -** **- - - - -**

P862018 870 c a c c t a g t c t a c a t c t g g a g c g t c t g a g g g g a a a g c g a a a g c t c t a c c a t

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

P862017 1083 **- - - - -** **- - - - -** **- - - - -** **- - - - -** **- - - - -** **G C C**

P862018 920 c c g a t c t t t a t a a g c t c c g c t a g c c t a g c t t t c a g a g a g c g c t g **g g a G C C**

* * *

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

P862017 1086 **G G A A G T G g c g** **g c c c g g a a c t** a c t c c c a c a g g g g g c g **g g g** a - - **A G G A A G A**

P862018 970 **G G A A G T G a c a** a g a g g a a g t c c c g c c t c a c t c a g a g g g c g g **g c t A G C A A G A**

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

P862017 1134 **T G G C G G C G C C** **C A G C G T C C C G** **T G A G G A G A G A** G G a c a c a - G G G A T C C C G G G G

P862018 1020 **T G G C G G C G C C** **C A G G A G C C C G** **T G A G G T G A G A** G G c g t c c t G G G G T C C T G G G G

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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

P862017 1183 A g c g g c c c a g a c t c G T A A A T T A T G G C C G C A T C T C C G C A C A c t c t c T C C T

P862018 1070 A c t g c t g c a c c a - - - G T A C G T T A T G G C C G C G T C C C C G C A C A C c a t t T C C T

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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

P862017 1233 C A C G C C T C C T G A C A G G T A C T G T A C C C G c c T T G G G C A C G A C C T T **G G G G G A A**

P862018 1117 C G C G C C T C C T C A C A G G T A T T G T A C C C G g - T T G G G A A T G A T C G T G G **A C G A A**

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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

P862017 1283 **A T T C T T C T C T T** **A T T a C C A C G** **T G C G A G** G C C G T G G T T C C G G C T G G C T G C A A C

P862018 1166 **T T G T T T C T T T** **T T T T g C C A T G** **T G C G G T A** C C G T G T T G C C G G C C G C C T G C A A C

P862017 (1501 bp)	1.000 22 %
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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 4.1.1

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

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

DiAlign professional TF Release 3.1 December 2004

Thu May 12 18:51:16 2005

Solution parameters:

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

- ALL user_defined.lib (0.75/Optimized)
- ALL vertebrates.lib (0.75/Optimized)

Selected groups
(core/matrix sim):

Aligned Sequences:

No.	Sequence Name	Sequence Description	Length
1	P911216	sym=COX11 loc=Loc1353 taxid=9606 spec=Homo sapiens chr=17 ctg=NT_010783 str=(-) start=11698832 end=11699832 len=1001 tss=501 comm=COX11 homolog, cytochrome c oxidase assembly protein (yeast); (NM_004375/502/bronze;)	1001 bp
2	P911219	sym=Cox11 loc=Loc69802 taxid=10090 spec=Mus musculus chr=11 ctg=NT_039521 str=(+) start=2038150 end=2039150 len=1001 tss=501 comm=COX11 homolog, cytochrome c oxidase assembly protein (yeast); (AK008096/529/gold;NM_199008/529/bronze;)	1001 bp
3	P911220	sym=na loc=Loc287621 taxid=10116 spec=Rattus norvegicus chr=10 ctg=NW_047336 str=(+) start=20039176 end=20040176 len=1001 tss=501 comm=similar to COX11 homolog; cytochrome c oxidase subunit 11; cytochrome c oxidase assembly protein COX11; (XM_213433/540/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\\$SMAD](#) [V\\$AHRR](#) [V\\$MYOD](#) [V\\$SEGRF](#) [V\\$DMTF](#) [V\\$BNCF](#) [V\\$SHIF](#) [V\\$STAF](#) [V\\$P53F](#) [V\\$GATA](#) [V\\$ZFIA](#) [V\\$PAX6](#)
[V\\$SRFF](#)

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alignment
position      1 . . . . . 1 1 . . . . . 2 1 . . . . . 3 1 . . . . . 4 1 . . . . .
P911216      1 g c a a g t t g t a a g g g g c a t c a g a G C A G G G G A A G C C G A C T G C C C A c - G G G C T
P911219      1 - - - - - - - - - - - - - - - - - - - - - - G C A G T G G G A G A C A T C T G C C C A T G G G G C T
    
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P911220	1	-----	-----	-----	-----	-----	CTGC	CC	TT	GG	GG	CT
alignment position	51	61	71	81	91		
P911216	50	GAGAAAATGC	AGGTGT	CGTG	-	GGt	g	c	c	c	a	t
P911219	29	GAGAAGATGC	ACAGGT	CGGG	-	GTGT	T	G	G	A	-	
P911220	15	GAGAAGACGC	ACAAGT	gga	g	a	G	T	G	T	G	G
		*****	*****	*****	*****	*****	*****	*****	*****	*****	*****	*****
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alignment position	101	111	121	131	141		
P911216	99	C-AAGGCTTTC	CTGAGAGAGG	tga	-	-	-	-	-	TACTTGA	AACT	AAAGTCCAGGG
P911219	77	T-AAGTGTTTC	CAGAAAAGAGG	GACGT	T	g	g	t	t	TGCCTG	CGCT	CAGTCAGCGG
P911220	64	taAAGTGTTTC	CTGAAAAGAGG	CAAGT	T	t	g	c	c	-	-	-
		*****	*****	*****	*****	*****	*****	*****	*****	*****	*****	*****
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alignment position	151	161	171	181	191		
P911216	141	CAGTGAGCAC	AGGAGC	cagc	gg	c	c	a	a	g	g	A
P911219	126	CGGAAAGCAA	C	GGGGC	T	G	A	G	A	-	-	-
P911220	110	CAGTAAGCGA	G	GGGGT	T	T	A	G	A	-	-	-
		*****	*****	*****	*****	*****	*****	*****	*****	*****	*****	*****
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alignment position	201	211	221	231	241		
P911216	191	GGAGAGC	gtc	gcc	-	-	-	GGGGC	TGCCG	GGT	CG	AGACAAAGGC
P911219	170	GCAGAGCTGC	CGCTGGGGC	CGCTA	GGT	CG	AGACAAAGGC	TGGCG	AAAGT	T	T	GGCAAGGC
P911220	154	GCAGAGCTGC	CGCTGGGGC	CGCTA	GGT	CA	AGACAAAGAC	TGGCG	GAGT	T	T	GGCAGGC
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alignment position	251	261	271	281	291		
P911216	239	Taaataaagata	cacagcgc	C	AA	CC	CAAGT	G	At	g	g	c
P911219	220	TGGGAGATG	GGGATA	-	-	-	C	AA	G	CC	CAAGT	G
P911220	204	TGGGAAGATG	AGAGTA	-	-	-	C	A	c	t	c	c
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alignment position	301	311	321	331	341		
P911216	289	ACGGGCG	AA	C	G	C	A	T	T	T	C	C
P911219	264	AAGGCCCA	AA	T	G	C	A	T	T	T	C	t
P911220	248	AAGGCCCA	AA	T	G	C	A	T	T	T	C	C
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P911216 580 c GTT CCT TTC TGT GGC TGGC GCTGGATCCA CCC TGGGTc t c c a a c c a g g g
P911219 550 g GTG GCT TCG TGT GGC CGGG GCTGGAGGCA GCCCGGGTGG TCAGGgCGGA
P911220 533 c a t c a CT TTG TGT GGC CGGG GCTGGAGCCA GCCCGGTGG TCGGGcCGGA
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alignment position 651 661 671 681 691

P911216 630 c t g c a g a g a g g g t AGAGCCG TTTCTTAGGC CAGAGTGGAG TGGGACAGGA
P911219 600 CTGTGGT GAA CGCAGAGCTG GTGCTTAGGC CCGGGTGGGA TGGGC TC GGA
P911220 583 CGGTGGT GAA CGCAGAGCGG GCTCTTAGGC CGGGATGGA A TGGGGTCGGA
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alignment position 701 711 721 731 741

P911216 680 Ggt GCCGAGA GAGGACTGAG GTGGCTTGGG ACATGGAAGC Gc t g c a g c c t
P911219 650 GGCGCGGAGC GGGGTC TGAG ACGCCTCGGG ACATGGAAGC GCCCGTGC GG
P911220 633 GGCGCGGAGC AGGGACTGAG ACGCCTCGGG ACATGGAAGC GCCCGAGCGG
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alignment position 751 761 771 781 791

P911216 730 t c g a g c c c g g c a t c c a g c a t t GCAGCCGCC GCGGCGGCC T AAGAGCTCGA
P911219 700 GGTCCGGGGG CCCGc g a C - - GCAGCCGCC ACGGCGGCC G AGGAGCAGCA
P911220 683 GGCCCGGGT CCCGt c g C - - GCAGCCGCC ACGGCGGCC AAGAGCAGCA
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alignment position 801 811 821 831 841

P911216 780 ACCCTTTCa c a CGCGCGCAG GAGGAGGAGC GGC GGC GGC A GAACAAGACG
P911219 747 ACCCTTTCCAg CGCGCGCAG GAGGACGAGT GGC GGC GGC G GAACAAGACG
P911220 730 ACCCTTTCCAg CGGGCGCAG GAAGACGAGT GGC GGC GGC G GAACAAGACG
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alignment position 851 861 871 881 891

P911216 830 a c c C TCACTT ACGTGGCCG C TG TCGCCGTG GGCATGCTGG GGGc g TCCTA
P911219 797 GTGC TCACTT ACGTGGCCG CG CCGCCGTG GGCATGCTGG GGGCCTCCTA
P911220 780 GTGC TCACTT ACGTGGCCG CG CCGCCGTG GGCATGCTGG GGGCCTCgTA
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P911216 (1001 bp)	0.370 58 %	0.374 56 %
P911219 (1001 bp)		1.000 83 %

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"/>

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GEMS Launcher 4.1.1

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

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

DiAlign professional TF Release 3.1 December 2004

Thu May 12 21:13:29 2005

Solution parameters:

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

- ALL user_defined.lib (0.75/Optimized)
- ALL vertebrates.lib (0.75/Optimized)

Selected groups (core/matrix sim):

Aligned Sequences:

No.	Sequence Name	Sequence Description	Length
1	P939218	sym=COX15 loc=Loc1355 taxid=9606 spec=Homo sapiens chr=10 ctg=NT_030059 str=(-) start=20239926 end=20240926 len=1001 tss=501 comm=COX15 homolog, cytochrome c oxidase assembly protein (yeast); (NM_078470/501/bronze;NM_004376/501/bronze;)	1001 bp
2	P939219	sym=Cox15 loc=Loc226139 taxid=10090 spec=Mus musculus chr=19 ctg=NT_039692 str=(-) start=4133505 end=4134589 len=1085 tss=501,585 comm=COX15 homolog, cytochrome c oxidase assembly protein (yeast); (AK051792/603/gold;NM_144874/519/silver;)	1085 bp
3	P939220	sym=na loc=Loc309391 taxid=10116 spec=Rattus norvegicus chr=1 ctg=NW_047566 str=(+) start=38313 end=39313 len=1001 tss=501 comm=similar to COX15 gene product; (XM_219882/587/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\$ZBPF
V\$OAZF
V\$SETSF
V\$E2FF
U\$NRF2
V\$AREB
V\$IRFF
V\$OCTP
V\$EBOX

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alignment position 1 . . . . . 1 1 . . . . . 2 1 . . . . . 3 1 . . . . . 4 1 . . . . .
P939218          1 a g g g g a c c c c g g g a c t c g a a c c t t g g c t c c a c a g c t g a g c c a t t c t c g c t
P939219          1 c t a g g t t g t a g a g - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
P939220          1 g g c g a g t g - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -

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alignment position 401 . . . . . 411 . . . . . 421 . . . . . 431 . . . . . 441 . . . . .
P939218 316 GTGCGCCTGC AGTTTccact t ggaatttgg gctccggcgc gcaccagcta
P939219 340 GCTCGCCTTC GGTTTCCACT GAGTCCC CGC G- - - - -
P939220 286 GCTCGCCTTC GGTTTCCACT GAGTCCC CGC G- - - - -
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alignment position 451 . . . . . 461 . . . . . 471 . . . . . 481 . . . . . 491 . . . . .
P939218 366 agaa g c g c g t c a a c a GCTGC GCGC GCC c g t g c - - - GCGC GTCCCCGACA
P939219 371 - - - - - - - - - - - GC CGC GCGAGC g AC G GAGGAGGCGC GTCCCCGACG
P939220 317 - - - - - - - - - - - GC TGC GCGAGCC AC C GAGAAGGCGC GGCCCGATG
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alignment position 501 . . . . . 511 . . . . . 521 . . . . . 531 . . . . . 541 . . . . .
P939218 412 CCTACGC CCC a GCAGCC - CC - - - - - - - - - CGCGA AAG CGGAGTCGCA
P939219 406 CCCGTGC CCG - GCAGCC t CC C AGGGAGT C G T GCGTGC ACG CGCAGTGGCC
P939220 352 CCGGTGC CCC - GCAGCC - CC C GCGGAGT C A T ATGCGC AAG CGCAGTGGCC
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alignment position 551 . . . . . 561 . . . . . 571 . . . . . 581 . . . . . 591 . . . . .
P939218 449 ACGCAGGCGC acttctgttc gctccgggtcc c c agagaagg cggggctccc
P939219 455 AACCTAGCGC gagggggcgc gcaacgac - - - - - - - - -
P939220 400 AGCCTcacta gca g - - - - - - - - - - -
* * * * *
* * * * *

```

```

alignment position 601 . . . . . 611 . . . . . 621 . . . . . 631 . . . . . 641 . . . . .
P939218 499 gct GCC CGAC CCGGAAGTGC TTC TCTTTT C TTG GCGGAG GAGggaGACC
P939219 482 - - - GCC TGAC CCGGAAGTGC TTG TCTTTT C GGAGCGGAG AAGCG- GACC
P939220 414 - - - GCC TGAC CCGGAAGTGT TTG T CCTTTT G Gt a - - - GAG AAGCG- GACC
* * * * *
* * * * *
* * * * *
* * * * *

```

```

alignment position 651 . . . . . 661 . . . . . 671 . . . . . 681 . . . . . 691 . . . . .
P939218 549 ACAGAGC CCT GGGTTGTGGA AGAGGTGGCt gttccctgtc a TCAGTATGC
P939219 528 GCAGCTC GCT GGGGC GC TCC GGCAGTGGC- GCTGTACTG- - TCAGCATGC
P939220 457 GCAGATC GCT GGCTGGT Gc g t t c c g c a g a g GCTGTACTG- - TCAGTATGC
* * * * *
* * * * *
* * * * *
* * * * *

```

```

alignment position 701 . . . . . 711 . . . . . 721 . . . . . 731 . . . . . 741 . . . . .
P939218 599 AGCGATTGCT CTTTCGCCG TTGAGGGCCTTGAAGGGGAG gcagtatctg

```


Extract aligned sequences

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GEMS Launcher 4.1.1

GEMS Launcher Task: *DiAlign TF*: Multiple alignment plus TF sites working on C4-COX17 (3 seq.)

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

DiAlign professional TF Release 3.1 December 2004

Thu May 12 21:56:38 2005

Solution parameters:

Sequence file: [C4-COX17](#) (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
1	P879435	P879435 sym=COX17 loc=Loc10063 taxid=9606 spec=Homo sapiens chr=3 ctg=NT_005612 str=(-) start=25890889 end=25891889 len=1001 tss=501 comm=COX17 homolog, cytochrome c oxidase assembly protein (yeast); (NM_005694/501/bronze;)
2	mCOX17	mCOX17 m5_dna range=chr16:38203020-38204074 5'pad=0 3'pad=0 revComp=FALSE strand=? repeatMasking=none
3	P879436	P879436 sym=Cox17 loc=Loc89786 taxid=10116 spec=Rattus norvegicus chr=11 ctg=NW_047356 str=(-) start=17580775 end=17581775 len=1001 tss=501 comm=cytochrome c oxidase, subunit XVII assembly protein homolog (yeast); (NM_053540/547/bronze;)

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\\$HESF](#) [V\\$SETSF](#) [U\\$NRF2](#) [V\\$SPIF](#) [V\\$ZNEP](#)

```

alignment position 1 . . . . . 1 1 . . . . . 2 1 . . . . . 3 1 . . . . . 4 1 . . . . .
P879435          1 c c a a t a g t t g t g g a c t c g g t g g t t c - - - - -
mCOX17          1 - - - - -
P879436          1 a c c a a t a t c t g c g g a a c a t a t a t t a a a c c a g a a a g a c c g g a a g a a g a t

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

```

P879435      26 - - - - -
mCOX17      1 - - - - - AGGG TGG AA C CCG GAT C TGC TAC TGC T T GTCCAGT AC
P879436     51 c a c a a a a t g c c c t AGGG TGG AA C C T G GAT C TGC CAC TGG T T GTCCAGG AC
                * * * * *
                * * * * *
                * * * * *

alignment position 101 . . . . . 111 . . . . . 121 . . . . . 131 . . . . . 141 . . . . .
P879435      26 - - - - -
mCOX17      38 C a a AGG T C A G C C C T G A A A A T A C G A A T A C A G T T A G C A T T A t a c T G G A C T G
P879436     101 C c a g A G G T C A G C C A T T A A A A T A T G A A T A C A G A T A G C A T T A c a g T G G A C T G
                * * * * *
                * * * * *
                * * * * *

alignment position 151 . . . . . 161 . . . . . 171 . . . . . 181 . . . . . 191 . . . . .
P879435      26 - - - - -
mCOX17      88 A A T G G G T C A T A T A G G A A T A T A T G T A T g c a t g t a t A C A T A T A A G C A T G C A A
P879436     151 A A C G G G T T A T A A A G G A A T A T A T G T A T - - - - - A C A T A T A T G C A T G C A A
                * * * * *
                * * * * *
                * * * * *

alignment position 201 . . . . . 211 . . . . . 221 . . . . . 231 . . . . . 241 . . . . .
P879435      26 - - - - -
mCOX17     138 T A A C A A T T A G G G A G G A A A G G C C A t G A A T T T G A A G G A T A G T G G G A A T G G
P879436     193 T A A C A A T T A G G G A G G A A A G G C C A c G A A T T T G A A G G A T A G T G G G A A C G G
                * * * * *
                * * * * *
                * * * * *

alignment position 251 . . . . . 261 . . . . . 271 . . . . . 281 . . . . . 291 . . . . .
P879435      26 - T A T G T C T T G C T A T T C A T T T T T A A A T A G G T C A A T G A A A G A G a g g a a a g g c
mCOX17     188 G T A T G T A T A T G T A A G G A T T T G T A G A A A G G A A A G G A A A G G A A A A T G A T G
P879436     243 G C G T G T A T A T G T g A G G A T T T G T A G A A A G G A A A C A G A A A G G A A A T G T T G
                * * * * *
                * * * * *
                * * * * *

alignment position 301 . . . . . 311 . . . . . 321 . . . . . 331 . . . . . 341 . . . . .
P879435      75 c t g c a g t g t g t g g g g a t c a g g a a g a a g g c g g a t a a a a g a a a a g g g g a a a
mCOX17     238 T A A t t A A A T T A C A A T C T C A A A A C A A - - - - -
P879436     293 C A A t c A A A T T A C A A T C T C A A A A C A A - - - - -
                * * *
                * * *
                * * *

alignment position 351 . . . . . 361 . . . . . 371 . . . . . 381 . . . . . 391 . . . . .
P879435     125 c t a g t c t g t t a t t c a a g g g a a c t g g c t t t c a c t t a t g g t t t c t c c t g t t t
mCOX17     264 - - - - -
P879436     319 - - - - -

alignment position 401 . . . . . 411 . . . . . 421 . . . . . 431 . . . . . 441 . . . . .
P879435     175 g g c t t g A A C A A A T C A T T T C A C C A T C T T G G G C T T C C G T T T c g a t a t t g g g t
mCOX17     264 - - - - - A A C A A A A C A A A A A C C A T T C T G G G T G A C C T T T T A A C C T - - - - -
P879436     319 - - - - - A C C A A A T A G C A A A A C C A c c c t a g a T G A C C T T T T A A C C T - - - - -
                * * * * *
                * * * * *
                * * * * *

alignment position 451 . . . . . 461 . . . . . 471 . . . . . 481 . . . . . 491 . . . . .
P879435     225 g g g g a g g a g c g g g t g t t a c g a g a t c t c t c a g t t g t c t t g c t g c t t t c t t t
mCOX17     302 - - - - -
P879436     357 - - - - -
    
```

```

alignment position 501 . . . . . 511 . . . . . 521 . . . . . 531 . . . . . 541 . . . . .
P879435      275 c t t c g t g a g c c c t c c c c a a g t t g a t t t a a c a a a t a c t c t a t g a c c t a g a g
mCOX17      302 - - - - -
P879436      357 - - - - -
    
```

```

alignment position 551 . . . . . 561 . . . . . 571 . . . . . 581 . . . . . 591 . . . . .
P879435      325 t c c t a g a g t g t a a a t a c c a c a g t c c a g g t g a g c g t t c a g c g g g c c t c c T T
mCOX17      302 - - - - - T T
P879436      357 - - - - - T T
                                     * *
                                     * *
    
```

```

alignment position 601 . . . . . 611 . . . . . 621 . . . . . 631 . . . . . 641 . . . . .
P879435      375 G C G C A T G C G C T G A A G g g g g c a c c c t c t c g t t a a g g c c c g a a t t t t g c c T C
mCOX17      304 G C G C C A G C G C T G A C G C C A C G C C C t t g g a g c g a g g c c t t g t a c c a c t - - T C
P879436      359 T G G T C T G C G C T A A A G C C A C G C C - - - - - - - - - - - - - - - - - - - - - - - -
          * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * *
          * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * *
    
```

```

alignment position 651 . . . . . 661 . . . . . 671 . . . . . 681 . . . . . 691 . . . . .
P879435      425 T T C T G C G C A C G C G C T C C T T t t a a a t t c c c c a c c t g t c a g a G A G A A G C A G G
mCOX17      352 T T T T G C G C A C G C G C T T C T T A G A C T t a C T T C C G T C C G - - - - G A G A G C G G G
P879436      382 T T T T G T G T G C G C G C T C C T T A G G C T c g C T T C C G T C C G - - - - G A G A G G A G G G
          * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * *
          * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * *
          * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * *
          * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * *
    
```

```

alignment position 701 . . . . . 711 . . . . . 721 . . . . . 731 . . . . . 741 . . . . .
P879435      475 A C T T C C T G T A C T T T T T A G A G C G A C T G C c G G A A G T G A C T G C G G A C G A A T C G
mCOX17      398 A C T T C C T G T C C C C C T T C G A T T G A C T G C - G G A A G T G G A G A C A G A C G G C T C A
P879436      428 A C T T C C T G T C T G C G T T C G C T T G A C T G C - G G A A G T G G A T A C A G A C A G C T C G
          * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * *
          * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * *
          * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * *
          * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * *
    
```

```

alignment position 751 . . . . . 761 . . . . . 771 . . . . . 781 . . . . . 791 . . . . .
P879435      525 G C G T T T G C C G A G - G C T G G c a t a g a t t t g g c t g t c t c C G C T C A T A G C T G C T
mCOX17      447 G G G T A G T C G G A G - T T T G G G A G C T T T G C G C G T G T G - - C G C T C A T A G T T G C T
P879436      477 G G T T G G T C T G A G t T T T G G G A G C T T T G C G C G T G T G - - C G a t c g t t a C T G C T
          * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * *
          * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * *
          * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * *
          * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * *
          * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * *
    
```

```

alignment position 801 . . . . . 811 . . . . . 821 . . . . . 831 . . . . . 841 . . . . .
P879435      574 T T T G C G C G A A A G A T G C C G G G T C T G G T T G a c t c a a a C C C T G C C C C G C C T G
mCOX17      494 T T C G C C T G G A A A G A T G C C G G G A C T G G C g G C C G C T A G C C C T G C C C C G C C G
P879436      525 T T C C T C T G G A A A G A T G C C G G G A C T G G C T G C C G C T A G C C C T G C C C C G C C G
          * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * *
          * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * *
          * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * *
          * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * *
          * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * *
          * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * *
          * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * *
          * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * *
          * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * *
    
```

```

alignment position 851 . . . . . 861 . . . . . 871 . . . . . 881 . . . . . 891 . . . . .
P879435      624 A G T C T C A G G A G A A G A A G C C G C T G A A G C C C T G C T G C G C T T G C C G G A G A C C
mCOX17      544 A G G C T C A G G A G A A G A A G C C a C T G A A G C C C T G C T G T G C C T G C C G G A A A C C
P879436      575 A G G C T C A G G A G A A G A A G C C t C T G A A G C C C T G C T G T G C C T G C C G G A G A C C
    
```


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 4.1.1

GEMS Launcher Task: *DiAlign TF*: Multiple alignment plus TF sites working on C4-CYCS (3 seq.)

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

DiAlign professional TF Release 3.1 December 2004

Fri May 13 03:44:13 2005

Solution parameters:

Sequence file: [C4-CYCS](#) (3 seq.)
Type of sequences: nucleotide sequences
Threshold T: 0.00
'*' signs below alignment denote: diagonal similarity (max. similarity is represented by 10 '*' signs)
Alignment output: complete alignment is shown
 # nucleic acids per line: 50
TF output: common TF matches located in aligned regions (common to 3 (100.0 %) sequences)
Family matches: yes
MatInspector library: Matrix Family Library Version 5.0 (February 2005)
 • ALL user_defined.lib (0.75/Optimized)
 • ALL vertebrates.lib (0.75/Optimized)
Selected groups
 (core/matrix sim):

Aligned Sequences:

No.	Sequence Name	Sequence Description
1	P882274	P882274 sym=CYCS loc=Loc54205 taxid=9606 spec=Homo sapiens chr=7 ctg=NT_007819 str=(-) start=24460128 end=24461228 len=1101 tss=601 comm=cytochrome c, som (NM_018947/501/bronze;)
2	P882275	P882275 sym=CyCS loc=Loc13063 taxid=10090 spec=Mus musculus chr=6 ctg=NT_039343 str=(-) start=2241526 end=2242696 len=1171 tss=601,644,669,670,671 comm=c, somatic; (AK005336/504/gold;AK010651/572/gold;AK088098/574/gold;AK003168/547/gold;NM_007808/573/bronze;)
3	rCYCS	rCYCS n3_dna range=chr4:79103604-79104758 5'pad=0 3'pad=0 revComp=TRUE strand=? repeatMasking=none

Alignment (DiAlign format):

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

V\$RORA
V\$RARF
V\$PERO
V\$HNF4

V\$E4FF
V\$CEBP
V\$ZF5F
V\$ZFIA
V\$ECAT
V\$PCAT
V\$HIF1
V\$GREF
V\$EREF
U\$EREF

```

alignment
position      1 . . . . . 1 1 . . . . . 2 1 . . . . . 3 1 . . . . . 4 1 . . . . .
P882274      1 - - - - -
P882275      1 T C A G G C G A A T C C T G C T T C T C C C T T A A A G C T T G C C T G C A C A C C C T C C T C G T
rCYCS        1 T C A G G C A A A T C C T G T T T C T T C C T T A A A G C T T G C C T G C A C A C C C T C C T T G T
    
```

	* * * * *	* * * * *	* * * * *	* * * * *	* * * * *
alignment position	5 1	6 1	7 1	8 1	9 1
P882274	1 - - - - -	- - - - -	- - - - -	- - - - -	- - - - -
P882275	51 T T T C T A C A A A	C A C T A G G G G A	A G A A A A C A G G	g a c t c t g g g t	a a G A T G T G A T
rCYCS	51 T T T T T C T A C A	A A C T A G G G G A	A G A A A A C A G G	- - - - -	- - G A T A A G A T
	* * * * *	* * * * *	* * * * *	* * * * *	* * * * *
	* * * * *	* * * * *	* * * * *	* * * * *	* * * * *
	* * * * *	* * * * *	* * * * *	* * * * *	* * * * *
alignment position	1 0 1	1 1 1	1 2 1	1 3 1	1 4 1
P882274	1 - - - - -	- - - - -	- - - T T C C T C	A G T C T T G G G G	C G T C C A t c a a
P882275	101 C C T G T C T G C C	A C T T G T G C G t	- A C C T T C C C C	A G C T T T G A G G	C T C T C A C T G -
rCYCS	89 C C C G T C T G C C	A C A T G T A C C g	c A C C A T C C C C	A G C T T T G A G G	C T T T C A C T G -
	* * * * *	* * * * *	* * * * *	* * * * *	* * * * *
	* * * * *	* * * * *	* * * * *	* * * * *	* * * * *
	* * * * *	* * * * *	* * * * *	* * * * *	* * * * *
alignment position	1 5 1	1 6 1	1 7 1	1 8 1	1 9 1
P882274	27 g c G G A G A G C T	G G A A t g t g a c t	g a a a g T A A C	A G A G T A T A G G	T g g a a c t a g a
P882275	149 - - G G A G A G C A	G G A A G A T G G T	T - - - - T A A C	A G A G T A A A G G	T - - - - - - -
rCYCS	138 - - G G A G A A C A	- G A A G A T G G T	T - - - - T A A C	A G A G T G A A G G	T - - - - - - -
	* * * * *	* * * * *	* * * * *	* * * * *	* * * * *
	* * * * *	* * * * *	* * * * *	* * * * *	* * * * *
	* * * * *	* * * * *	* * * * *	* * * * *	* * * * *
alignment position	2 0 1	2 1 1	2 2 1	2 3 1	2 4 1
P882274	77 a c a a g g t C A C	G A G C T G G T G C	C C A a c t c g t g	t a a c t c c t g g	t t c c a g g c t g
P882275	183 - - - - - C A C	C A G C A G G C G T	C C A c t g c G A G	G C C A G T G C A G	T T - - - - -
rCYCS	171 - - - - - C A C	C A G C A t - - - -	- - - - - G A G	T C C G G T G C A G	T T - - - - -
	* * * * *	* * * * *	* * * * *	* * * * *	* * * * *
	* * * * *	* * * * *	* * * * *	* * * * *	* * * * *
	* * * * *	* * * * *	* * * * *	* * * * *	* * * * *
alignment position	2 5 1	2 6 1	2 7 1	2 8 1	2 9 1
P882274	127 t c c c t c t a g g	a t g c t g t t g G	C G C C A G C C g t	g g t a g t a g G A	C A G A G T C T G G
P882275	218 - - - - -	- - - - - G	C G C C A G C C A G	G a a g c c t t G A	C C A A G C C T G G
rCYCS	195 - - - - -	- - - - - A	C G C T A G T C A G	G g a a t c t a G A	C C A A G C C T G G
	* * * * *	* * * * *	* * * * *	* * * * *	* * * * *
	* * * * *	* * * * *	* * * * *	* * * * *	* * * * *
	* * * * *	* * * * *	* * * * *	* * * * *	* * * * *
alignment position	3 0 1	3 1 1	3 2 1	3 3 1	3 4 1
P882274	177 G T A A A G G T C G	C C T G C T G A C a	a g a t g g t a g c	t a g g a g a c c t	c t a g g t g c g c
P882275	249 G T A A A G G T C G	C C A G C A C A C C	G G C C G G C a G T	C T C A G C A C T C	C C C G T G G G C G
rCYCS	226 G T A A A G G T C G	C C T T C A G A C T	G G G C G G C g G T	C T T A G C A C T A	C C C G T G G G C G
	* * * * *	* * * * *	* * * * *	* * * * *	* * * * *
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	* * * * *	* * * * *	* * * * *	* * * * *	* * * * *
alignment position	3 5 1	3 6 1	3 7 1	3 8 1	3 9 1
P882274	227 c a a a a t t a g g	g c g t c t t t t c	c t g g a c c g g c	a a a a c g c c c t	g c t c a a a g c t
P882275	299 G A G G C C G A A G	G A G T C C T A g g	g c c g g g c - - -	- - - - -	- - - - -

rCYCS 276 G A G G C A G A A G G A G T C C T A a g a 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

P882274 277 c a t t a c a t c a c c a c g c c c a a g a a c T G A T A C T T T A G C A G G G C A A C G C A C C A
P882275 326 - - - - - G T T A C C T G A G C C G A G C C A C A C C C G G
rCYCS 302 - - - - - T G T T A C C T G A G C C C A G C C G C A C C C A A
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alignment position 4 5 1 4 6 1 4 7 1 4 8 1 4 9 1

P882274 327 A C C A A G C G a c t c c g c c - - C C A C C C T C C C C G C T C C T C C A G C A C A C G C a a g c
P882275 351 A T C C C A A G G G A G C a t c g g C C C C G C T A C T T G C - C C T C G C C A T C T C G C - - -
rCYCS 328 A T C C C G A G G G A G C g a c c a C C C C G C T A C T C G C T C C T C C C C A A C A C G C - - -
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alignment position 5 0 1 5 1 1 5 2 1 5 3 1 5 4 1

P882274 375 g c a c a g A G G C C G C G A G T G A C G T C A C c t t c t c c g a c a c c a c c t c g t t g t c
P882275 396 - - - - A G G C C A G A G G G T G A C G T C A C g C A C G T C C A C G C C T - - - - -
rCYCS 374 - - - - A G G C C G G A G G G T G A C G T C A t c C A C G T C C A C G C C T - - - - -
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alignment position 5 5 1 5 6 1 5 7 1 5 8 1 5 9 1

P882274 425 g T A C G A C C A A A G G C C T G T C G T A A C G G C C G G G A A A A - - - G C C T C G A G A A G
P882275 430 - T A C G T C C T A A G G C C T G T C G T A A G T G T C G G G C A A A C G A G G C C T C T G A A G G
rCYCS 408 - T A C G T C C A A G G G C C T G T C G T A A G T G T C G G G C A A A C G A G G C C T C T A G A G G
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alignment position 6 0 1 6 1 1 6 2 1 6 3 1 6 4 1

P882274 471 A A G G G C A C G C A C g c c G T A C A C C C T A A C A T G C T C G C C A G C A T G C G C G C G C A
P882275 479 A A G G G C G C C C T C T g G G C A C A T C C T A C C A T G C T A G C T C G C A T G C G C G C G C A
rCYCS 457 A A G G G C G C C C T C T c G G T A C A A C C T A C C A T G C T A G C C C G C A T G C G C G C G C A
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alignment position 6 5 1 6 6 1 6 7 1 6 8 1 6 9 1

P882274 521 g g t c c t t g g c g c a g g c a t t g g g a C T G G A G C C A A T G A G G T G C G G C G A C G T T
P882275 529 C a a a c c t g - - - - - T C - - - C T G G A G C C A A T G A G G T G C G G T T A C G T C
rCYCS 507 C c t t g c t a g c g c t c c c a a T C - - - C T G G A G C C A A T G A C A T G C G G C T A C G T C
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alignment position

7 0 1 7 1 1 7 2 1 7 3 1 7 4 1
P882274 571 A C T G C G T A G C c g c c a g e t e g G C C G C A C G T C A G G G C G C G G G A G C G C G G A G C
P882275 566 A C G G C G C A G C a g a C G G C G C T A C C G C A C G T C G G G C G C G G A C G G G C G G A A C
rCYCS 554 A C G G C G C A G t g c c C G G C G C T G C C G C A C G T C C G G C C G C G G G A G G G C A G A A C
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alignment position

7 5 1 7 6 1 7 7 1 7 8 1 7 9 1
P882274 621 G A G T T T G G T T G c a c t t A C A C C G G T A C T T A A G C G C G G A C C G G C G G T G T C C T T
P882275 616 A A G T G T G G T T G C A C C G A C A C C G G T A C A T A G G C G C G G G C C G G C G G T G T C C T T
rCYCS 604 A A G T G T G G T T G C A T T G A C A C C G G T A C A T A G G C G C G G G C C G G C G G T G T C C T T
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alignment position

8 0 1 8 1 1 8 2 1 8 3 1 8 4 1
P882274 671 G G A C T t a g a g a g t g G G G A C G T C C G G C T T C G g a g c g g g a g t G T T C G T T G T G
P882275 666 G G G C T A G A G C G C - - G G G A C G T C T G T C T T C G A G T C C G A A C - G T T C G T G G T G
rCYCS 654 G G G C T A G A G A G C - - G G G A C G T C T c c c t a a G A G T C T G A T C - C T T T G T G G T G
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alignment position

8 5 1 8 6 1 8 7 1 8 8 1 8 9 1
P882274 721 c c a g c g a c t a a a a - - - - - - - - - - - - - - - - G A G G T G A G A G C G
P882275 713 T T G A C C A G C C C G G A A C G G T G A G C G C G C G A C G G G G A T G C G G A C C G G G A A C G
rCYCS 701 T T G A C C A G C C C G G A C C G G T G A G C G C G C G A C G G G G A C G C G G G G C G G G A A G A
* * * * *
* * * * *
* * * * *

alignment position

9 0 1 9 1 1 9 2 1 9 3 1 9 4 1
P882274 747 G G T C G C G G A G G C C G C A C C T G G T T A G A g - - - - - - - - - - G C A G A G C T G T G
P882275 763 G G G C G A G G A G G C C G G G C A G G C C T A A C C T A C A A G C C A T G C A G A A C T G T G
rCYCS 751 G G G C G A G G A G A C C G A G G C A G G C C T G A C C T A C A A G A C A T G C G G A A C T G T G
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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 . . . . .
P882274 1102 - - - - -
P882275  996 G T G A G A C G G T   T C C T T C C C c a   g t c c t c c c t c   G C C T T C C C G T   G C C G G A C T A A
rCYCS    993 G T G A G A A G G T   T C C T T C C C t t   - - - - -   G C C T T C C C G G   G C C G G A C T A A
                * * * * *
                * * * * *
                * * * * *
                * * * * *

alignment
position      1 4 0 1 . . . . . 1 4 1 1 . . . . . 1 4 2 1 . . . . . 1 4 3 1 . . . . . 1 4 4 1 . . . . .
P882274 1102 - - - - -
P882275 1046 A G C A A G A G a g   a a g a   G A C T T A   A C C T C C T A A T   G A G A C C G G A G   C A G G c - - - G G
rCYCS    1033 T G C A A G A G t -   - - -   G A C T T A   A C C T C C A A A T   G A G A C C A G A G   C A G G a g g a G G
                * * * * *
                * * * * *
                * * * * *
                * * * * *

alignment
position      1 4 5 1 . . . . . 1 4 6 1 . . . . . 1 4 7 1 . . . . . 1 4 8 1 . . . . . 1 4 9 1 . . . . .
P882274 1102 - - - - -
P882275 1093 A A G C A C T T A G   G A T C a c c c c c   a g c c - - - - -   - - - - -   T C C C T T A
rCYCS    1078 A A G C A C T T A G   G A T C t t c a g c   c c c c g a g c c c   c a t t g a t g t a   t t t T C C C T T A
                * * * * *
                * * * * *
                * * * * *
                * * * * *

alignment
position      1 5 0 1 . . . . . 1 5 1 1 . . . . . 1 5 2 1 . . . . . 1 5 3 1 . . . . . 1 5 4 1 . . . . .
P882274 1102 - - - - -
P882275 1124 T C T T T G G A A G   T G A C T T T A A t   c g g c a g c a c t   g a c a g c a g t t   t a g c a t t c
rCYCS    1128 T C T T T G G A A G   T G A C T T T A A a   t g a c a 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.

	P882275 (1171 bp)	rCYCS (1154 bp)
P882274 (1101 bp)	0.178 33 %	0.182 28 %
P882275 (1171 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

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GEMS Launcher 4.1.1

GEMS Launcher Task: *DiAlign TF*: Multiple alignment plus TF sites working on C4-HCCS (3 seq.)

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

DiAlign professional TF Release 3.1 December 2004

Fri May 13 00:43:02 2005

Solution parameters:

Sequence file: [C4-HCCS](#) (3 seq.)
Type of sequences: nucleotide sequences
Threshold T: 0.00
'*' signs below alignment denote: diagonal similarity (max. similarity is represented by 10 '*' signs)
Alignment output: complete alignment is shown
nucleic acids per line: 50
TF output: common TF matches located in aligned regions (common to 3 (100.0 %) sequences)
Family matches: yes
MatInspector library: Matrix Family Library Version 5.0 (February 2005)

- ALL user_defined.lib (0.75/Optimized)
- ALL vertebrates.lib (0.75/Optimized)

Selected groups
(core/matrix sim):

Aligned Sequences:

No.	Sequence Name	Sequence Description
1	P928091	P928091 sym=HCCS loc=Loc3052 taxid=9606 spec=Homo sapiens chr=X ctg=NT_011757 str=(+) start=7095486 end=7096548 len=1063 tss=501,563 comm=holocytocrome c synthase (cytochrome c heme-lyase); (AK097815/501/gold;NM_005333/563/silver;)
2	P928092	P928092 sym=Hccs loc=Loc15159 taxid=10090 spec=Mus musculus chr=X ctg=NT_083046 str=(-) start=4043347 end=4044347 len=1001 tss=501 comm=holocytocrome c synthetase; (NM_008222/501/silver;)
3	rHCCS	rHCCS rn3_dna range=chrX:45670319-45671118 5'pad=0 3'pad=0 revComp=FALSE strand=? repeatMasking=non

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\$STAT
V\$SETSF
V\$NFKB
U\$NRF2
V\$SPIF

```

alignment position 1 . . . . . 1 1 . . . . . 2 1 . . . . . 3 1 . . . . . 4 1 . . . . .
P928091          1 t t a t t g c c t a c a t c c C T G A T G G A A G A A A A T G C T A A A T T T C T G T T G G A G G T
P928092          1 g - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
rHCCS            1 c c t a t - - - - - - - - - - C T G C T G G T T T A C C A T A C A C A A A T A C T A T A A A A G C T
                  * * * * *
alignment position 5 1 . . . . . 6 1 . . . . . 7 1 . . . . . 8 1 . . . . . 9 1 . . . . .
P928091          5 1 A A a - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -

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P928092      16 -----
rHCCS       41 TAc t t t a t a t a a t g t g a a a t a t a a t a c t t t t a t t a t a t g a a a g c T G A A A A
      * * * * *
alignment position 1 0 1 . . . . . 1 1 1 . . . . . 1 2 1 . . . . . 1 3 1 . . . . . 1 4 1 . . . . .
P928091     60 TACAGACATT c a a a a t c a c a t a c c c a g t t a a g a a g a a t t t a g c a g c c a g a
P928092     16 -----
rHCCS       91 TTCAACGATT g c a t g c a c t a - - - - -
      * * * * *
alignment position 1 5 1 . . . . . 1 6 1 . . . . . 1 7 1 . . . . . 1 8 1 . . . . . 1 9 1 . . . . .
P928091    110 a c a c t g t c t t g t t c a c t t t t g g a t c t c c a c c a c c g a a g t t a t g g g C A C C T
P928092     16 -----
rHCCS      111 ----- C A C T C
      * * * * *
alignment position 2 0 1 . . . . . 2 1 1 . . . . . 2 2 1 . . . . . 2 3 1 . . . . . 2 4 1 . . . . .
P928091    160 ACTAACGTTT C TTGAATCAT T GCTACAATT A a a a c c g a t a a g a t t t a - - -
P928092     16 -----
rHCCS      116 ACAACTGTTA C TAGAGT CCT T GAAAGGACT A c g c a c a g a a g t t t a a g t g c
      * * * * *
alignment position 2 5 1 . . . . . 2 6 1 . . . . . 2 7 1 . . . . . 2 8 1 . . . . . 2 9 1 . . . . .
P928091    207 -----
P928092     16 -----
rHCCS     166 g t g t a t t g a a t t a t a g c a c t t t a t t c c a t a a a t a a g c a c a a a t a t c a c t t
alignment position 3 0 1 . . . . . 3 1 1 . . . . . 3 2 1 . . . . . 3 3 1 . . . . . 3 4 1 . . . . .
P928091    207 -----
P928092     16 - - - - - AA A AAATACAAG T TGACCTTTC AA g AACCT AA GGAGAT GACT
rHCCS     216 g t t c g t c a AA A AAATACAAA T CGACCTTTC AA a AACCG AA GGAGAT GACT
      * * * * *
      * * * * *
      * * * * *
alignment position 3 5 1 . . . . . 3 6 1 . . . . . 3 7 1 . . . . . 3 8 1 . . . . . 3 9 1 . . . . .
P928091    207 - - - A A A A A A A A A A C A A A T T T A A A A - A C T C C T C C A A A G C - A C T C C T T C T G C C
P928092     58 T A G A A A A A C A C A G C G A C G T G c c t t A C C C C T C G G A A G C G A C A C C C c g c g g t
rHCCS     266 G T G A A A A A C A C A G C A A C T T G A C A - A C T C C T C C A A A G C G A C T C C C T C T G C T
      * * * * *
      * * * * *
      * * * * *
alignment position 4 0 1 . . . . . 4 1 1 . . . . . 4 2 1 . . . . . 4 3 1 . . . . . 4 4 1 . . . . .
P928091    252 G C A T A A a g c a t a c a t a g t a g a g c t c t t c a c t c t a g g g a a g c c t c t g g a g c
P928092    108 t c c c t a a c t t c t c a c c c t g a g c g g c t t a c c g g c c g g c c g G C G G A G T T a a -
rHCCS     315 A C C T A A g t c c a a a c c - - - - - G C G G A G T T t c t
      * * * * *
alignment position 4 5 1 . . . . . 4 6 1 . . . . . 4 7 1 . . . . . 4 8 1 . . . . . 4 9 1 . . . . .
P928091    302 a g a c a a c c t t c c c t g c c a c c g c c a c a t t T T G A A A A A G G C T C C T G G C C T G G
P928092    157 ----- - A A A A C A C C G C C T G G C C C G T
rHCCS     341 c a a a g a g a g c c g c a g a g - - - - - T T G A A A A C A C C G C C C A G C C C T T
      * * * * *
      * * * * *
      * * * * *
alignment position 5 0 1 . . . . . 5 1 1 . . . . . 5 2 1 . . . . . 5 3 1 . . . . . 5 4 1 . . . . .
P928091    352 A G G G G C G G G C C A G A A A G c g g c c c c c g c a - - - - -
P928092    176 A G G G G C G G A G A C G A G A G A A G g c t c g g g c g c c t a t a g g c c g c g g a g c g a g
rHCCS     380 A G A G G C G G A G A C G A G A G A A G g c g g - - - - -
    
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alignment position 551 . . . . . 561 . . . . . 571 . . . . . 581 . . . . . 591 . . . . .
P928091 381 - - - - -
P928092 226 a a g g g g t g g a c c g a c c c g c c c t t a a a c a c a c c g c c c c g c a c g t a g g g g c g
rHCCS 405 - - - - -

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alignment position 601 . . . . . 611 . . . . . 621 . . . . . 631 . . . . . 641 . . . . .
P928091 381 - - - - - G C A G T T A C A G G C C G G G C G A G G A G G G G - A C
P928092 276 g a g a c g g a g a g a a g g c t c G G G C G G C T C G A G G C C T C G G A G C G G A A G G g G T
rHCCS 405 - - - - - G G G C G G C T A T T G G C C T C G G A G C G G A A G G G - G T
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alignment position 651 . . . . . 661 . . . . . 671 . . . . . 681 . . . . . 691 . . . . .
P928091 410 G G A A C C C G C T C T C C G T G A T T G A C g g a a a a t a t t a C T C T T C A G C C C G c c t c
P928092 326 G G G A G C G A T C C G C C G A C C T G A C G A c c - G T T C C T C T C C T C A G C G C G a g c t
rHCCS 436 G G G A C C G A T C C T C C C T G A C T G A C A A g a g G T T C C T T T C C T C A G C t t g c g g t
*****
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alignment position 701 . . . . . 711 . . . . . 721 . . . . . 731 . . . . . 741 . . . . .
P928091 460 c c g c g t g - - - - - C C C G G A A G T C C C G C C T T C T A A A A A G G A A G T A G G G G T G
P928092 375 t g c c t c g t - - - - - G C T C C C G G A A G T C C C G C C T T C G G A A C A G G A A G T A A C G G C G
rHCCS 486 t t g t g t c a g g G C T C C C G G A A G T C C C G C C T T C G G A A A A G G A A G T A A C G G C t
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alignment position 751 . . . . . 761 . . . . . 771 . . . . . 781 . . . . . 791 . . . . .
P928091 504 C G T G A G A A C G C C G G C G G T G A C C G c a g c c a c A G C G G T G A C C G A G T G A G A G G
P928092 423 C C C G A G A A C G C C G G C T G T G A C C G g a - C G T T A G C G G T G A C C C C G C G T G A G G
rHCCS 536 c a C G A G A A A G C C G G C C G T G A C C c g g t C G T T A G C G G T G A C C C C G T G T G T G G
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alignment position 801 . . . . . 811 . . . . . 821 . . . . . 831 . . . . . 841 . . . . .
P928091 554 A A g g c g g c g g c g g c g g c g g c g t g a a g t c a c t g c t g c t c T G G G T T
P928092 472 A A A A A C C G C G G G T G C a g c c g a g c g a c - - - - - T T
rHCCS 586 A A A A G C G G C A G G T G C g g t t g g t g g c t g t g g a g - - - - - T G T G T T
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alignment position 851 . . . . . 861 . . . . . 871 . . . . . 881 . . . . . 891 . . . . .
P928091 604 C G G T T G G C G A C T G A A G G C G G T A C C G G C C T C C C G G a a c - - - - - A G C C C G
P928092 500 C G G C T G G G C G G T T C G A C G C G C T C G C G G C C G C G C C G c g c g g g a c a A G T C G G
rHCCS 624 C G G C T T G G C G G T T C A A C G C G G T C G C G G C C G C G C G - - - - -
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alignment position 901..... 911..... 921..... 931..... 941.....
P928091 648 GGGGAGGGCT T AGGTGCAGa a g g g c a g g c t GGCCGCGGCC GGT TTGGTCT
P928092 550 AGCGGAGACT T GGGGGCAG- - - - - GGCGGCGC CC GGGTTC GGCT
rHCCS 658 - - - - -
          *****
alignment position 951..... 961..... 971..... 981..... 991.....
P928091 698 GGGGACCACG - - - - -
P928092 589 GGAGCCGCGG g c t g c c g a g t g a g t t c g g c t g g g c a g g t t g a c g c g c t c g g
rHCCS 658 - - - - -
          *****
alignment position 1001..... 1011..... 1021..... 1031..... 1041.....
P928091 708 - - - - -
P928092 639 g g c c g c g c g g c g c g GGACAG T CGGC GAGGT GACT TGGG GA CAGg AC GGCG
rHCCS 658 - - - - - GGACGG T TGGAGAGGA GACT CGGG GA CAG- AC GGTG
          *****
          *****
alignment position 1051..... 1061..... 1071..... 1081..... 1091.....
P928091 708 - - - - - G GCTGGAGCAG GTGg g c a a g c g c c g g g a c g g t - - - - -
P928092 689 TCCGGGTCCG GCTGGAGCCG GTGCACTGTG CAGAc c g - - - - CGGT GCCG
rHCCS 693 TCCAGGTTAG GCTGGAGTCT GTGACCTGTG GACAc c t c g g a c CGGT AGAG
          *****
          *****
alignment position 1101..... 1111..... 1121..... 1131..... 1141.....
P928091 740 - - - - - G T GGGGAAGAC ACTTGGCa g c t t - - - - -
P928092 734 GTGGGACGCG C ATAGACGGg a a GGCAACAC TGGTGGCT TC CTGCCC TTCG
rHCCS 743 GTGGGCGCGC C TTAGACAGG T GGT AAGAT TGTGGCT CC CTGCCC TTTG
          *****
          *****
alignment position 1151..... 1161..... 1171..... 1181..... 1191.....
P928091 763 - - - - - CTCGACCTC T GGTGTCCCT TCGTTTCT TC GAATTC CTAT
P928092 784 CCGCTc c t t g c CTCCCGTTT T GGTGACTTT TTTT TTTT TA ACCTTC CTAT
rHCCS 793 CCTCTt g t - - - - -
          *****
          *****
alignment position 1201..... 1211..... 1221..... 1231..... 1241.....
P928091 802 Tc a t g c g c c g c a - - - - CCC T TCTCGGACC CCCAGCCC CT CGCTAa g g c t
P928092 834 Tt t c c c t g a g g c g c c t g CCC T ACTGGGAAC ACGGGTTC GA GGCTA- - - -
rHCCS 801 - - - - -
          *****
alignment position 1251..... 1261..... 1271..... 1281..... 1291.....
P928091 847 c t g g g g a t g g g g g t c a a g t c t a g GCTCAAT GGACCTCC CC TCCTCC ACCC
P928092 879 - - - - - GTT CAGT GTATTTTC CC TTGGAC CCCA
rHCCS 801 - - - - -
          *****
alignment position 1301..... 1311..... 1321..... 1331..... 1341.....
P928091 897 GGGTCAACCAC T CCt c g g a a t c c t c g c c c c a c t c c c g c c t c a g g c c t g t a
P928092 906 CCATCAAGAC T ACa c c c g t c t t c a c - - - - -
rHCCS 801 - - - - -
          *****
alignment position 1351..... 1361..... 1371..... 1381..... 1391.....
P928091 947 c c t c c t g g c t g t GACGTGGT T t c t c a g e g a c t g c c t c a c c t e a g t c c c a a
P928092 931 - - - - - GACGTGGT T g c a t c t t a c a a g t t t c c a g a c t c t g g c - -
rHCCS 801 - - - - -
          *****
alignment position 1401..... 1411..... 1421..... 1431..... 1441.....

```

```

P928091 997 a a t c c t c a c t   g c c t t a g a t a c a t A C G T G C C C C C A G A G G T T G G C C T G G G T T
P928092 967 - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
rHCCS   801 - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
                                     * * * * *
alignment position 1 4 5 1 . . . . . 1 4 6 1 . . .
P928091 1047 TCACAGTAt t t c c c t a a
P928092 994 TCAAGGTA- - - - - - - - - - -
rHCCS   801 - - - - - - - - - - - - - - - -
                                     * * * * *
    
```

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.

	P928092 (1001 bp)	rHCCS (800 bp)
P928091 (1063 bp)	0.260 26 %	0.282 33 %
P928092 (1001 bp)		<u>1.000</u> <u>51 %</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

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

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

DiAlign professional TF Release 3.1 December 2004

Tue May 3 21:44:27 2005

Solution parameters:

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

Aligned Sequences:

No.	Sequence Name	Sequence Description	Length
1	P881957	sym=SURF1 loc=Loc6834 taxid=9606 spec=Homo sapiens chr=9 ctg=NT_035014 str=(-) start=3000201 end=3000801 len=601 tss=501 comm=surfeit 1; (NM_003172/501/silver;)	601 bp
2	P881959	sym=Surf1 loc=Loc20930 taxid=10090 spec=Mus musculus chr=2 ctg=NT_039206 str=(-) start=4344877 end=4345492 len=616 tss=503,516 comm=surfeit gene 1; (AK002469/503/gold;NM_013677/516/bronze;)	616 bp
3	P881961	sym=Surf1 loc=Loc64463 taxid=10116 spec=Rattus norvegicus chr=3 ctg=NW_047651 str=(-) start=5813658 end=5814275 len=618 tss=501 comm=Surfeit 1; (NM_172068/501/bronze;)	618 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\$EGRF V\$OAZF V\$SETF U\$NRF2

```

alignment position 1 . . . . . 1 1 . . . . . 2 1 . . . . . 3 1 . . . . . 4 1 . . . . .
P881957          1 t - - - - -
P881959          1 - - - - - TGGG CACAAT GTGT
P881961          1 g c a t t g g c c g g c c a t c t a c g t a c c g a t t c t t t g t g c TGGG CACAAT GTGT
    
```



```
alignment position 51 . . . . . 61 . . . . . 71 . . . . . 81 . . . . . 91 . . . . .
P881957 2 - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
P881959 15 GGC TCGAAA G CT GCGTAA TC GAAGt t AG AG AAGGAACTT G ACAGCCGTT G
P881961 51 GGC TCGAAC G CT GTGTAAT C GAAGg c AG AG AAGGCACTT G AGAGCCGCT G
*****
*****
*****
*****
```

```
alignment position 101 . . . . . 111 . . . . . 121 . . . . . 131 . . . . . 141 . . . . .
P881957 2 - - - - - TTG CC GCGGGT GT A GACC TGG AG CTCCGGCAGG CGGCAGGGC A
P881959 65 GTACTTCTT G CC GCGGGT GT ATTCC TGG AG CTCGGGCAGA CGGCAGGGC A
P881961 101 GTACTTCTT G CC GCTAGT GT AGACT TGG AG GTCCGGCAGA CGGCAGGGAA
*****
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*****
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*****
*****
```

```
alignment position 151 . . . . . 161 . . . . . 171 . . . . . 181 . . . . . 191 . . . . .
P881957 45 GCT CGTGACC TGTCA GGA TG C ACCT CAC CT GCGGACGc g t g g g c g g g c a g
P881959 115 GCT CATGGCC AGTTA GGG AG C AGC G AAC CT GCGGATGAGC ATCTG- - - - -
P881961 151 GCT CATGACC GGTTA GCG AG C AGC GTAC CT GTGGATGAAC CGCTG- - - - -
*****
*****
*****
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*****
*****
*****
*****
```

```
alignment position 201 . . . . . 211 . . . . . 221 . . . . . 231 . . . . . 241 . . . . .
P881957 95 g a c GTCAGGA GGg c c a g g g c t c c g c t c c c t g g t g c c c c t c c t g c c g e g e
P881959 160 - - - GTCAGAA GGTGGt TCTT GCCAGCTC CG - - - - - - - - - - - - - - - - - - - - - - - -
P881961 196 - - - GTCAGAA GGTGGa TCTT GCCAGCTC CG - - - - - - - - - - - - - - - - - - - - - - - -
*****
*****
*****
*****
```

```
alignment position 251 . . . . . 261 . . . . . 271 . . . . . 281 . . . . . 291 . . . . .
P881957 145 CCCCTTCCCT ct c c t c c c c t g a t c c e g c e g c g c c c t c t c c c t g c c c t c c
P881959 187 CCCCTTCCCT GCA - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
P881961 223 CCCCTTCCCT GCA - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
*****
*****
*****
*****
```

```
alignment position 301 . . . . . 311 . . . . . 321 . . . . . 331 . . . . . 341 . . . . .
P881957 195 c c t c t c t c c t g e t e t c c c c t c t c c c e t e t c c CTGCCCTC TCCTCT- - - -
P881959 200 - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
P881961 236 - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
*****
*****
*****
*****
```

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

```

P881957 241 - - - - - C CC CTGCCTCC c t c a g c c c t
P881959 218 c g c t t t c c a g g c a c a a t a c t c c c g g g t C CC CCTCCTTCT GGCCAc t g t C
P881961 250 - - - - - C CC CTTCCTTTC GGCCA- - - - C
          * * * * *
          * * * * *

```

```

alignment position 4 0 1 . . . . . 4 1 1 . . . . . 4 2 1 . . . . . 4 3 1 . . . . . 4 4 1 . . . . .
P881957 264 c a t c c c a a C T G C G C C C T T C T C C G C C A C T C C G T T C C C C T C C G C G C T G c g a
P881959 268 G G T C - - - C T C C G A G G T T C C G C T C C T C C C A G A T C C C G T T C C T T C C T G G C C
P881961 269 G G T C - - - C T C C G A G G T C C C A A T C C T T C C A G G T C C C G T T C C T T C C T G G C C
          * * * * *
          * * * * *
          * * * * *
          * * * * *
          * * * * *

```

```

alignment position 4 5 1 . . . . . 4 6 1 . . . . . 4 7 1 . . . . . 4 8 1 . . . . . 4 9 1 . . . . .
P881957 314 - - - - - A C C T T G C G G G C G T C C G T C T G G
P881959 314 C T A C T C T T C C g - G T C A C G G T T C T C T T C C G A C C T T G C G G G T G T T G G G C A G T
P881961 315 C T A C T T T T C C c c G T C A C G G T T C T C T T T C G A C C T T G T G G G T G T T G G G C A G C
          * * * * *
          * * * * *
          * * * * *
          * * * * *
          * * * * *
          * * * * *
          * * * * *
          * * * * *
          * * * * *
          * * * * *

```

```

alignment position 5 0 1 . . . . . 5 1 1 . . . . . 5 2 1 . . . . . 5 3 1 . . . . . 5 4 1 . . . . .
P881957 335 A G C C G C A G G C T C G G G T G C T c c G C G A G A A A C G C C C G C A C G T C G C C C G G C A A
P881959 363 A G T C T C A A G C T G G G G T G C T G G C G C A A G A A T G C A A G C A C A T C A G A G G G T G G
P881961 365 A G T C T C A A G C T G G G G T G C T G A C G C A G A A A T G C A A G C A C A T C A G A A G G T G G
          * * * * *
          * * * * *
          * * * * *
          * * * * *
          * * * * *
          * * * * *
          * * * * *
          * * * * *
          * * * * *
          * * * * *

```

```

alignment position 5 5 1 . . . . . 5 6 1 . . . . . 5 7 1 . . . . . 5 8 1 . . . . . 5 9 1 . . . . .
P881957 385 C T C G C T C A T G g c c g a c g c g c c c g C G G A G C A G C C C G G C G G A A G C C G C T C G C
P881959 413 T T C G T C C A T G A T - - - - - - - - C G G A G A T G C C C A T C T G A C G C C G C A G C C
P881961 415 T T C G T C C A T G A T - - - - - - - - C G G A G a c g - C C A T C T G A C G C C A C A G C C
          * * * * *
          * * * * *
          * * * * *
          * * * * *
          * * * * *
          * * * * *
          * * * * *
          * * * * *
          * * * * *
          * * * * *

```

```

alignment position 6 0 1 . . . . . 6 1 1 . . . . . 6 2 1 . . . . . 6 3 1 . . . . . 6 4 1 . . . . .
P881957 435 A G A A C C T G G A G C C G G G G G C G G g g g c t c t g g g c g g g a c t c a g c g g c g C C C C G
P881959 452 A C C A C G T G A G A C A G A G C G C c G T - - - - - - - - - - - - - - - - - - - - - - C C C G G
P881961 453 A C C A C G T G A G G C G G A G C G C G G T - - - - - - - - - - - - - - - - - - - - - - C C C G G
          * * * * *
          * * * * *
          * * * * *
          * * * * *
          * * * * *
          * * * * *
          * * * * *
          * * * * *
          * * * * *
          * * * * *

```

```

alignment position 6 5 1 . . . . . 6 6 1 . . . . . 6 7 1 . . . . . 6 8 1 . . . . . 6 9 1 . . . . .
P881957 485 G A T G C A G A T G C C T C C T G C G T C C C G G A A G C G C C C G c g g g g c c G G G T G C G A T
P881959 479 A A G G A A G C A G A T T T C T C G G T C C C G G A A G T G C T C A A A G A T - - G G T G C T G T
P881961 480 A A G G A A G C A G G T T T C T C C G C C C C G G A A G T G t T C A A A G A T - - G G T G C T G T
          * * * * *
          * * * * *
          * * * * *
          * * * * *
          * * * * *
          * * * * *
          * * * * *
          * * * * *
          * * * * *
          * * * * *

```

```

alignment position 7 0 1 . . . . . 7 1 1 . . . . . 7 2 1 . . . . . 7 3 1 . . . . . 7 4 1 . . . . .
P881957      535 GGC GGC GGT G GCT GC GTT GC AGCT G GGG CT Gc g g c - - - - - GG
P881959      527 GAT GGC TTT G GCT GT GCT GC C GCGA CGG AT GACGCGGTGG TCGCAATGGG
P881961      528 AAT GGCTTT G ACT GT CCT GC g a a g t CGG AT AACGCGATGG CCGCAGTGGG
          * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * *
          * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * *
          * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * *
          * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * *

alignment position 7 5 1 . . . . . 7 6 1 . . . . . 7 7 1 . . . . . 7 8 1 . . . . . 7 9 1
P881957      573 CGGGGCTGGG ACGGGTGAGC GCCGGGTg c - - - - - - - - -
P881959      577 CCT ACGCGGG ACGGGTAA GC GGGGGTTC AG AGAGGATCCT -
P881961      578 CCT GCGCGGG GC CGGTAA GC GGGGGTTC AG AGAGGATCCT 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.

	P881959 (616 bp)	P881961 (618 bp)
P881957 (601 bp)	0.181 41 %	0.155 40 %
P881959 (616 bp)		<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"/>
Extract aligned sequences	

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