This Supplementary Material shows the Core Promoters of Complex I 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 additional file 3 (in the “Matrix Family Library” Excell sheet).

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GEMS Launcher Task: *DiAlign TF*: Multiple alignment plus TF sites
working on NDUFA1_HMR.seq (3 seq.)

[Alignment] [Pairwise similarities]

DiAlign professional TF Release 3.1 December 2004 **Mon Mar 14 20:25:14 2005**

Solution parameters:

Sequence file:	NDUFA1_HMR.seq (3 seq.)
Type of sequences:	nucleotide sequences
Threshold T:	0.00
'*' signs below alignment denote:	diagonal similarity (max. similarity is represented by 10 '*' signs)
Alignment output:	complete alignment is shown # nucleic acids per line: 50
TF output:	common TF matches located in aligned regions (common to 3 (100.0 %) sequences)
Family matches:	yes
MatInspector library:	Matrix Family Library Version 5.0 (February 2005)
Selected groups (core/matrix sim):	• ALL user_defined.lib (0.75/Optimized) • ALL vertebrates.lib (0.75/Optimized)

Aligned Sequences:

No.	Sequence Name	Sequence Description	Length
1	P914042	P914042 sym=NDUFA1|loc=Loc4694|taxid=9606|spec=Homo sapiens|chr=X|ctg=NT_011786|str=(+)|start=3272907|end=3273632|len=726|tss=538|comm=NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 1, 7.5kDa; (NM_004541/538/bronze;)	726 bp
2	P914043	P914043 sym=Ndufa1|loc=Loc54405|taxid=10090|spec=Mus musculus|chr=X|ctg=NT_039702|str=(-)|start=4319612|end=4320330|len=719|tss=599,619|comm=NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 1; (AK007840/619/gold;NM_019443/599/bronze;)	719 bp
3	P914044	P914044 sym=na|loc=Loc363441|taxid=10116|spec=Rattus norvegicus|chr=X|ctg=NW_048033|str=(+)|start=100444|end=101164|len=721|tss=501|comm=similar to NADH dehydrogenase; (XM_343760/501/bronze;)	721 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$VMYB V$SMAD V$FKHD V$EBOX V$HESF V$MYT1 V$PAX2 V$CREB V$ZBPF V$SP1F V$GLIF V$EGRF V$HAML

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alignment position 1 . . . . . . . . .  1 1 . . . . . . . .  2 1 . . . . . . . .  3 1 . . . . . . . .  4 1 . . . . . . . .
P914042          1 t c t - - - T T C T  C T G T G T C C A G  C T C A T A G A C A  G C T G T C G C T C  C C A T A T C C T C
P914043          1 - - - - - - - T C T  C A G T G T C C A G  T T C G T A G A C G  G C G G T C G C C C  C C A T A T C C T C
P914044          1 c g t t c c T T C T  C A G T G T C C A G  T T C A T A G A C A  G C G G T C G C C C  C C A T A T C t T C
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alignment position      51........ 61........ 71........ 81........ 91........
P914042              48 TGGTCCCACG GGTTTCGCCG AACGGGTGGA TTTATAAACC ACGCCGAGAC
P914043              44 GGGCCCCACG GGTTTTGCCG AACGGGTAGA CTTGTAGACG ACGCCGAGAC
P914044              51 GGGCCCTACG GGTTTTGCTG AACGGGTAGA CTTGTAGgtC ACGCCAAGAC
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alignment position      101....... 111....... 121....... 131....... 141.......
P914042              98 TCTCGGGCTC ATTTTCctct tccTCTTCGC TGCTCAAGTC GCCGTAAGCC
P914043              94 CCTCCGGTTC ATTCTCG--- ---TCCTCGC TACTCAAGCC GCCATAGGTT
P914044             101 CCTCAGGTTC ATTCTCA--- ---TCCTCAC TACTCAAACC GCCGTAGTTT
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alignment position      151....... 161....... 171....... 181....... 191.......
P914042             148 GCCTTCTGTT TACCACTGTC ACGGGTCTTC TGTATCATTG GATTGTGGGT
P914043             138 GCCTTCTGTT TAGCGCTGCC ACGCGTCTTC TGGATCATCG GATTGTGGGT
P914044             145 GtCTTCTGTT TAGCGCTGCC ACGCGTCTTC TGTATCATCG GGTTGTGGGT
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alignment position      201....... 211....... 221....... 231....... 241.......
P914042             198 CACCCGCTTC TTTTCCGGTC GAACCACAGT GCAGCCTTCG TCGCTACTGC
P914043             188 CGCTTGCTTC TTCTCCGGGC GGACCACAGA GCTGCCTTCA TCACTGCTGC
P914044             195 AGCCTGCTTC TTCTCGGGGC GGACCACAGc GCTGCCTTCG TCACTGCTGC
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alignment position      251....... 261....... 271....... 281....... 291.......
P914042             248 TGCCGCTTTC TCCGGGCTCT GGGTCGCAGG CCGGGCGCTT TCTGCGTCCA
P914043             238 TGCAGCTGTC CCCGGAGCCT GCATCACAGA GCCGGCGCTT TCGGCGGCCC
P914044             245 TGCCGCTGTC CCCGGACCCc tCATCACAGA GCGGGCGCTT TCGGCGGCCA
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alignment position 301....... 311....... 321....... 331....... 341.......
P914042        298 GCAGCCCCTT TCCGCCCAGG CTTTTTGAAA AGGAAGGTGC ACACCTGAtc
P914043        288 GCCGCTCCTT TCCGCCCAGG CTTTTTGAAG AGGAACGTGC ACACCTGACG
P914044        295 GCCGt TCCTT TCCGGCCAGG CTTTTTGAAG AGAAAAGTGC ACACCTt ACC
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alignment position 351....... 361....... 371....... 381....... 391.......
P914042        348 caccgccTTT CCTGGAGAAA GCTGCTCTGC CA-TTttAGA GTCCTGAGCT
P914043        338 GGTAGAATTC CCGGGAGAAA GTTGCTCCGC CAtTTAGAGA TCCCCAAGTT
P914044        345 GGTAGAATTC CCTGGAGAAA GTTGCTCCGC CA-TTAGAGA TCCCCAAGTT
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alignment position 401....... 411....... 421....... 431....... 441.......
P914042        397 CCGAAACAGC CGTGGCTGCC TGGgttgcac ttgGCCCCTG CACGTCACTC
P914043        388 CTGAAACTGC CGCGACGTCC GGGACC---- ---GCTTCGC GTCGTCACAC
P914044        394 CTGAAACTGC TGTGACCTAC GGGACC---- ---GCTTCCG GTCGTCACAC
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alignment position 451....... 461....... 471....... 481....... 491.......
P914042        447 CACGTTGCGC GCTCCGCCGg gagtcgaagc ---------- ----------
P914043        431 TCCGTGGTGG TCTCTGATGC AGCGGATCAG ATAGGAGGag taggacgaca
P914044        437 CTCTTGGTGG TCTCTGCTGC AGTGAATCGG ACAAGAGGgg gttaaa----
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alignment position 501....... 511....... 521....... 531....... 541.......
P914042        477 -AAAAGACAC TGACGGAAGA GGACTGCGAG AGCCCGAgCG CCCGTCTCTC
P914043        481 gAAAGAATCC TGTCCGGGAA CGCTTGCTGG ACCGCGAACG CCAGTCACTT
P914044        483 -AAAATACAC CGCCGGGGAA TGCTTGCCAG ACCGCGAACG CCAGTTACTT
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alignment position 551....... 561....... 571....... 581....... 591.......
P914042        526 TTGTGCCCTA GCAGATTCCG TCGCTTCt-- -TCCGGAGCC GTACGTGGCA
P914043        531 TTGGGCCCCC ACAGCCACCG TCGCTTCCTC CTCCGGAGCC GTACGGGGCA
P914044        532 TTGGGCCCTC GCAGCCGCCG TCGCTTCCTA CT---GAGCG GTACGGGGCA
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alignment position 601....... 611....... 621....... 631....... 641.......
P914042        573 CCGCCCCGCT CGCGGGCGGC CGcggggctt gctggGAAGA GAGGCGAAGC
P914043        581 CCGCCCCTCC CGCGTGCTGC CG-------- -----GAAGA GAGGTAAAGC
P914044        579 CCGCCCCTCT CGCGTGCTGC CG-------- -----GAAGA GCGGTGAAGC
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alignment position 651....... 661....... 671....... 681....... 691.......
P914042        623 CA--GGTCAC CTttcaagga cccagaagta gggttttggc ctag----GT
P914043        618 CG--GGTCAC CTCTGAGGAG CCGGT----- -GACGGGTTG GCGTGCGAGT
P914044        616 CcccGGTCAC CTCTGAGGAG CCGGTaacgg tGACGGGTTG GAGTGTGAGT
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alignment position 701....... 711....... 721....... 731....... 741.......
P914042        667 AACGGGGCAG AGATGTGGTT CGAGATTCTC CCcGGACTCT CCGTCATGGG
P914043        660 AACGGTGCGG AGATGTGGTT CGAGATTCTC CCTGGCCTCG CCATTATGGG
P914044        666 AACGGTGAGG AGATGTGGTT CGAGATTCTC CCTGGCCTCG CCATTATGGG
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alignment position 751.......
P914042        717 CGTGTGCTTG
P914043        710 GGTGTGCTTG
P914044        716 GGTGTG----
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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.

	P914043 (719 bp)	**P914044 (721 bp)**
P914042 (726 bp)	0.526 68 %	0.467 67 %

P914043 **(719 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: ☐ to: ☐
Output file	dialign.seq

Extract aligned sequences

For questions or bug reports, please contact support@genomatix.de

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GEMS Launcher 4.1.0

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GEMS Launcher Task: *DiAlign TF*: Multiple alignment plus TF sites
working on ndufa2 (3 seq.)

[Alignment] [Pairwise similarities]

DiAlign professional TF Release 3.1.1 September 2005 **Fri Oct 20 20:30:09 2006**

Solution parameters:

Sequence file:	ndufa2 (3 seq.)
Type of sequences:	nucleotide sequences
Threshold T:	0.00
'*' signs below alignment denote:	diagonal similarity (max. similarity is represented by 10 '*' signs)
Alignment output:	complete alignment is shown # nucleic acids per line: 50
TF output:	common TF matches located in aligned regions (common to 3 (100.0 %) sequences)
Family matches:	yes
MatInspector library:	Matrix Family Library Version 6.1 (June 2006)
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	Lengt
1	GXP_123839	GXP_123839 loc=GXL_103357|sym=NDUFA2|geneid=4695|acc=GXP_123839|taxid=9606|spec=Homo sapiens|chr=5|ctg=NC_000005|str=(-)|start=140006924|end=140007924|len=1001|tss=501|descr=NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 2, 8kDa|comm=GXT_2834145/NM_002488/871/bronze	10
2	GXP_83080	GXP_83080 loc=GXL_69065|sym=Ndufa2|geneid=17991|acc=GXP_83080|taxid=10090|spec=Mus musculus|chr=18|ctg=NC_000084|str=(-)|start=36869998|end=36871022|len=1025|tss=501,525|descr=NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 2|comm=GXT_13006391/AK018732/570/gold;GXT_13017074/AK003608/546/gold;GXT_13131667/NM_010885/546/bronze	10
3	GXP_309531	GXP_309531 loc=GXL_260322|sym=Ndufa2_predicted|geneid=291660|acc=GXP_309531|taxid=10116|spec=Rattus norvegicus|chr=18|ctg=NC_005117|str=(-)|start=29443334|end=29444334|len=1001|tss=501|descr=NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 2 (predicted)|comm=GXT_21781541/XM_214570/566/bronze	10

Alignment (DiAlign format):

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

V$GATA V$STAF V$ZBPF V$SP1F V$YY1F V$PARF V$ZNFP V$CLOX V$HEAT **TSS**

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alignment position                       1.........  11........  21........  31........  41........
GXP_123839 (NDUFA2)                   1  gcccatcatc  acttggagta  gg--------  -------AGT  GAGGACTGGG
GXP_83080 (Ndufa2)                    1  aaccacgtcc  ctaaaagaga  ggcacaagcc  atggtttACT  AAGGAAGGGA
GXP_309531 (Ndufa2_predicted)         1  ----------  ----------  ----------  ----------  ----------
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alignment position                       51........  61........  71........  81........  91........
GXP_123839 (NDUFA2)                  36  GACGGAGTTT  Ggagctg---  ----------  ----------  ----------
GXP_83080 (Ndufa2)                   51  TAGGGAGGTA  GAGCTGCctc  aaaaaaTTCA  AAACGCCGGT  CCTCCACAAA
GXP_309531 (Ndufa2_predicted)         1  ----GAGGTG  GGGCTGC---  ------TTCA  AAACGCCGGT  CCTCAACAAA
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alignment position           101....... 111....... 121....... 131....... 141.......
GXP_123839 (NDUFA2)       53 ---------- ---------- -------TCG GCCTCACTTA GGACCCTGTG
GXP_83080 (Ndufa2)       101 aGAAATGAAA CTTGAGGGCA GCTCAGCTGG GCCTCTCCTA AGGACCAATG
GXP_309531                38 -GAAACAAAA TTTGAGGGCA GTTCAGCAGG GCCTCTCCTA AAGGCCAATG
(Ndufa2_predicted)
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alignment position           151....... 161....... 171....... 181....... 191.......
GXP_123839 (NDUFA2)       76 GCTTCTCCGG GCTCAagcgt cacacataca tacatacaca cacacacaca
GXP_83080 (Ndufa2)       151 GTTCGCGCGG CTCCA----- ---------- ---------- ----------
GXP_309531                87 GTTCGCGCGC CTCCA----- ---------- ---------- ----------
(Ndufa2_predicted)
                             ********** *****
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alignment position           201....... 211....... 221....... 231....... 241.......
GXP_123839 (NDUFA2)      126 cacacacaca cACACACACA C---ACCCGG CTTAAGCTCA GAAgctacaa
GXP_83080 (Ndufa2)       166 ---------- -TCAGTCACA CgacACCTTG CTTAAATTCA GCAAACTCGA
GXP_309531               102 ---------- -ACAGTCACA C---AACTGG CTTAAATTCA GCAAACTCAA
(Ndufa2_predicted)
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alignment position           251....... 261....... 271....... 281....... 291.......
GXP_123839 (NDUFA2)      173 taatGCGCCA AGTGCCCCAA GTGCCATGGG GAAGAAATAA CGGatggcct
GXP_83080 (Ndufa2)       205 C---GAGCCT AGCGTCTCTA GTCCCGCGGG CAGGAAAGAG TGGTcGACTC
GXP_309531               138 C---AAGCCT AGTGTCTCTA GTCCCGCGGG CAAGAAAGAG TGGTtGACTC
(Ndufa2_predicted)
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alignment position           301....... 311....... 321....... 331....... 341.......
GXP_123839 (NDUFA2)      223 GAGCCTTACT ATCTCGCTCC GGCATTTTGt tatcgttctt tcgctgtcaC
GXP_83080 (Ndufa2)       252 GAGCCTTACT ATCTCGTTCT GGCATTTTGG CAGCGGCCTC TCAACG---T
GXP_309531               185 TAGCCTTACT ATCTCGCTCC GGCATTTcGG CCGCGGTCTC TCAGCG---C
(Ndufa2_predicted)
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alignment position           351....... 361....... 371....... 381....... 391.......
GXP_123839 (NDUFA2)      273 CAACAATCGa gtctccaa-- CAG--CAACA CCGCAGCGAC AAGCTCTTTC
GXP_83080 (Ndufa2)       299 CCGCAATCGC GAAATGTCCc cctaaCAAGA CAGCGGCGAC AAACTTTTAT
GXP_309531               232 CAGCAATCGC GAAATATCCt CAA--CAAAA CAGCGGCGAC AAACTTTTAT
(Ndufa2_predicted)
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alignment position           401....... 411....... 421....... 431....... 441.......
GXP_123839 (NDUFA2)      319 CCACAGTGCA CCtcagaatc aacCCACACT GCTTTGCGTT CGCAGCCTTT
GXP_83080 (Ndufa2)       349 CCACAATGCA CCACGAAAac ctgt------ ---------- ----------
GXP_309531               280 CCACAATGCA CCACGAAAgc ctgCGACAGA GCTTTGCCTT CCGTGCCTTC
(Ndufa2_predicted)
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alignment position                451....... 461....... 471....... 481....... 491.......
GXP_123839 (NDUFA2)           369 CCGCTTCCTg tttttccctc cgaccaaccc cgagcgcaaa gaaattgacc
GXP_83080 (Ndufa2)            373 ---CTTCCTT CGCGTCACCA Cacgatgcct cctg------ ----------
GXP_309531 (Ndufa2_predicted) 330 CGGCTTCCTT CGCGTCACTA Ccattctgcc cctataaagg cctcatttaa
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alignment position                501....... 511....... 521....... 531....... 541.......
GXP_123839 (NDUFA2)           419 tcgcagcggt cctacaatac ttttataTCA TTGGCCAAGC TTTACCCCGC
GXP_83080 (Ndufa2)            404 ---------- ---------- -------TCA TTGGCTAAGA TTTATCCCGC
GXP_309531 (Ndufa2_predicted) 380 tt-------- ---------- ---------- ---GCTAAGA TTTGTCCCGC
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alignment position                551....... 561....... 571....... 581....... 591.......
GXP_123839 (NDUFA2)           469 CCCT--GCC- ---TCATGCA GCCTATGGGC TAGGCTTTAG GGTCCGCGGT
GXP_83080 (Ndufa2)            427 CCCTttCCCT GCGTCATCCA ATCGACGGCG AAGACTGGAG GGCCCGCTAT
GXP_309531 (Ndufa2_predicted) 399 CCCT--CCCC GCGTCATCCA ATCGATGACG GAGACTAGAG GGT-CGCTAT
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alignment position                601....... 611....... 621....... 631....... 641.......
GXP_123839 (NDUFA2)           513 TGGTCAGAcc ggagcacttg gcCTGAAGAC CTGGAATTGG CGACTTCGAT
GXP_83080 (Ndufa2)            477 TGGTCCGATT GAGGG----- ---TGAAAGG TCGTGATTGG GCGCTCCTTT
GXP_309531 (Ndufa2_predicted) 446 TGGTCCGATT GAGGGag--- --CTGAAAGG CCGTGATTGG GTGCTCCTTT
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                                  ********                 ******* ********** **********
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alignment position                651....... 661....... 671....... 681....... 691.......
GXP_123839 (NDUFA2)           563 ATTAACAAGG ATGGCGGCGG CCGCAGCAAG TCGAGGAGTC GGGGCAAAGC
GXP_83080 (Ndufa2)            519 GCTAACAAAG ATGGCGGCTG CCGCTGCTAG CCGAGCGGTC GGCGCAAAGC
GXP_309531 (Ndufa2_predicted) 491 GCTAGCAAAG ATG------G CGGCCGCAAG CCGAGTAGTC GGTGCAAAGC
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alignment position                701....... 711....... 721....... 731....... 741.......
GXP_123839 (NDUFA2)           613 TGGGCCTGCG TGAGATTCGC ATCCACTTAT GTCAGCGCTC GCCCGGCAGC
GXP_83080 (Ndufa2)            569 TGGGGTTGCG TGAGATTCGC GTTCACTTAT GCCAGCGTTC CCCAGGCAGC
GXP_309531 (Ndufa2_predicted) 535 AGGTACTGCG TGAGATTCGC ATTCACTTAT GCCAGCGTTC CCCAGGCAGC
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alignment position                751....... 761....... 771....... 781....... 791.......
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GXP_123839 (NDUFA2)  663 CAGGGCGTCA GGTGAGGCGC -GGCGTGGTG AGGCGGGCGG GCTTCGGGAc
GXP_83080 (Ndufa2)   619 CAGGGTGTGA GGTGAGGCGg aAGCGTGGGA AGGCGAGTGA GCTTCGGAA-
GXP_309531           585 CAGGGTGTGA GGTGAGTCGT -AGCGTGGGA AGGCGAGTGA GCTTCGGAA-
(Ndufa2_predicted)
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alignment position       801....... 811....... 821....... 831....... 841.......
GXP_123839 (NDUFA2)  712 GCCAGGGTCA CGACCTCGAC CTCCCTGAAG TTGAGGGaag cccccgccca
GXP_83080 (Ndufa2)   668 GCTGGAGCTA TGACCTTGAC CTCCGGGCAG GGGCGGGGGc ----------
GXP_309531           633 GgTGGAGCTC TGACCTTGAC CTCCGGa--- -GGCGGGGGg tgtcagggtc
(Ndufa2_predicted)
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alignment position       851....... 861....... 871....... 881....... 891.......
GXP_123839 (NDUFA2)  762 cagcacgc-- ---------- -GCGGCGCTC TCTCCg---- -------GCC
GXP_83080 (Ndufa2)   708 --TGTGTACC TTTGCCCGCT AGCGGCAGTC TCTCtcttcc ccccCCCCCC
GXP_309531           679 agTGTGTACC TTTGCCCGCT AGCGACAGTC TCTCCt---- ----CCCGCC
(Ndufa2_predicted)
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alignment position       901....... 911....... 921....... 931....... 941.......
GXP_123839 (NDUFA2)  788 CCGCAGGGAC TTCATTGAGA AACGCTACGT GGAGCTGAAG AAGGCGAATC
GXP_83080 (Ndufa2)   756 CCGCAGGGAT TTCATCGTGC AACGGTACGT GGAGCTGAAG AAGGCGCACC
GXP_309531           721 CCGCAGAGAT TTCATCCAGC AACGGTACGT GGAGCTGAAG AAGGCGCACC
(Ndufa2_predicted)
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alignment position       951....... 961....... 971....... 981....... 991.......
GXP_123839 (NDUFA2)  838 CCGACCTACC CATCCTAATC CGCGAATGCT CCGATGTGCA GCCCAAGCTC
GXP_83080 (Ndufa2)   806 CCAACCTGCC CATTCTGATC CGCGAATGCT CGGAGGTGCA GCCCAAGCTT
GXP_309531           771 CCGACCTGCC CATTCTAATC CGCGAATGTT CAGAGGTGCA GCCCAAGCTC
(Ndufa2_predicted)
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alignment position       1001...... 1011...... 1021...... 1031...... 1041......
GXP_123839 (NDUFA2)  888 TGGGCCCGCT ACGGTGAGTg cgGGACGCCA GGGGTCTGGG GCTCCGGTAG
GXP_83080 (Ndufa2)   856 TGGGCCCGCT ATGGTGAGTA CTGGTCGCCG GAGGTCAGGG GCCCGGGTTG
GXP_309531           821 TGGGCCCGTT ATGGTGAGTA CTGGTCGttG GAGGTCAGGG GCCCGGGTTG
(Ndufa2_predicted)
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alignment position                 1051...... 1061...... 1071...... 1081...... 1091......
GXP_123839 (NDUFA2)             938 GGGAACAAGG GTTTGAGAAG -AGAAGGGAC CGCCCAAGGT CGTGCAGAAA
GXP_83080 (Ndufa2)              906 CAGAATACGG GATGGAGAGA -TGAAGGGGC CTCCCAACGT CCTGGGGAAA
GXP_309531 (Ndufa2_predicted)   871 CAGAATACGG GATAGAAAAa cATAAGGAGC CTCCCCACGT CATGGGAAGA
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alignment position                 1101...... 1111...... 1121...... 1131...... 1141......
GXP_123839 (NDUFA2)             987 Cccgtggaga aacta----- ---------- ---------- ----------
GXP_83080 (Ndufa2)              955 CGGGGCTGAA GGACCAAAAC TCGTACTGAT AAAGgAATTC ACATTTACTT
GXP_309531 (Ndufa2_predicted)   921 CGGGGCTGAA GGACCAAAAC TCCAACTGAT AAAGaAATTC ACATTTACTT
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alignment position                 1151...... 1161...... 1171...... 1181
GXP_123839 (NDUFA2)            1002 ---------- ---------- ---------- -
GXP_83080 (Ndufa2)             1005 AGTTGTGTGA TGCTTTTTAT T--------- -
GXP_309531 (Ndufa2_predicted)   971 AGTTGTGTGA TGCCTTTTAT Tcatggcaac 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.

	GXP_83080 (1025 bp)	**GXP_309531 (1001 bp)**
GXP_123839 (1001 bp)	0.341 49 %	0.334 46 %
GXP_83080 (1025 bp)		1.000 79 %

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

Extract Alignment Region	
Positions in alignment	from: to:
Output file	dialign.seq

Extract Aligned Sequences

For comments, questions, or bug reports, please contact support@genomatix.de.

GEMS Launcher 4.3.0

License Agreement

GEMS Launcher Task: *DiAlign TF*: Multiple alignment plus TF sites
working on CVW-ndufa3 (3 seq.)

[Alignment] [Pairwise similarities]

DiAlign professional TF Release 3.1.1 September 2005 **Fri Oct 20 20:31:45 2006**

Solution parameters:

Sequence file:	CVW-ndufa3 (3 seq.)
Type of sequences:	nucleotide sequences
Threshold T:	0.00
'*' signs below alignment denote:	diagonal similarity (max. similarity is represented by 10 '*' signs)
Alignment output:	complete alignment is shown # nucleic acids per line: 50
TF output:	common TF matches located in aligned regions (common to 3 (100.0 %) sequences)
Family matches:	yes
MatInspector library:	Matrix Family Library Version 6.1 (June 2006)
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	Lengt
1	P914067	P914067 sym=NDUFA3|loc=Loc4696|taxid=9606|spec=Homo sapiens|chr=19|ctg=NT_011109|str=(+)|start=26873850|end=26874850|len=1001|tss=501|comm=NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 3, 9kDa; (NM_004542/501/bronze;)	1001 b
2	mNDUFA3	mNDUFA3 m6_dna range=chr7_random:9785301-9786471 5'pad=0 3'pad=0 revComp=FALSE strand=? repeatMasking=none	1171 b
3	P914068	P914068 sym=na|loc=Loc361494|taxid=10116|spec=Rattus norvegicus|chr=1|ctg=NW_047555|str=(-)|start=9304776|end=9305776|len=1001|tss=501|comm=similar to NADH-ubiquinone oxidoreductase B9 subunit (Complex I-B9) (CI-B9); (XM_341773/501/bronze;)	1001 b

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$STAT V$BRNF V$ZBPF V$YY1F V$NKXH V$EKLF V$RARF V$RORA V$MZF1 TSS

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alignment
position          1.........  11........  21........  31........  41........
P914067
(NDUFA3)        1 agagcc----  ----------  ----------  ----------  ----------
mNDUFA3         1 ttaatg----  -----CCCTG  TCTCAAAATA  AAAAGTAATG  AAAGGGCTGA
P914068
(na)            1 agatacttaa  tgagaCCCTA  TCTCAAAATA  AAAAGCAATG  AAAGGGTTGA
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alignment position      51........ 61........ 71........ 81........ 91........
P914067 (NDUFA3)      7 ---------- ---------- ---------- ---------- ----------
mNDUFA3              42 AAAATGTGGC TCAACAATAA AAGATATGCC TAAAATCCAC CAGCagggac
P914068 (na)         51 CAAATGTGGC TCAACAATAC AAAATATGCC TAGAATCCAC CAGCcggagc
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alignment position      101....... 111....... 121....... 131....... 141.......
P914067 (NDUFA3)      7 ---------- ---------- ---------- ---------- ----------
mNDUFA3              92 ctgggatagt aGAATCTATC ACCAAGTGGA CGGAGGAGTG GCTCAATCgg
P914068 (na)        101 ctgggtcatg -GAATCTACC AGCAAGTGGA CCGAGGAGTG CCTCAGTCat
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alignment position      151....... 161....... 171....... 181....... 191.......
P914067 (NDUFA3)      7 ---------- ---------- ---------- ---------- ----------
mNDUFA3             142 AGATGGGTAG CCTAgcctgT CCTGGTTTCA GTTTTCAGCA CTAAGGGGCA
P914068 (na)        150 AGATGGGTAG CCTA-----T CCTGGTTTCA ATCTGCAACA CTGAGGGGCA
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alignment position      201....... 211....... 221....... 231....... 241.......
P914067 (NDUFA3)      7 ---------- ---------- ---------- ---------- --CGCAGAAA
mNDUFA3             192 GATGGAGGgA AAAGCCATGA TCTGCATGCT AGTAACACAA AGCACAGGCA
P914068 (na)        195 GAGGGTGGaA AAAACCATGA GCCGCATGCT AGTAACATAA AGCACAGACT
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alignment position      251....... 261....... 271....... 281....... 291.......
P914067 (NDUFA3)     15 GCTCCTAACC CATCTGGGAT GAgaccTAGC GCTTCCAGGA CGAGCCGATG
mNDUFA3             242 GTCCTTAATA TATTTGGGAT TAATT-TAGA ATTTCCAGAA TGAGCTTATG
P914068 (na)        245 GTTCTTAATC TATTTGGGAT CAATT-TAGA ATTTCTGGAA TGAGTTCATG
                        ********** ********** ***** **** ********** **********
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alignment position      301....... 311....... 321....... 331....... 341.......
P914067 (NDUFA3)     65 TTGAGCTGAG ACCTCGAa-- ---------- ---------- ----------
mNDUFA3             291 TCTAGATGTG ATCTCAATGT AAAGCTGACT TTTTTttttt taaggtttat
P914068 (na)        294 TCTAGACGCG ACCTCAATGT AATGAGGACT TTCTTgcaga agatcttgaa
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alignment position        351....... 361....... 371....... 381....... 391.......
P914067 (NDUFA3)       83 ---------- ---------- ---------- ---------- ----------
mNDUFA3               341 ttatgagtac actgttgcag tcttcagaca caccagaaga gggcgtcaga
P914068 (na)          344 ---------- ---------- ---------- ---------- ----------

alignment position        401....... 411....... 421....... 431....... 441.......
P914067 (NDUFA3)       83 -------GGA CAGGTTAGTC ATTCACCTTC Tcccgggctc agtttcttcg
mNDUFA3               391 tcccattGCA GATGGTTGTC AGTCACCATG Tggttactgg aaattaaacc
P914068 (na)          344 ---------- ---------- ---------- ---------- ----------
                                 *** ********** ********** *
alignment position        451....... 461....... 471....... 481....... 491.......
P914067 (NDUFA3)      126 tctgtaaaat gggctttcat ac-------- ---------- ----------
mNDUFA3               441 tttggaagag cagacagagc tctgagccat ctctccagcc caaagctgac
P914068 (na)          344 ---------- ---------- ---------- ---------- ----------

alignment position        501....... 511....... 521....... 531....... 541.......
P914067 (NDUFA3)      148 ---------- ---------- ---------- ---------- ---------A
mNDUFA3               491 tttattacag gagaacgtta tGTTACTTCT CCGATGCATT TGCTGAGTTA
P914068 (na)          344 ---------- ---------- -GTTACTTCT CTGACGCATC TTCTAAGGTA
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alignment position        551....... 561....... 571....... 581....... 591.......
P914067 (NDUFA3)      149 TAAACTATAA aatggggact attttgttcc gccttaggtg ggtcgcagca
mNDUFA3               541 TAAACTATAA Gaaaat---- ---------- ---------- ----------
P914068 (na)          373 TAAGCTATAA Gaga------ ---------- ---------- ----------
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alignment position        601....... 611....... 621....... 631....... 641.......
P914067 (NDUFA3)      199 ggaggactag tcactccgga gcgacttctA GGCTGAGACT AAGGAGATTC
mNDUFA3               557 ---------- ---------- ---------- -GGTGAGGCC AGCAGGTGTT
P914068 (na)          387 ---------- ---------- ---------A AGGTGAGACC AGGAGGTGTG
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alignment position        651....... 661....... 671....... 681....... 691.......
P914067 (NDUFA3)      249 CACGCAGGTc cgcaaagtca ggcttgcgct tgctcctgac accacttcct
mNDUFA3               576 CAAGGTGGTT TAAATCTTTC agtCCTCTTA AGC------- ----------
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P914068        408 CAAGGTGGTT TAATTCTTTC tggCCTCCTA AGC------- ----------
(na)
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alignment          701....... 711....... 721....... 731....... 741.......
position
P914067        299 ttacctccac ggctccatct ttgttctgcg cgagtgcgca cgcgcaggct
(NDUFA3)
mNDUFA3        609 ---------- ---------- ---------- ---------- ----------
P914068        441 ---------- ---------- ---------- ---------- ----------
(na)

alignment          751....... 761....... 771....... 781....... 791.......
position
P914067        349 ccgaaagcgg gccgtCGCAC AGAGGGACCA CAACTCCCAG AGTGCTCCGC
(NDUFA3)
mNDUFA3        609 ---------- -----CTCAC TCCAGAACTA CAACTCCCGA AAGGGTCCAC
P914068        441 ---------- -----CTCAC TCTAGAACTA CAACTCCCGA AAGGCTTCAC
(na)
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alignment          801....... 811....... 821....... 831....... 841.......
position
P914067        399 GTCCTTGCtt tcgcctctac ttgtgctcca gggcgcacgc gcagcCCTGG
(NDUFA3)
mNDUFA3        644 GTCCTCGC-- ---------- ---------- ---------- -----CCAAG
P914068        476 GTCCTTGC-- ---------- ---------- ---------- -----CCAAG
(na)
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alignment          851....... 861....... 871....... 881....... 891.......
position
P914067        449 GAGCGGGTTC TCGCGCAtag ----GGACCA CAACTCCCAG GGTGCTCCGC
(NDUFA3)
mNDUFA3        657 GGGCGGGGCC TCACGCAAGG AGAAGGACCA CAACTCCCAG AGAGCTCCGC
P914068        489 GGGCGGGGCC TCATGCAAGG AAAAGAACCA CAACTCCCAG AGAGCTCCct
(na)
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alignment          901....... 911....... 921....... 931....... 941.......
position
P914067        495 gtcctcgccg ctgtcgcCGC CGCGGAGACA AAGATGGCTG CGAGTAAGTG
(NDUFA3)
mNDUFA3        707 tccttgt--- -------CGC CGCCAAGAAC AAGATGGCCG GGAGTAAGTA
P914068        539 gctcttgt-- ---------- --CCAAGACC AAGATGGCTG CTAGTAAGTA
(na)
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alignment position      951....... 961....... 971....... 981....... 991.......
P914067 (NDUFA3)    545 CAGGTTCCGG TGGCGcaCGG GGCTCGGGTA GTTCTGGGAA CCTCTGGGCG
mNDUFA3             747 CAGGTTtgga GCTCG--CGG GGATCAAGTA GTTCCAGGAA ACTGTGGGCT
P914068 (na)        575 CGCGTTCTGG GCGCG--CGG GGACCAAGTA ATTCCAGGAA ACCGTGGCTT
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alignment position      1001...... 1011...... 1021...... 1031...... 1041......
P914067 (NDUFA3)    595 GTCCTGGGAC TGAGGtgcgg cagggcaggg gtGGAAGCGA TGGGGTCCGT
mNDUFA3             795 GATCCGTGGC TGAGTCTCAG TGGAGCCTTG --GGGACCGG Ta--ATCCGT
P914068 (na)        623 GACCCGTGGC TGAGGCTCAG TAGAGCCTTG --GGGAGCGG TAGGATCCGT
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alignment position      1051...... 1061...... 1071...... 1081...... 1091......
P914067 (NDUFA3)    645 g-CTGGAGGG GAACGCAGAA GTCACGAGGG GGctcctcCA GGGCAGGGGT
mNDUFA3             841 CCCAGAATAG GGGCGCGGCA GTCACGAGGG TG------CA GAGCAGGGGT
P914068 (na)        671 CCCAGAAGAG GGGCGCAGCA GCCAATAGGG TG------CA GAGCAGGGGT
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alignment position      1101...... 1111...... 1121...... 1131...... 1141......
P914067 (NDUFA3)    694 GGCACGAGAG GGTTAGAGGT CACCGggggc agctacttgC AGGGGTGACg
mNDUFA3             885 GATACGAGAG TGTTAGAGGT CACCGCAGTA GTCCC----C AAGGGTGACT
P914068 (na)        715 GATACGAGAG TGTTAGAGGT CACCGCAGCA GTCCC----C AAGGGCGACT
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alignment position      1151...... 1161...... 1171...... 1181...... 1191......
P914067 (NDUFA3)    744 ctTCTTGCCA CCCCTTCAGG AGTCggCGCC TTCCTCAAGA ATGCCTGGGA
mNDUFA3             931 G-TCTTCTCA CCTCTCTAGG AATCTCTGCC TTCCTCAAGA ATGCCTGGGC
P914068 (na)        761 T-TTTTCTCA CCTCT--AGG AATCTCCGCC TTCCTTAAGA ATGCCTGGGC
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alignment position    1201...... 1211...... 1221...... 1231...... 1241......
P914067 (NDUFA3)  794 CAAGGAGCCa GTGCTGGTCG TGTCCTTCGT CGTCGGGGGC CTCGGTGCGT
mNDUFA3           980 GAAGGAGCCG GTGCTGGTGG TGTCCTTCTC TGTCTGGGGC CTCGGTGAGT
P914068 (na)      808 AAAGGAGCCG GTGCTGGTGG TGTCCTTCAC TGTCTGGGGC CTCGGTGAGT
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alignment position    1251...... 1261...... 1271...... 1281...... 1291......
P914067 (NDUFA3)  844 gagtgct--C CAGGCGCAAA CTTGCATCGT CCACCCccgt ccccctacat
mNDUFA3          1030 gccccctTCC CCGGCGCGAA AGTGCATCCT CCACCCGGAA GTCATCAgca
P914068 (na)      858 ac-----TCC CCGGAGCGAA CGTGTATCCT CCACCCTGAA GTCATCAata
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alignment position    1301...... 1311...... 1321...... 1331...... 1341......
P914067 (NDUFA3)  892 ccctccatct tgtaccccta aagccctatc gccgccctcg ggtcccctct
mNDUFA3          1080 ttccacggca cagtttcaTC TC-------- ---------- ----------
P914068 (na)      903 ttc------- --------TC TC-------- ---------- ----------
                                         ** **
                                         ** **
                                         ** **
                                         ** **
alignment position    1351...... 1361...... 1371...... 1381...... 1391......
P914067 (NDUFA3)  942 agtgtgtctg cacccccacg GCATCCCCTT atctatcccc atacccatta
mNDUFA3          1102 ---------- ---------- GCATCCCCTT GCCAGCCATA TCCTGACATt
P914068 (na)      910 ---------- ---------- GCATCCCCTT GCCAGCCATA TCCTGACATg
                                            ********** ********** *********
                                            ********** ********** *********
                                            ********** ********** *********
                                            ********** ********** *********
alignment position    1401...... 1411...... 1421...... 1431...... 1441......
P914067 (NDUFA3)  992 taacctctcc ---------- ---------- ---------- ----------
mNDUFA3          1132 ACTGTCGCTC TTCCCTCACC ACA------- -CACAAGAGG TGCACATT--
```

```
P914068      940  ACTGTCGCTC TTCCCTCACC ACAt acacct a CACAAGAAG TGCACATTt a
(na)
                  ********** ********** ***            ********* ********
                  ********** ********** ***
                  ********** ********** ***

alignment         1451...... 1461
position

P914067     1002  ---------- --
(NDUFA3)
mNDUFA3     1172  ---------- --
P914068      990  acccagcttg ta
(na)
```

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.

	mNDUFA3 (1171 bp)	**P914068 (1001 bp)**
P914067 (1001 bp)	0.227 36 %	0.193 36 %
mNDUFA3 (1171 bp)		1.000 79 %

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

Extract Alignment Region	
Positions in alignment	from: ☐ to: ☐
Output file	dialign.seq

Extract Aligned Sequences

For comments, questions, or bug reports, please contact support@genomatix.de.

GEMS Launcher 4.3.0

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GEMS Launcher Task: *DiAlign TF*: Multiple alignment plus TF sites
working on C1-NDUFA4 (3 seq.)

[Alignment] [Pairwise similarities]

DiAlign professional TF Release 3.1.1 September 2005 **Fri Oct 20 20:35:27 2006**

Solution parameters:

Sequence file:	C1-NDUFA4 (3 seq.)
Type of sequences:	nucleotide sequences
Threshold T:	0.00
'*' signs below alignment denote:	diagonal similarity (max. similarity is represented by 10 '*' signs)
Alignment output:	complete alignment is shown # nucleic acids per line: 50
TF output:	common TF matches located in aligned regions (common to 3 (100.0 %) sequences)
Family matches:	yes
MatInspector library:	Matrix Family Library Version 6.1 (June 2006)
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	P876208	P876208 sym=NDUFA4|loc=Loc4697|taxid=9606|spec=Homo sapiens|chr=7|ctg=NT_007819|str=(-)|start=10274926|end=10275986|len=1061|tss=501,552,561|comm=NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 4, 9kDa; (AK024837/552/gold;AK130950/561/gold;NM_002489/501/silver;)
2	P876209	P876209 sym=Ndufa4|loc=Loc17992|taxid=10090|spec=Mus musculus|chr=6|ctg=NT_039340|str=(-)|start=8662756|end=8663771|len=1016|tss=501,505,514,516|comm=NAD dehydrogenase (ubiquinone) 1 alpha subcomplex, 4; (AK005084/533/gold;AK008357/546/gold;AK008506/548/gold;NM_010886/537/silver;)
3	rNDUFA4	rNDUFA4 n3_dna range=chr4:37251038-37252042 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$P53F V$ZF5F V$AHRR V$HESF V$CLOX V$ETSF V$DMTF V$XBBF V$E2FF V$NRSF V$HEAT **TSS**

```
alignment
position              1.........  11........  21........  31........  41........
P876208
(NDUFA4)           1  cgtaacacag  gaagcagctg  cagtcttctc  aaaccgcagC  CGCTGACCTT
P876209
(Ndufa4)           1  ----------  ----------  ----------  ---------C  CGTTGACCCC
```

```
rNDUFA4               1 ---------- ---------- ---------- ---------C CGTTGACCCC
                                                                  * **********
                                                                  * **********
                                                                  * **********
                                                                  * **********
                                                                  * **********

alignment position        51........ 61........ 71........ 81........ 91........
P876208 (NDUFA4)     51 AGCGGCAAGA GGCCCGACCT GCCCTCCAGg cgcccGGCGC TCGGCTCCCA
P876209 (Ndufa4)     12 GGCGGCTGGA GACTCGACCT GTCCTGCGGg atcTGGGCGC TGAGCCTGCA
rNDUFA4              12 AGCGGCTGGA GACTCGACCT GTCCTGCGGg attTGGGCGC TGCGCCTGCA
                        ********** ********** *********     ******* **********
                        ********** ********** *********     ******* **********
                        ********** ********** *********     ******* **********
                        ********** ********** *********       ***** **********
                        ********** ********** *********       ***** **********
                                                              ***** **********

alignment position        101....... 111....... 121....... 131....... 141.......
P876208 (NDUFA4)    101 GAGGCGCCGC GCAGCTCCCT Cagcggcagt cacagctggC CAGCGCGCAC
P876209 (Ndufa4)     62 GAGGCGCCTG GCAGCTCCCT CcGGGGCCCT CCGGGCGGCG CGGCGCGCGC
rNDUFA4              62 GAGGCGCCTG GCAGCTCCCT CtGGGGCTCT CTGAGAGGCC CAGCGCGCGC
                        ********** ********** * ******** ********** **********
                        ********** ********** *                   * **********
                        ********** ********** *                       ********
                        ********** ********** *
                        ********** ********** *
                        ********** ********** *

alignment position        151....... 161....... 171....... 181....... 191.......
P876208 (NDUFA4)    151 CCGGCACGCG CGCCCCCA-G GGCCTCTGCG CGCGGACCCG GCTCTCAGGC
P876209 (Ndufa4)    112 CCCACACGCG CGCCCCCAAG CGCGTCCACG CGCGGCCCTG GCCGGGAGGC
rNDUFA4             112 ACCGCACGCG CGCCCCCAAG CGCGTCAGCG CGCGGCCCAG GCCTAGAGGC
                        ********** ********** ********** ********** **********
                        ********** ********** ********** ********** **********
                        ********** ********** ********** ********** ***  *****
                           ******* ********    ********* ********** ***  *****
                           ******* ********

alignment position        201....... 211....... 221....... 231....... 241.......
P876208 (NDUFA4)    200 GCCGCGGGAG Aggcccccta CTCACGGAGC GCGCGGCCCG TGCGCCCACG
P876209 (Ndufa4)    162 GCCGCTAAGG AAGCCGCG-- CCCGCCGAGC GCACTGCCAG CGGACCGCCG
rNDUFA4             162 GCCGCTAGGG AAGCCGCG-- CTCGCCAAGC GCACTtCCAG CCGACCGCCG
                        ********** ********   ********** ********** **********
                        ********** ********   ********** ***** **** **********
                        ********** ********   ********** ***** **** **********
                        ****

alignment position        251....... 261....... 271....... 281....... 291.......
P876208 (NDUFA4)    250 ctccgaccgc attcctcagt acgtggcacc CTTGGAAAGT GCCTGTCTGG
P876209 (Ndufa4)    210 GATGACCCTG GTCTATACGC ATGCcGT--- CCTGAAAAGT GCCTGTCTCA
rNDUFA4             210 GATGACCCTG ATCTACACGC ATGCtGT--- CCTGAAAATT GCCTGTCTTA
```

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

alignment        301....... 311....... 321....... 331....... 341.......
position
P876208     300  TCAATCGaag agtcctcgtt tcgac-C--- ------AAAA AAATTCCCCT
(NDUFA4)
P876209     257  CCAGTCGAGA CGCTCTGcct gctatgcaaa aaataaAAAA ATAAACCTAT
(Ndufa4)
rNDUFA4     257  TCAGTCGAGA CGCTCTGatt tctgtgC--- ------AAAA ATAATCCTAT
                 ********** *******          *          **** **********
                 ********** *******                     **** **********
                 ********** *******                     **** **********
                 *******                                **** **********

alignment        351....... 361....... 371....... 381....... 391.......
position
P876208     340  CAGAAATATG CATGGCACGG CAATGAaggc atttcactat gaagtggaat
(NDUFA4)
P876209     307  CAAAAAGATG CATGGTGGAG AACTGAtgga tcatgAACTC AAAAATGCGA
(Ndufa4)
rNDUFA4     298  CAAAAATATG CATAGTGGAG AACTaaagga tgtttAGCTT AACAATGGGA
                 ********** ********** ******          ***** **********
                 ********** ********** ****
                 ********** ********** ****
                 ********** ***

alignment        401....... 411....... 421....... 431....... 441.......
position
P876208     390  gatgatggtc cgaccagGTC AGGACGAACA TATGAGGGGT TAg-ATCTAA
(NDUFA4)
P876209     357  AGAAGTGGTC GGGACA-TTT AGGGCaatCG CGCGAGGGCT GACTACCTAT
(Ndufa4)
rNDUFA4     348  AGAAGTGCTG GTACCA-GTT AGGGCGACCG CGCGAGGGCT GAACACCCAT
                 ********** ****** *** ********** ********** **********
                                               ** ********** **********

alignment        451....... 461....... 471....... 481....... 491.......
position
P876208     439  GCAGGCACTA TTAAAGACAG TCGCATCCGG GCCCTCCTGC CGCAAGCTGC
(NDUFA4)
P876209     406  TCAGGCACCT TAGAGGACAG CCGCATCCGG GCTTTCCTGC TGCAGGCTGC
(Ndufa4)
rNDUFA4     397  TCAGGCACCA TAGAGGACAG CCGCATCCGG GCTTTCCTAC TGCAGGCTGC
                 ********** ********** ********** ********** **********
                 ********** ********** ********** ********** **********
                  ********* ********** ********** ********** **********
                                ****** ********** ********** **********
                                ****** ********** ********** **********
                                 ***** ********** ********** **********
                                 ***** ********** **    ****** **********

alignment        501....... 511....... 521....... 531....... 541.......
position
P876208     489  CCTCCCAGCC AAGGGTCCTT CAGGTAGGAG GTCCTGGGTG ACTTTGGAAG
(NDUFA4)
P876209     456  CCTCagcGCC AGGGGTCCTT CAGGTAGGAG GTCCTGGGTG ACTTTGGACG
(Ndufa4)
rNDUFA4     447  CCTCCCAGCC AGGGGTCCTT CAGGTAGGAG GTCCTGGGTG ACTTTGGACG
                 ********** ********** ********** ********** **********
                 ********** ********** ********** ********** **********
                 ****   *** ********** ********** ********** **********
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                 ****   *** ********** ********** ********** **********
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                     ****** ********** ********** *******
```

```
                                                          ****  *******   
alignment position   551....... 561....... 571....... 581....... 591.......
P876208 (NDUFA4) 539 TCCGTAGTGT CTCATTGCAG ATAATTTTTA GCTTAGGGCC Tggtggctag
P876209 (Ndufa4) 506 TCCGCTCAGC CAGGTTGCAG AAGCGGCTTA GCGTGTGTCC TAATCTTCTC
rNDUFA4          497 TCCGCTCAGC CAGGTTGCAG AAGCGGTTTA GTGTGTGTCC TAATCTTCTC
                     ********** ********** ********** ********** **********
                     ********** ********** ****** *** ********** **********
                     ********** ********** ******
                     ********** ********** ******
                     ****
                     ****
                     ****

alignment position   601....... 611....... 621....... 631....... 641.......
P876208 (NDUFA4) 589 gtcggttctc tcctttccag tcggAGACCT CTGCCGCAAA CATGCTCCGC
P876209 (Ndufa4) 556 TCTgcGTGTA GGT------- ----AGGCCT GTGCCGCAAA CATGCTCCGC
rNDUFA4          547 TCTcgGTGTA GGT------- ----AGGCCT GTGCCGCAAA CATGCTCCGC
                     ***  ***** ***            ****** ********** **********
                     ***  ***** ***            ****** ********** **********
                          ***** ***            ****** ********** **********
                          ***** ***            ****** ********** **********
                                               ****** ********** **********
                                               ****** ********** **********
                                               ****** ********** **********
                                               ****** ********** **********

alignment position   651....... 661....... 671....... 681....... 691.......
P876208 (NDUFA4) 639 CAGATCATCG GTCAGGCCAA GAAGCATCCG AGCGTAAGTT Cgtgaccgct
P876209 (Ndufa4) 595 CAGATCCTCG GGCAAGCCAA GAAGCATCCC AGCGTAAGTT CACGgTCTTT
rNDUFA4          586 CAGATCCTCG GGCAAGCCAA GAAACATCCC AGCGTAAGTT CACGaTCTTT
                     ********** ********** ********** ********** **** *****
                     ********** ********** ********** ********** **** *****
                     ********** ********** ********** ********** ****
                     ********** ********** ********** ********** *
                     ********** ********** ********** ********** *
                     ********** **** ***** ********** ********** *
                     ****** *** **** ***** ********** ********** *
                     ******

alignment position   701....... 711....... 721....... 731....... 741.......
P876208 (NDUFA4) 689 ctcctaatgt tttcccttgt ccttcttgcg tcgGGGTGCG CCTCTTTCTG
P876209 (Ndufa4) 645 GCCAGGGTGG CCTCTTAGCT GT-------- ---GGTTGCT CCTGCCCGTG
rNDUFA4          636 GCCAGAGTGG GCTCTTAGCT GT-------- ---GATTGCG CCTTCCCGTG
                     ********** ********** **            ******* **********
                     ********** ********** **            ******* **********
                                                         ******* *** ******
                                                            **** *** ******
                                                                     ******

alignment position   751....... 761....... 771....... 781....... 791.......
P876208 (NDUFA4) 739 TTCCCTGGGA ACGTCCTCAT TTacagccac ttaccgtccg tcagaccaga
P876209 (Ndufa4) 684 TCCCCTGGGG ACGTTCTCTT TTCTCTGTTc cttggggtta cattctgttG
rNDUFA4          675 TCCCCTGGGG ACGTTCTCTT TTCTCTGTTt ctgag----- ---------G
```

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

alignment position      801....... 811....... 821....... 831....... 841.......
P876208 (NDUFA4)    789 cccctgcctcg cctagtgttt gtcatcttag ttgtcccagg cctctgtgac
P876209 (Ndufa4)    734 TTGGGATGAC CTGATTGCTT GAAGCCTCTA CCTGGGGTGg ag--------
rNDUFA4             711 TTGGCCTAAC CTGATAGCTC GAAGTCTCTA CTGGGGGTGg ggaagg----
                        ********** ********** ********** *********
                        ********** ********** ********** *********

alignment position      851....... 861....... 871....... 881....... 891.......
P876208 (NDUFA4)    839 cctctacgcc atgcattGTG GGGTTTTGTC TGACAGGAGG AAGGAGAcgg
P876209 (Ndufa4)    776 ---------- -------GTG AGGTTGCCTG AAGCAGAAGG TGGCAGAGAT
rNDUFA4             757 ---------- ---------- -GGTTGCCTG AAGCCGAAGG TGTCAGACAT
                                          *** ********** ********** **********
                                               ********* ********** **********

alignment position      901....... 911....... 921....... 931....... 941.......
P876208 (NDUFA4)    889 acactgctcg gaaaaaaaac ctagtttttt ctagtTAGTG AATATTGGAA
P876209 (Ndufa4)    809 CAGGGAgAAA GGTAAACA-- ---------- -----TTCTG AGTGTTGGAA
rNDUFA4             786 CAGGGAaAAA GGTAAACA-- ---------- -----TTCTG AGTGTTGGAA
                        ****** *** ********                   ***** **********
                        ****** *** ********                   ***** **********
                               *** ********                   ***** **********
                               *** ********                   ***** **********

alignment position      951....... 961....... 971....... 981....... 991.......
P876208 (NDUFA4)    939 CAGTCTGGTG GCCGCTCTCT tttgcaggtt gtgcggtCCA GGAGGGATAG
P876209 (Ndufa4)    842 CACTGTGGC- -------TCT CAGATTACTT GGTCC--CAA GAGGGGTGAG
rNDUFA4             819 CACTGTGGCC ACCGATCTCT CAGGTTACTT GGTCC--CAA GAAGGGTGAG
                        ********** ********** ********** *****  *** **********
                        *********         *** ********** *****  *** **********
                        *********         *** ********** *****  *** **********
                        *********

alignment position      1001...... 1011...... 1021...... 1031...... 1041......
P876208 (NDUFA4)    989 ATGTGCGCTG TGTgGGTCAG AGACTAGCAT AGGTCAGGTT CCCTATGtgt
P876209 (Ndufa4)    882 TGGTACGTTG AGT-GATTAG AATCCAAGAG AGGCCAAGTT TGTTATGCtg
rNDUFA4             867 TGGTAtaTTG AGT-GATTAG AATCCAAGAG AGACCAAGTT TGTTATGCtg
                        ********** *** ****** ********** ********** ********
                        *****  *** *** ****** ********** ********** ********
                        *****  *** *** ****** ********** ********** ********
                               *** *** ****** ********** ********** ********

alignment position      1051...... 1061...... 1071...... 1081...... 1091......
P876208 (NDUFA4)   1039 tataccatct ctggaggttc ttg------- ---------- ----------
P876209 (Ndufa4)    931 -CTCTTTGCG GCTTTTAGAG TCACTGcATT GCACCACCAA ACCTTCAGAA
rNDUFA4             916 cCTTTTTGAG GCTATTATAT TCACCGgATT GCACCACCAA GCCTTCAGAA
```

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

alignment          1101...... 1111...... 1121...... 1131......
position
P876208      1062  ---------- ---------- ---------- ----------
(NDUFA4)
P876209       980  GTGCAAGGGa ---TCGTCAT CGTGTAATCC CCACTTTGCT
(Ndufa4)
rNDUFA4       966  ATACAAGGGg tcgTCGTCAT CTTGTAATCA TAACTTTGCT
                   *********     ******* ********** **********
                   *********
```

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.

	P876209 (1016 bp)	**rNDUFA4 (1005 bp)**
P876208 (1061 bp)	0.238 38 %	0.262 40 %
P876209 (1016 bp)		1.000 85 %

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

Extract Alignment Region	
Positions in alignment	from: ☐ to: ☐
Output file	dialign.seq

Extract Aligned Sequences

For comments, questions, or bug reports, please contact support@genomatix.de.

GEMS Launcher 4.3.0

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

[Alignment] [Pairwise similarities]

DiAlign professional TF Release 3.1 December 2004 **Mon Jun 6 23:08:24 2005**

Solution parameters:

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

Aligned Sequences:

No.	Sequence Name	Sequence Description	Length
1	P921898	sym=NDUFA5|loc=Loc4698|taxid=9606|spec=Homo sapiens|chr=7| ctg=NT_007933|str=(-)|start=48380931|end=48382034|len=1104| tss=501,604| comm=NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 5, 13kDa; (AK022209/645/gold;NM_005000/542/bronze;)	1104 bp
2	P921899	sym=Ndufa5|loc=Loc68202|taxid=10090|spec=Mus musculus|chr=6| ctg=NT_039340|str=(-)|start=21360789|end=21361930|len=1142| tss=501,522,608,609,618,620,629,632,633,636,641,642| comm=NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 5; (AK011579/642/gold;AK019201/632/gold;AK008155/632/gold; AK008414/636/gold;AK011947/642/gold;AK008156/636/gold; AK009985/618/gold;AK019207/641/gold;AK019215/632/gold; AK010090/632/gold;AK019242/633/gold;AK010092/618/gold; AK019324/522/gold;AK019430/620/gold;AK009338/618/gold; AK008286/636/gold;AK019245/620/gold;AK009461/632/gold; AK019084/632/gold;AK009608/632/gold;AK009642/620/gold; AK019354/629/gold;AK019364/618/gold;AK019291/632/gold; AK009652/632/gold;AK009840/618/gold;AK019359/609/gold; AK009493/632/gold;AK009396/632/gold;AK019368/620/gold; AK010024/632/gold;AK009775/608/gold;NM_026614/501/bronze;)	1142 bp
3	P921900	sym=Ndufa5|loc=Loc25488|taxid=10116|spec=Rattus norvegicus| chr=4|ctg=NW_047689|str=(-)|start=21329033|end=21330033| len=1001|tss=501| comm=NADH dehydrogenase (ubiquinone) 1 alpha subcomplex 5; (NM_012985/508/bronze;)	1001 bp

Alignment (DiAlign format):

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

V$NRF1 U$NRF1 V$SP1F V$HOXC V$RORA V$FKHD V$NF1F

```
alignment position 1.........  11........ 21........ 31........ 41........
P921898        1   gagg------ ---------- ---------- ---------- ----------
P921899        1   caaagaacaC ATGCATCTTT TATAAAGCCA TGATTCCACA TTCTAGAACA
P921900        1   ---------C ATGCATCTTT TATAAAGCCA TGATTCCACA TTCTAGAACA
                            * ********** ********** ********** **********
                            * ********** ********** ********** **********
                            * ********** ********** ********** **********
                            * ********** ********** ********** **********
                            * ********** ********** ********** *********
                            * ********** ********** ********** *********
                            * ********** ********** ********** *********

alignment position 51........  61........ 71........ 81........ 91........
P921898        5   ---------- ---------- ---------- ---------- ----------
P921899       51   CACTCAACAA TGACAGATGT TCTTGGGATC TGGAggGACA GAGAACAGGG
P921900       42   CACTTAACAA TGACAGATGT TCTTAGGACC TGGAaaGACG GAGAATAGAG
                   ********** ********** ********** ****  **** **********
                   ********** ********** ********** ****  **** **********
                   ********** ********** ********** ****  **** **********
                   ********** ********** ********** ****  **** **********

alignment position 101.......  111....... 121....... 131....... 141.......
P921898        5   ---------- ---------- --TAGGAAAA AGTGGTATGG TCTGATATCA
P921899      101   ACTATGACCT CATAAACACC CAcTGGAACA AAGACTACGA CTTCATAACC
P921900       92   ACTATGACCT CATAAACTCC CATTGGAACA AAGACTATGA CTTCATAACC
                   ********** ********** ********** ********** **********
                   ********** ********** ** ******* ********** **********
                   ********** ********** ** ******* ********** **********
                   ********** ********** ** ******* ********** **********
                                            ******* ********** **********
                                            ******* ********** **********

alignment position 151.......  161....... 171....... 181....... 191.......
P921898       33   TTTCATctgg aaa------- ---------- ---------- ----------
P921899      151   TTTCATTCAt CAGTCTCCTC AAGAGAAAAC GGATGCATCA GATGGTTAAT
P921900      142   TTTCATTCAc CAGCCTCCAC AGGAGCAAAC GGATATATCA GATGGTTAAT
                   *********  ********** ********** ********** **********
                   *********  ********** ********** ********** **********
                   *********  ********** ********** ********** **********
                   *********  ********** ********** ********** **********
                   *********
                   ******

alignment position 201.......  211....... 221....... 231....... 241.......
P921898       46   ---------- ---------- TAAGATGATG TATTTCAGCC AGTGAAATCG
P921899      201   TCCACTTTAT AATTTCCACT TATGAGTATG CATTCACACA c-GTGGAGGG
P921900      192   TCCACTTTAT AGTTCCCATT TATGAATATG TATTCACGCA AGGGGGAGAG
                   ********** ********** ********** ********** **********
                   ********** ********** ********** **********
                   ********** ********** ********** **********
                   ********** ********** ********** **********

alignment position 251.......  261....... 271....... 281....... 291.......
P921898       76   Aaaagagcga tggaaaatga cctcacactc catagggctt tggttcgtaa
P921899      250   AAAGCATTCT TCATGGTGCT C--------- ---------- ----------
P921900      242   AGCATTTTTT TCATGATGCT C--------- ---------- ----------
                   ********** ********** *

alignment position 301.......  311....... 321....... 331....... 341.......
P921898      126   gacacagaga atactgatat cctgtgcga  agaactaact tgctgttgag
P921899      271   ---------- ---------- ---------- ---------- ----------
P921900      263   ---------- ---------- ---------- ---------- ----------
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alignment position 351....... 361....... 371....... 381....... 391.......
P921898        176 agatcaattc agaggatgct caAGCTCCGT TATCACTTTC ATTTTACTAA
P921899        271 ---------- ---------- --AGGcctgc TTCCACCCTC ATTTCCATAA
P921900        263 ---------- ---------- --AGGTCCGT TTCCACCCTC ATTTCAATCA
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alignment position 401....... 411....... 421....... 431....... 441.......
P921898        226 ACTGAGAAAG gaaggttgag gaATGCATCA ACGGTTAAGC ACAGTGCAGG
P921899        299 CCTGAGGAAG TCCGggTAAA ATAGCAGTCG AAGGCTGAGC AAAATCAAAG
P921900        291 GCTGAGGAAG TGCGcaTAAA ACATCAATCA AAGGCTGAGC AAAATCAAAG
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alignment position 451....... 461....... 471....... 481....... 491.......
P921898        276 TTCCTACAGC GACTgg---- --AGTTTTTT GGTAGTTGGG AGTGTTTCcc
P921899        349 TCCCTGCAGT GACTACGTTG CAAGTTTTTC CGTAGCGTAG CGCTTTTCTT
P921900        341 TCCCTG-AGT GACTACATTG AAAGTTTTTC -GTAGCGCAG CGTTTTTCTT
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alignment position 501....... 511....... 521....... 531....... 541.......
P921898        320 tcaatctttg ggcaagccgt cagcagtggc aggaacagga acagacagct
P921899        399 AACCTTTAGT ACT--CAGAG ACGTCAGTCG GTCTCTACTA CACCAAAGCC
P921900        389 AACCTTTAGT CCTaaCAGAG GCGTCAGTCT GTCTCTGTTG CGCCAAAACC
                   ********** ***  ***** ********** ********** **********
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alignment position 551....... 561....... 571....... 581....... 591.......
P921898        370 gggaaaccct tctttccccc aatcgtcttc tagcttagct ttaggcttgt
P921899        447 CTgCGTGGAG CCGCTTGTGT GAGCT----- ---------- ----------
P921900        439 CTaCGTGGAG CCACGCGTAT GAGCT----- ---------- ----------
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alignment position 601....... 611....... 621....... 631....... 641.......
P921898        420 atgcccatcG CGCATGCGTC AATTTTTCTC TTTTAAGATG GGCGGGGCag
P921899        472 ---------G CGCAGGCGCA AATCTACCTC TCCTAGGTGG GCGGGAGCTG
P921900        464 ---------G CGCAGGCGCA AATCTCTCCC TCCTAGGTGG GCGGGAGTTA
                            * ********** ********** ********** **********
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alignment position 651....... 661....... 671....... 681....... 691.......
P921898        470 agtctttgct cctttggcga tCCTGAAGGG GTGGAGCTAA GCTGTTTCCA
P921899        513 CCCCTACCCa gcccgagc-- --------GG TTGGAGCCAA GAGTGTTCTT
P921900        505 CCCCTAGCCc cg-------- -CCTGAGAGG TGGGAGCCAA GTGCTTTCTT
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alignment position 701....... 711....... 721....... 731....... 741.......
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P921898        520 GGGTGACAGA GTGGCgacct cggtggTCGA TTGAGCAGGT CTGAGAATTG
P921899        553 AGGTGACTCA GGGGCAGCat cgACGCTCGA TTGAGCGGGC TTGGGAAAGG
P921900        546 GGGTGACACA GGAGCAGCtt ctACGTTCGA TTGAGCGGGC CTGGGAAAGG
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alignment position 751....... 761....... 771....... 781....... 791.......
P921898        570 TTCCCAAAGG GTTGTGcgtc accgagtcgt tgGCGCTGTC ATGGCGGGTG
P921899        603 TTCCCAGAGG GCTGTGCGCT GGAGGCGCTG G-ACGCTGTC ATGGCGGGCT
P921900        596 TTCCCAGAAG GCcgcGCGCT GGAGTCTCTG A-GCGCAGTC ATGGCGGGCT
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alignment position 801....... 811....... 821....... 831....... 841.......
P921898        620 TGCTGAAGAA GGTGAGacga aTGGAGGTCA CTGTtggaat ttagactgtg
P921899        652 TGCTGAAAAA GGTGAGCGTG -TGGAGGTCA CCGTGATGCT GcgaatgGGG
P921900        645 TGGTGAAGAA GGTGAGCGTC -TGGAGGTCA CCATGGTGCT Gaggac-GGG
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alignment position 851....... 861....... 871....... 881....... 891.......
P921898        670 ggggtagact cagtccgata gccctacttc ccgcgggtgt tgacccctac
P921899        701 ACCGTAGGCA GCCGCGTCTC CCTCATCGGT Gggcagagac -------GCT
P921900        693 GCGGTAGGCA GCCTTGTCTC CCTCATCCGT Gttaagagga tggagaaGCT
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alignment position 901....... 911....... 921....... 931....... 941.......
P921898        720 tgtcgcgggc tcggcggtgc tttTCGGGGA CTCGTTCTGC ATGCCTTACC
P921899        744 AAGAGGAGGG G--------- ---TTGGGGG AGTGTTCCGC TGTCCTGGCA
P921900        743 AAGAGGACGG G--------- ---TTGGGGG AGTGTTCCGC TGTCCTGACA
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                   ********** *             ******* ********** *******
alignment position 951....... 961....... 971....... 981....... 991.......
P921898        770 GGGTAGGGCA GGttagtggt tccgctccga gagtcaggaa aaaagctcca
P921899        782 GGGGGCGACA GGGTGCGTAG TTGTGTCGGG AGGGTCGGct aaccag----
P921900        781 GGGGGCGACA GGGTTCGTAG TTGTGTCTGG AAGTTCGGct aatcagcggg
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alignment position 1001...... 1011...... 1021...... 1031...... 1041......
P921898        820 aacaagcgag actgagagac cagtagctgg ctttagacca gttttaGCCG
P921899        828 ---------- ---------- ---------- ---------- ----------
P921900        831 ccaggactgg gg-------- ---------- ---------- ------GCCC
                                                                     ****

alignment position 1051...... 1061...... 1071...... 1081...... 1091......
P921898        870 GGGGATTCGT GGTTTTGTAT TTCCTTAGCG tgctggatgt atggaaaccg
P921899        828 ---------- ---------- ---------- ---------- -GGGATTACG
P921900        847 CGGGATGGGC GGGCTGGCTT TTCCTGCGCG ctgttacgcg tGGGATGACG
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alignment position 1101...... 1111...... 1121...... 1131...... 1141......
P921898        920 taGTAAACAG CAtgaaTCGT GTTTTGTTTT TGAACAGACC ACTGGCCTTG
P921899        837 --GTAAACAT CACGG-TCCT GTTTTGTCTC TGCACAGACA ACTGGCCTGG
P921900        897 --GTAAACAG CACGG-TCTT GTTTTGTTTC TGAACAGACT ACTGGCCTGG
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alignment position 1151...... 1161...... 1171...... 1181...... 1191......
P921898        970 TGGGATTGGC TGTGTGCAAT ACTCCTCACG AGGTATGTAc ctttgttctt
P921899        884 TGGGGTTGGC GGTGTGCGAC ACTCCACACG AGGTAAGTGC GACTTTTTGT
P921900        944 TGGGATTGGC CGTTTGCGAC ACTCCACACG AGGTAAGTAC GGCTTTTTGT
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alignment position 1201...... 1211...... 1221...... 1231...... 1241......
P921898       1020 tcttcgttct tgaaTTCCCA AGGAAGACTa aattcctgtc actttgctta
P921899        934 GTCgtcc--- ----TTCTCA AGCAAGACTg tgatcgaccg aacttgccc-
P921900        994 GTCtttgc-- ---------- ---------- ---------- ----------
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alignment position 1251...... 1261...... 1271...... 1281...... 1291......
P921898       1070 TTGCAGGGTT AACGGGAtac agatgtttca agccc----- ----------
P921899        976 TTGCAAGATT AACGAGAccc ccgtgagctc tggcctccgg ggcagcgctg
P921900       1002 ---------- ---------- ---------- ---------- ----------
                   ********** *******

alignment position 1301...... 1311...... 1321...... 1331...... 1341......
P921898       1105 ---------- ---------- ---------- ---------- ----------
P921899       1026 agcttcgctg accccgtggc atcctttttg caatgcctcc ttttgccttc
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P921900      1002 - - - - - - - - - -   - - - - - - - - - -   - - - - - - - - - -   - - - - - - - - - -   - - - - - - - - - -

alignment  position 1 3 5 1 . . . . . .   1 3 6 1 . . . . . .   1 3 7 1 . . . . . .   1 3 8 1 . . . . . .   1 3 9 1 . . . . . .
P921898      1105 - - - - - - - - - -   - - - - - - - - - -   - - - - - - - - - -   - - - - - - - - - -   - - - - - - - - - -
P921899      1076 g c c g t g a c c t   c t t a a t t a a g   a c g c g t t t c t   t c a c g g c a t t   c t c t t a g c g t
P921900      1002 - - - - - - - - - -   - - - - - - - - - -   - - - - - - - - - -   - - - - - - - - - -   - - - - - - - - - -

alignment  position 1 4 0 1 . . . . . .   1 4 1 1 . . .
P921898      1105 - - - - - - - - - -   - - - - - - -
P921899      1126 c a g t g g t g t g   g a g t a t t
P921900      1002 - - - - - - - - - -   - - - - - - -
```

Pairwise similarities:

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

	P921899 (1142 bp)	**P921900 (1001 bp)**
P921898 (1104 bp)	0.158 31 %	0.177 35 %
P921899 (1142 bp)		1.000 77 %

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

Extract alignment region	
Positions in alignment	from: ______ to: ______
Output file	dialign.seq

Extract aligned sequences

For comments, questions or bug reports, please contact support@genomatix.de

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License Agreement

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 **Mon Jun 6 23:21:05 2005**

Solution parameters:

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

Aligned Sequences:

No.	Sequence Name	Sequence Description	Length
1	P855595	sym=NDUFA6|loc=Loc4700|taxid=9606|spec=Homo sapiens|chr=22|ctg=NT_011520|str=(-)|start=21876764|end=21877764|len=1001| tss=501| comm=NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 6, 14kDa; (NM_002490/577/bronze;)	1001 bp
2	P855596	sym=Ndufa6|loc=Loc67130|taxid=10090|spec=Mus musculus|chr=15|ctg=NT_039621|str=(-)|start=43832732|end=43833737| len=1006|tss=501,506| comm=NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 6 (B14); (AK002749/558/gold;AK010988/558/gold;AK012328/558/gold; NM_025987/553/bronze;)	1006 bp
3	P855597	sym=na|loc=Loc315167|taxid=10116|spec=Rattus norvegicus|chr=7|ctg=NW_047781|str=(-)|start=1179476|end=1180476| len=1001|tss=501| comm=similar to NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 6 (B14); NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 6 (14kD, B14); (XM_235518/597/bronze;)	1001 bp

Alignment (DiAlign format):

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

V$NRF1 U$NRF1 V$ECAT V$PCAT V$YY1F V$NEUR V$PLAG V$HICF V$E2TF V$NFKB V$CREB V$RORA
U$T3R U$T3Rbis V$E4FF V$STAT V$ETSF

```
alignment
position         1.........  11........  21........  31........  41........
P855595        1 a---------  ----------  ----------  ----------  ----------
P855596        1 tc--------  ----------  ----------  ----------  ----------
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P855597     1 acaagttcgg tggacacaaa cctgcagagg cagagaaatc actgcaagtt

alignment
position      51........ 61........ 71........ 81........ 91........
P855595     2 ---------- ---------- ---------- ---------- ----------
P855596     3 ---------- ---------- ---------- ---------- ----------
P855597    51 ctgaggccaa cctggctggt ctacataagt gagtttaagg tcagccgcaa

alignment
position      101....... 111....... 121....... 131....... 141.......
P855595     2 ---------- ---------- ---------- ---------- ----------
P855596     3 ---------- ----AAAACA ATGGCATGAA GTAAGTAAAC AAA-------
P855597   101 tcagacgaca acgaAAAACA ATGACAATAA GTAAACAAAC AAAcaatatg
                              ****** ********** ********** ***

alignment
position      151....... 161....... 171....... 181....... 191.......
P855595     2 ---------- ---------- ---------- ---------- ----------
P855596    32 ---------- --------CG GGGCTGAGAA ACGCCAAAAA GCTCAAGCCa
P855597   151 gagttttcat tataatccCG GGGCTGAGAA ACGGCACAAA GCTCAAGCCg
                                  ** ********** ********** *********
                                  ** ********** ********** *********

alignment
position      201....... 211....... 221....... 231....... 241.......
P855595     2 ---------- ---------- ---------- ---------- ----------
P855596    64 GAGGCGCTTT TGCGATCGAC ACCATGTCTA CAAGAAAACg gttttccgga
P855597   201 GAGGCGCTTT TGCGATCTAC ACCAAGTCTA GAAGAAAAC- ----------
              ********** ********** ********** *********
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alignment
position      251....... 261....... 271....... 281....... 291.......
P855595     2 ---------- ---------- ---------- ---------- ----------
P855596   114 agcacataca caatatgctc agcagtacgc acTGTTGCTG CGGAAAGACT
P855597   240 ---------- ---------- ---------- --TGTTTCTG CGGAAAGACC
                                                 ******** **********

alignment
position      301....... 311....... 321....... 331....... 341.......
P855595     2 ---------- ---------- ---------- ---------- ----------
P855596   164 GCCATtgccg cctggcaccg ttatctatgc ccgaggtctt ctcctccgag
P855597   258 GCCATca--- ---------- ---------- ---------- ----------
              *****

alignment
position      351....... 361....... 371....... 381....... 391.......
P855595     2 ---------- --GCCGCCAG GCGGCAGGAc aa-------- ----------
P855596   214 cctgccaacc acGGCGCCTG GCTGAAGGAA CAAACttttg gtaagagcag
P855597   265 ---------- ------CCCG GCTGGAACAA CAAACcg--- ----------
                           ******** ********** *****

alignment
position      401....... 411....... 421....... 431....... 441.......
P855595    22 -------GCC CCACCGCAGC Ccaggcgcca ttatctgcct cagcagttaC
P855596   264 acagagcGCC TCACCGCTGC CTGAAG---- ---------- ---------C
P855597   286 ---------- --ACCGCTGC CGGAAG---- ---------- ---------C
                     *** ********** ******                          *
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alignment
position      451....... 461....... 471....... 481....... 491.......
P855595    65 CTCGGGGTCC CGCCACGAGG AGGTTCTTCA AGGCCTGCGc gcccacggac
P855596   291 CTCGACGCTG CGCCTCCTGG TGGTTCCTCA GCGCCGCCGT TGAACGAG--
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P855597     301 CTCGACGCTG CGCTCCCTGG TGGTTCTTCA GCGCCGCGGT CGAAGGAG--
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alignment
position        501....... 511....... 521....... 531....... 541.......
P855595     115 actaccaagg agcgcggcgg gcagccggat agcaggacgc tgagggaaac
P855596     339 ---------- ---------- ---------- ---------- ----------
P855597     349 ---------- ---------- ---------- ---------- ----------

alignment
position        551....... 561....... 571....... 581....... 591.......
P855595     165 cccgcagtcg ctcggcgtcc ccggcgccag ctcacgaccc agcgacctcc
P855596     339 ---------- ---------- ---------- ---------- ----------
P855597     349 ---------- ---------- ---------- ---------- ----------

alignment
position        601....... 611....... 621....... 631....... 641.......
P855595     215 tgcggcccga gcgtcccctg gcggcaacgc cggctcgtta gagcgagcga
P855596     339 ---------- ---------- ---------- ---------- ----------
P855597     349 ---------- ---------- ---------- ---------- ----------

alignment
position        651....... 661....... 671....... 681....... 691.......
P855595     265 cagatggtgt agtCCAAAGG CCAAGCGGCG TTTCTGTAGA TGAGCATGCG
P855596     339 ---------- ---CCAACCc cggATCGGTG TTTCCGCGGT AGAGCATGCG
P855597     349 ---------- ---CCAACCA CCAATCGGTG TTTCCGCGGT AGAGCATGCG
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                              ******     ******* ********** **********
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alignment
position        701....... 711....... 721....... 731....... 741.......
P855595     315 CAgcacccac cgttcgctca gccagagaga ggcttcCCAG CCAATCCGAG
P855596     376 CATTGCAGAG CCCgaggctt ---------- ------CCAG CCAATCAGAG
P855597     386 CATGGCAGAG CCCgt----- ---------- ---------- CCAATCGGAG
                ********** ***                         **** **********
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alignment
position        751....... 761....... 771....... 781....... 791.......
P855595     365 AGCCTCAGag tcatcctccc gcccacccag cataca---G GCGGGGCGTt
P855596     410 AGCCCTAGTC cagtcagtcc ttccctcTGC ACTGCAGGAG GCACGGCAGC
P855597     411 AGCCCCAGTC aa-------- -------TCC ACCGCAGAGG GCGTGGCGTC
                **********                   *** ********** **********
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alignment
position        801....... 811....... 821....... 831....... 841.......
P855595     412 cctccttagc caatgggaaa agacattcgc ccgcggtccG CACGCGCTGc
P855596     460 GAGTCCCGTg gcaccgCGCG T--------- ---------G CGCACGCTGA
P855597     446 GCGTCCTGTa acgctaCGCG T--------- ---------G CGCGCGCTGA
                *********        **** *                  * **********
                                 **** *                  * **********

alignment
position        851....... 861....... 871....... 881....... 891.......
P855595     462 ttgcaaaggg gtggggttgt GGAGTGGATG CTTTGGCAAG ATGGCGGgg-
P855596     492 AGG------- ---------- GGCGGGGCTT CCTCGGCAAG ATGGCGGCCG
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P855597    478 GAG------- ---------- GGCGGGGCTT CCTTAGCAAG ATGGCGGCCG
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alignment
position       901....... 911....... 921....... 931....... 941.......

P855595    511 -----AGCGG CGTCCGCCAA GCTACTTCT- --ACCGCCAG CACCTTCGTG
P855596    525 CGGCCACCGG CCTGCGCCAA GCTGCTGCTg cgGCAGCCAG TACCTCGGTG
P855597    511 CGGCCAGCGG CCTGCGCCAG GCTGCTTCT- --GCAGCCAG TACCTCGGTG
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alignment
position       951....... 961....... 971....... 981....... 991.......

P855595    553 AAGCCCATTT TCAGTCGGGA CATGAACGAG GCCAAGCGGA GGGTGCGCGA
P855596    575 AAGCCCATTT TCAGTCGCGA CCTGAACGAG GCCAAGCGGA GGGTGCGCGA
P855597    558 AAGCCCATTT TCAGTCGGGA CCTGAAAGAG GCCAAGCGGA GGGTGCGCGA
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alignment
position       1001...... 1011...... 1021...... 1031...... 1041......

P855595    603 GCTCTACCGC GCcTGGTATC GGGAGGTGCC GAACACTGGT GAGAGGTAGC
P855596    625 GCTCTACCGC GCTTGGTATC GGGAGGTGCC GAACACCGGT GAGAGGCAGG
P855597    608 GCTCTACCGC GCTTGGTACC GGGAGGTGCC AAACACTGGT GAGAGGCAGG
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alignment
position       1051...... 1061...... 1071...... 1081...... 1091......

P855595    653 GGcttacgtG GGGACCCGGA GGCCGCCGCT CAAGGTcgta gccggcccgg
P855596    675 GGTGCATTCG GGGCGCCGGA GGCACCTGCC CAAGGTctc- ----------
P855597    658 GGTGCATTCA GGGCCCCGGA GTCACCAGTC CAAGGT---- ----------
               ********** ********** ********** ******
               ********** ********** ********** ******
               **       * ********** ********** ******
               **
               **
               **
               **

alignment
position       1101...... 1111...... 1121...... 1131...... 1141......

P855595    703 ccggggtttc tcaTGGGCCC AGCTGAGGTC ACCAACTTGG GCAGAGGCGA
P855596    714 ---------- ---TCGGCCG AGCTGAGGTC ACGTAGTGGG ACAGAAACGA
P855597    694 ---------- ------GCCG GGCTGAGGTC ACCTACTAGG ACAGAAAtGA
```

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

alignment
position      1151...... 1161...... 1171...... 1181...... 1191......
P855595  753 ctgcgggtGC TTCAGGGGAA GAGGGTCACC CGAGCCtacc atgggccgga
P855596  751 GCCCTGG-GC TTCGGGGGAA GGGGGTCACC CGAGCCAGAG TGCCCCACAC
P855597  728 GCCCTGG-GC TTCGGGGGAA GGGGGTCACA CGgaCCAAAG TGCCCCACCC
             ******* ** ********** ********** ********** **********
             ******* ** ********** ********** ********** **********
             ******* ** ********** ********** **  ****** **********
                     ** ********** *********      **
                     ** ********** *********

alignment
position      1201...... 1211...... 1221...... 1231...... 1241......
P855595  803 cctggcggcg gcgcggtggt cagaccggcc gtgcctagca ttcgtacGTG
P855596  800 CGGGACAGGG CTTCCGA--- ---------- ---------- -------GCG
P855597  777 CGGGACAGGG CTTCCGA--- ---------- ---------- -------GAG
             ********** *******                                ***
             ********** *******                                ***
             ********** *******                                ***

alignment
position      1251...... 1261...... 1271...... 1281...... 1291......
P855595  853 CTATCGGAGC TTTGGTCTCT TTTGTCCTTc gcaattggcg ggaggacgat
P855596  820 CCCcAGTTGC TTTGGTGGCC TTTGTTCCTt a-TTTCTTAT GGAGCCCCTG
P855597  797 CCCTAGTCGC TTTGGTGGCC TTTGTTCCTa tgTTTCTTAC AGAGCCCCAG
             ********** ********** *********    ******** **********
             *** ****** ********** *********
             ***

alignment
position      1301...... 1311...... 1321...... 1331...... 1341......
P855595  903 gactgtcagt gacacactca ctttgtgggt gaggcagcgg aggcaccgag
P855596  869 GGAGGGGCG- ---------- ---------- ---------- ----------
P855597  847 GGAGGAGCGa gcagggacta tgagaaag-- ---------- ----------
             *********

alignment
position      1351...... 1361...... 1371...... 1381...... 1391......
P855595  953 aggtGAAGTG ATGTGCCCAG GGCCCAGGCC GAGCCACTGT TGTacccag-
P855596  878 ---------- -----TCCGC GGTCCTGAGC TAGCCCCGGG TGCTTCTTGA
P855597  875 ----GAATTG ACGCGTCCGC GGTCCCACGC TAGCCCCAGG TGTTTCTGGA
                 ****** ********** ********** ********** **********
                             ***** ********** ********** **********

alignment
position      1401...... 1411...... 1421...... 1431...... 1441......
P855595 1002 ---------- ---------- ---------- ---------- ----------
P855596  913 ACCCagCTTT ACAGTTCCAG AGAAGGTTCT AGATGCCCAT TCGAtTTTGT
P855597  921 ACCCgaCTTT ACAGTTCCAG AAAATGTTCC AGATGCCCAT TAGAcTTTGT
             ****  **** ********** ********** ********** **** *****
             ****  **** ********** ********** ********** **** *****
                   **** ********** ********** ********** **** *****

alignment
position      1451...... 1461...... 1471...... 1481...... 1491
P855595 1002 ---------- ---------- ---------- ---------- ----
P855596  963 AACTAAAGTG GCGAAGGGCT TTAGCAGTTA Tctgttactt agtc
P855597  971 AACTAAAGTG GCAAAGGGCT TTAGCAGTTA 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.

	P855596 (1006 bp)	**P855597 (1001 bp)**
P855595 (1001 bp)	0.298 32 %	0.277 34 %
P855596 (1006 bp)		1.000 71 %

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

Extract alignment region	
Positions in alignment	from: to:
Output file	dialign.seq

Extract aligned sequences

For comments, questions or bug reports, please contact support@genomatix.de

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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 **Mon Jun 6 23:42:11 2005**

Solution parameters:

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

Aligned Sequences:

No.	Sequence Name	Sequence Description	Length
1	P878819	sym=NDUFA7|loc=Loc4701|taxid=9606|spec=Homo sapiens|chr=19|ctg=NT_077812|str=(-)|start=989762|end=990762|len=1001| tss=501| comm=NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 7, 14.5kDa; (NM_005001/517/bronze;)	1001 bp
2	P878820	sym=Ndufa7|loc=Loc66416|taxid=10090|spec=Mus musculus|chr=17|ctg=NT_039649|str=(+)|start=10247921|end=10248946| len=1026|tss=501,524,526|comm=NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 7 (B14.5a); (AK010299/526/gold;AK002476/501/gold;AK003468/501/gold; NM_023202/524/bronze;)	1026 bp
3	P878821	sym=na|loc=Loc299643|taxid=10116|spec=Rattus norvegicus|chr=7|ctg=NW_047773|str=(+)|start=16320701|end=16321701| len=1001|tss=501| comm=similar to NADH oxidoreductase; (XM_216859/524/bronze;)	1001 bp

Alignment (DiAlign format):

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

V$AHRR V$HIFF V$P53F V$SP1F V$ECAT V$HESF V$MTF1 V$YY1F V$CREB V$EBOX V$TBPF V$STAF
V$WHZF V$NFKB

```
alignment
position        1 .........  11 ........  21 ........  31 ........  41 ........
P878819      1  agatatgaat  tcagagaacg  tgtcggggcc  agaatacaga  tcgttaaagg
P878820      1  nnnnnnnnnn  nnnnnnnnnn  nnnnnnnnnn  nnnnnnnACC  AAAGCTTTCA
P878821      1  aaaa------  ----------  ----------  -------ACC  AAAGCTTTCA
```

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

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

P878819   51  gaaccatcag aacccc---- ---------G TGATGAAATG AGAATCGGCT
P878820   51  AAGGCAGtct tactacggTA TCCGCGTTTC TTACAAAGTC ATATCCTc--
P878821   18  AAGACAGaca ttgtaaatTA TCCAGGTTTG TGACAAAGTT ATATCCTTCT
              *******            ** ********** ********** **********
              *******            ** ********** ********** *******

alignment
position      101....... 111....... 121....... 131....... 141.......

P878819   88  CCCGGATTCC GGCTGGCAGg ggttagggca gggtagaggt cacatcaggg
P878820   99  -CCTGAACCT AGCTACTAGA ATTAAACGTC ACCAAATCCA G-TTATAATC
P878821   68  TCCTAAACCT AGCAGTTAGG ATTAAACATC ACCAAACCCA GcTAATAAGC
              ********** ********** ********** ********** * ********
               ********* ********** ********** ********** *

alignment
position      151....... 161....... 171....... 181....... 191.......

P878819  138  tttaggt--- ---------- ---------- --CGCCGGCA GTCGGCCAAA
P878820  147  CTGGTACTCG GGAGGA---- CTCCGCTCCG ACCCCAGGAA GTGGTCCGAA
P878821  118  CTGGTATTTA GGAGGAcccg CTCCGACCGG ACCCCAGGAA GTGGTCGGAA
              ********** ******     ********** ********** **********
                                  ********** ********** **********
                                  ********** ********** **********

alignment
position      201....... 211....... 221....... 231....... 241.......

P878819  163  TGCCCCCACC CGATTACCTG CGTGCACTGT CCCTGAGAAC CGGTCCTGCC
P878820  193  TGTTCCCATC a-CTCACCTG CGTGCACTGT CCCTGCGAAC CGGTCCTGCC
P878821  168  AGTTCCCATC CGCTCACCTG CGTGCACTGT CCCTGCGATC CGGTCCTGCC
              ********** ********** ********** ********** **********
              ********** ********** ********** ********** **********
              ********** ********** ********** ********** **********
                  ******   ******** ********** ********** **********
                  ******   ******** ********** ********** **********
                           ******** ********** ********** **********
                           ******** ********** ********** **********
                              ***** ********** ********** **********
                              ***** ********** ******** * **********
                              ***** ********** ******** * **********

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

P878819  213  CAGGACCTTG GTGACCTGGA GGAAAGAAGc tgggttcaga cccggcccgt
P878820  242  CAGCACTTTG GTTACCTACA GGAAATAAGG GAAAGTTAgg ctCGACATGT
P878821  218  CAGCACTTTA GTTACCTACA GGAAAGAAGA GACAGTTAaa ccCGACAGGT
              ********** ********** ********** ********     ********
              ********** ********** ********** ********     ********
              ********** ********** ********** ********     ********
              ********** ********** *********
              ********** ********** *********
              ********** ********** *********
              **
              **
              **
              **

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

P878819  263  ttggctcctc taatccctcc ccctgccccc aaattcgggc ccc-CACCTC
P878820  292  TCAGCTTTCT TCTCTCTTTA TTCAGGTTTC TAAACACCCG CAGTCGCCTC
P878821  268  CCAGCTTTCT TCTTTCTTTA TTCAGGCTTC TAAACACCCG TAGTCACCTC
              ********** ********** ********** ********** **********
              ********** ********** ********** ********** **********
              ********** ********** ********** ********** **********
                                                 ******** **********
                                                              ******
```

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

P878819 312 ACCCTGGCCA GCTTGATAGG CTGCACACGG CTgGTGTCCA TGATGGCGGC
P878820 342 ACCCTAGCCA GCTTGATGGG CTGCACGCGA CTCGTGTCCA TGATGGCGGC
P878821 318 ACCCTAGCCA GCTTGATGGG CTGCACGCGA CTCGTGTCCA TGATGGCGGA
            ********** ********** ********** ********** **********
            ********** ********** ********** ********** **********
            ********** ********** ********** ********** **********
            ********** ********** ********** ********** **********
            ********** ********** ********** ** ******* **********
            ********** ********** ********** ** ******* *********
            ********** ********** ********** **
            ********** ********** ********** **
            ********** ********** ********** **

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

P878819 362 Gcggcggcgg TCTGGCGGAG AGGAGTCACG TGCTTCGGGG AGAGCCTTTA
P878820 392 GA-------- TCTGGCGGAG AGGAGTCACG TGAGCAGGGG ATGCCTTTTA
P878821 368 GA-------- TCTAGCGGAG AGGAGTCACG TGAGCAGGGG ATGCCATTTA
            **         ********** ********** ********** **********
            **         ********** ********** ********** **********
            **         ********** ********** ********** **********
            **         ********** ********** ********** **********
            *          ********** ********** ********** **********
                       ********** ********** ********** **********
                           ****** ********** **
                           ****** ********** **

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

P878819 412 TAGGACGTTC TAGCACCGCC cac--TCCCG TCTCGCGATA CCacgccgcg
P878820 434 TAGTCGGCTC TGACCACGCC TCACTTTCGC TCTCGCGAGA CCGCACGCgG
P878821 410 TAGTCGGCTC gGACCACGCC TCACTTCCGC TCTCGCGAGA CCGCACGCaG
            ********** ********** ********** ********** ******** *
            **********  ********* ********** ********** ******** *
            **********  ********* ********** ********** ******** *
            **********  ********* ********** ********** ********
            **********
            ***

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

P878819 460 tctTTCCCAG CAGCCCCAGC GGTGGAGACG TCACCGGCtg cgcccttcag
P878820 484 ---TACCCAG GAATCCTCGG GACAGAGTCG TCACCAGCGT CCTTCGGA--
P878821 460 ---TACCCAG GAACCCTCGG GGCAGAATCG TCACCGGCGT CCTTCGGA--
               ******* ********** ********** ********** ********
               ******* ********** ********** ********** ********
               ******* ********** ********** ********** ********
               ******* ********** ********** ********     ******
                                                          ******

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

P878819 510 tatcGCGGAC GGAAGATGGC GTCCGCCACC CGTCTCATCC AgcgGCTGCG
P878820 529 ----GCGGAA GGAATATGGC GTCCGCTACT CGCGTTATCC AAAAGCTGCG
P878821 505 ----GCGGAA GGAATATGGC GTCCGCTACT CGCGTTATCC AAAAGCTTCG
                ****** ********** ********** ********** **********
                ****** ********** ********** ********** **********
                ****** ********** ********** ********** **********
                ****** ********** ********** ********** **********
                ****** ********** ********** ********** *   ******
                ****** ********** ********** ********** *   ******
                ****** ********** ********** ********** *   ******
                ****** ********** ********** ********       ******
```

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

P878819 560 GAACTGGGCG TCCGGGGTGC Gcggggcgga cagggctgca ccatGGGGGG
P878820 575 GAACTGGGCG TCTGGGGTGC GTGTGCTGtT CCGATCCGGG CCG-GGAAGG
P878821 551 GAACTGGGCG TCTGGGGTGC GTGTACTG-T CCGACCCCGG CCG-GGAAGG
            ********** ********** ******** * ********** *** ******
            ********** ********** ******** * ********** *** ******
            ********** ********** ******** * ********** *** ******
            ********** ********** ********
            ********** ********** *
            ********** ********** *
            ********** ********** *
            ********** ********** *

alignment
position    651....... 661....... 671....... 681....... 691.......

P878819 610 CTTCGGGCTC CGTGTGTCCG GGAcccgctc ctgctcctca ccTCCCTCCT
P878820 624 ATTTGGGTTC TGTACGCCCT TGAATCCTA- ---------- --TCCCCCTT
P878821 599 CTTTGGGTTC TGTAAGCCCT CGAAACCTA- ---------- --TCCCTCTT
            ********** ********** *********              ********
            ********** **********  ********              ********
            ********** **********  ********              ********

alignment
position    701....... 711....... 721....... 731....... 741.......

P878819 660 AAgccgggac ccttcgctct ccccgaatct ccctgGGAAC CCCCAGCTAG
P878820 661 AACATCTCCT TAGTTCAGTG gataaTCCA- -----GGATC CCTGAATTTG
P878821 636 AACATCTGCT TAGTTCGGTG cggagTCCA- -----GGATC CCTGAATTTG
            ********** **********      ****       ***** **********
            ********** **********      ****       ***** **********
            ********** **********      ****       ***** **********

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

P878819 710 TCACCCCTTC AGCC---CGg gaccctctcc tggcctggga accactcagg
P878820 705 TGACTCCAGT AGTC---AGA CTCAAGGTCC TAAATGTTTT Tgg-CCGGGT
P878821 680 TGACTtccaa tagacagAGA CTCAATGTCC TAAATGTTTT TtgaCCGGAT
            ********** ****   *** ********** ********** *   ******
            *****             *** ********** ********** *   ******
            *****

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

P878819 757 c-CTGGGATT TCCccagtcc ccgaccttcT TAGCCTTGGA Tctgtgggcc
P878820 751 TACTGGGATT TCC------- ---------T TGGCCTTAGA TTGc------
P878821 730 TCTTGGAATT CCC------- ---------T TGGCTTTAGA TTGtcc----
            ********** ***                 * ********** ***
            ********** ***                 * ********** ***

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

P878819 806 cggactCTGG CTTTgctctt cacctgcagg acccacatcc gtttccccga
P878820 779 ------CTGG CTTTAGCTCC C--------- ---------- ----------
P878821 760 --------GG TTTTAGCTTC C--------- ---------- ----------
                  **** ********** *
                    ** ********** *

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

P878819 856 gtgttcatcc cctgccttcc cttaaaatgc gcatccccgg accatccctg
P878820 794 ---------- ---------- ---------- ---------- ----------
P878821 773 ---------- ---------- ---------- ---------- ----------

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

P878819 906 gTCCCTTGCC CTCTCCTTTC CTCTCTC--C tggggtgcct tgcaggccga
P878820 794 -CCCCGCCCC GCCCCTCTTC CTATCccttT ---------- ----------
```

```
P878821       773 -TCCCTCCCC TCCTCCTTTC CTATCTC--T ---------- ----------
                   ********* ********** *******  *
                   ********* ********** *****    *
                                                 *

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

P878819       954 cCTCTCCTCT CCTCttccca cagcatgacc t--------- ----------
P878820       823 -CTCTCTTCG CCTCATTTGT CTCCCACGTg ------AGAC CAGGTGTTTC
P878821       800 -CTCTCCTTG CCTCATTTGT CTTCCACGTt ccactcAGAA CTGGTGTTTC
                   ********* ********** *********        **** **********
                   ********* ********** *********

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

P878819       985 ---------- ---------- ---------- ---------- ----------
P878820       866 ctcatcCCCC GTATCAGCTT GGAATCTTtg tttgtt---- ----------
P878821       849 tttct-CCCT GTATCAGCTT TGAATCTTgt gcccctattt tcggaaggtc
                        **** ********** ********
                        **** ********** ********

alignment
position          1101...... 1111...... 1121...... 1131...... 1141......

P878819       985 ---------- ---------- ---------- -----GCAGG GGAAGCTGca
P878820       902 ---------- ---------- ---------- ---------- ------TGTT
P878821       898 gaaggccagt ttttagattt tggaagaaaa cagagGCCGG GGAAGCTGTA
                                                       ***** **********

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

P878819      1000 gc-------- ---------- ---------- ---------- ----------
P878820       906 TGTTTTTGTT TTTGTTTTTC TTTTTCGAGA CAGGgtttct ctgtgtagcc
P878821       948 AATTTCTGTA TCTTAATTTA GGGTCTAAGA AAGGaagtat atctagagct
                  ********** ********** ********** ****

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

P878819      1002 ---------- ---------- ---------- ---------- ----------
P878820       956 ctggctgtcc tggaactcac tttgtagacc aggctggcct tgaactcata
P878821       998 cagc------ ---------- ---------- ---------- ----------

alignment
position          1251...... 1261...... 1271

P878819      1002 ---------- ---------- -
P878820      1006 aatccgcctg cctctgcctc c
P878821      1002 ---------- ---------- -
```

Pairwise similarities:

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

	P878820 (1026 bp)	**P878821 (1001 bp)**
P878819 (1001 bp)	0.253 33 %	0.248 32 %
P878820 (1026 bp)		1.000 73 %

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

Extract alignment region	
Positions in alignment	from: ☐ to: ☐
Output file	dialign.seq

Extract aligned sequences

For comments, questions or bug reports, please contact support@genomatix.de

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GEMS Launcher 4.1.1

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

[Alignment] [Pairwise similarities]

DiAlign professional TF Release 3.1 December 2004 **Tue Jun 7 00:08:43 2005**

Solution parameters:

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

Aligned Sequences:

No.	Sequence Name	Sequence Description	Length
1	P884734	sym=NDUFA8|loc=Loc4702|taxid=9606|spec=Homo sapiens|chr=9|ctg=NT_008470|str=(-)|start=32242802|end=32243802|len=1001| tss=501| comm=NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 8, 19kDa; (NM_014222/501/silver;)	1001 bp
2	P884735	sym=Ndufa8|loc=Loc68375|taxid=10090|spec=Mus musculus|chr=2|ctg=NT_039206|str=(-)|start=13477407|end=13478407|len=1001| tss=501| comm=NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 8; (AK002744/590/gold;NM_026703/590/bronze;)	1001 bp
3	P884736	sym=na|loc=Loc296658|taxid=10116|spec=Rattus norvegicus|chr=3|ctg=NW_047653|str=(-)|start=1194484|end=1195484| len=1001|tss=501| comm=similar to Aa2-258; (XM_216044/581/bronze;)	1001 bp

Alignment (DiAlign format):

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

V$SORY V$BRNF V$SP1F V$ZBPF V$NRF1 U$NRF1 V$MINI V$GATA

```
alignment position 1.........  11.........  21.........  31.........  41.........
P884734          1 tacatctcca  actggattat  aaactccata  agagcaagga  tcttgacatt
P884735          1 cgcgctcg--  ----------  ----------  T---------  ----------
P884736          1 gggatacacg  cgctcatacg  gatacacaca  T---------  ----------
                                                       *
                                                       *
                                                       *
```

```
alignment position  51........ 61........ 71........ 81........ 91........
P884734         51  ttaaatattc ttattcctat gtttaaaact ggcagatagc ACACACACAC
P884735         10  ---------- ---------- ---------- ---------- ACACACACAC
P884736         32  ---------- ---------- ---------- ---------- ACACACACAC
                                                               **********
                                                               **********
                                                               **********

alignment position  101....... 111....... 121....... 131....... 141.......
P884734        101  Agtcaatg-- ---------- ---------- ---CACACAC ACATataagt
P884735         20  ACACACACAC ACACACgaat gaatgaatga aagaat---- ----------
P884736         42  ACACACACAC ACACACacac acacacacac acaCACACAC ACATcacta-
                    ********** ******                    ******* ****
                    ********** ******
                    ********** ******

alignment position  151....... 161....... 171....... 181....... 191.......
P884734        126  atatatgGAA TGAATGCATC TTAGCTTTGC TGCTTATTAG ATATg-GTCC
P884735         56  -------GAA TGAGTGAATC CTACCTATGC GACTTATTAG GTATCTGTGC
P884736         91  -------GAA TGAATGAATC CCACCTATGC GGCTTATTAG GTATCTGTGT
                           *** ********** ********** ********** **********
                           *** ********** ********** ********** **********
                           *** ********** ********** ********** *******
                           *** ********** ********** ********** *******
                           *** ********** ********** ********** ****
                           *** ********** ********** ********** ****

alignment position  201....... 211....... 221....... 231....... 241.......
P884734        175  TTGAAAAAAT TACTCGGGCA AGTTTGTGAA AGTGCCTGGC ACAAGGTGTT
P884735         99  TTGAGCACTA TAGTTGAACA AGTTTTTGAA AGCATTTGGC TGAGGGTCCT
P884736        134  TTGAGCACGT TAGTTGAACA CGTTTTT-AA AGTGCTTGGC TTAGGGTCCT
                    ********** ********** ********** ********** **********
                    ********** ********** ******* ** ********** **********

alignment position  251....... 261....... 271....... 281....... 291.......
P884734        225  TCGCAGAAgc ----AAAAAG CCGTCTTTTT CCAGTCacag ctattcaagg
P884735        149  TGGCGGAGgc ttaaAAACAG TTGTCTTTCA CTAGCCtgaa AGTGGAGACA
P884736        183  AGTCTGAGag ---------- ---------- ---------- AGTGGGTACA
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alignment position  301....... 311....... 321....... 331....... 341.......
P884734        271  tatagtaagt gaatcaaatg agccCCTTAC CTCCCATCTA caTATTCCCC
P884735        199  TGGACGAATG GGG------- ----GCTTAC CTCCCGTTTA TGTATTCCCC
P884736        203  TGGACGAAAG GGG------- ----CCTTAC CTCCCATTTT TGTATGCCCC
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alignment position  351....... 361....... 371....... 381....... 391.......
P884734        321  GATATATTTG CTCCCTGTGT ACTCCATGgc gcctgttttt agcttccagc
P884735        238  GAAATACTGG CTCCCGGTGT ACTGCATGTT AACAGCTAGT GTCTAACAGA
P884736        242  GATATATTTG CTCCCGGTGT ACTGCATGTT AACAGCTAGA GTCTAACAGA
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alignment position  401....... 411....... 421....... 431....... 441.......
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P884734         371 tgttaggaTC CGGAGTCTCA GTggatacGG CATCACTATG ACAACCTGGA
P884735         288 CACCAACTTC AGCtgtctt- --------GG CGTCACTATG ACAACCAGGA
P884736         292 CACCAACTTC AGCACTCTCA GT-------- -GTCACTATG ACAACTAGGA
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alignment position  451....... 461....... 471....... 481....... 491.......
P884734         421 GGGGTGGGCG GAGCCgaatc GAAGCCCCAC CCCGCTGGAg gCTGAAAAGT
P884735         329 GATGTGGGCG GAGACCAGAT GAAGCCCCGC CCCTCGGGAC -CGCTAGACT
P884736         333 GATGTGGGCG GGGCCCATAT GAAGCCCCGC CCCGCGGCCC -CAGTAGACT
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alignment position  501....... 511....... 521....... 531....... 541.......
P884734         471 TCTTGGTATT GCGCACGCTC CCTCGCTCgt ggttggg-CA GGGCAATACG
P884735         378 TCCTGGAATG GCTTACGCTT CGCCTCCTCC AGCGGCCCTA GAGCAGTGCG
P884736         382 TCCTGGAATG GCGTAAGCTC CGTCTTTCCG AGCGGCTCCA GAACAGTGCG
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alignment position  551....... 561....... 571....... 581....... 591.......
P884734         520 CCTGCGTGTT GCCGGATGCG CATGCGCAGg cgccgtgtgg cactcggcgg
P884735         428 CTTGCGCGTC GCTGGAGACG CATGCGCAGA TGGTACCGGG CAGTCTtggc
P884736         432 CATGCGCCTC GCCGGAGACG CATGCGCAGA TGGTATTGGG CAGTCTgaga
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alignment position  601....... 611....... 621....... 631....... 641.......
P884734         570 tcg--AAAGG GGAGTTCAAG GAGACGGGgg CGACGCGGCT GAGGGCTTCT
P884735         478 cAGCCAAAGG GGACTTGAAG GAGACGGG-- CGACACGGCC GAGGGCACCT
P884736         482 aAGCCAAAGG GGAATTGAAG GAGACGGG-- CGACACTGCC GAGGGCACCT
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alignment position  651....... 661....... 671....... 681....... 691.......
P884734         618 CGTCGGGGTC GGGGCTGCaG CCGTCATGCC GGGGATAGTG GAGCTGCCcA
P884735         526 GGTCAGGGTC GCGGCTACCG CCGTCATGCC GGGGATAGTG GAGCTGCCAA
P884736         530 GGTCAGGGTC GCGGCTGCCG CCGTCATGCC GGGGATAGTG GAGCTGCCAA
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alignment position 701....... 711....... 721....... 731....... 741.......
P884734        668 CTCTAGAGGA GCTGAAAGTA GATGAGGTGA GGCTa-TCCG GAGGACAGGC
P884735        576 CTCTGGAAGA GCTGAAAGTG GAGGAGGTGA GGCTCTTCCT GAGGGCAGGC
P884736        580 CTCTGGAAGA GCTGAAAGTA GAGGAGGTGA GGCTTTACCT GAGGGCAGGC
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alignment position 751....... 761....... 771....... 781....... 791.......
P884734        717 aaGGGAGACA TGGGGCTGCG GCTTctcggg cctgggccta gccccccttg
P884735        626 --GGGAAGCC TGGGATTGCA GCTTTCAGGC GGGCCcaggc aCGGTTCCGG
P884736        630 --GGG-AGCC TGGGATTGCA GCTGTCAGGC GGGCCatact -CGGTTCCGG
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alignment position 801....... 811....... 821....... 831....... 841.......
P884734        767 ggctccgcgg atcctgggac ccgggccccc ctccccagtc ctccaacgca
P884735        674 ---------- ---------- ---------- ---------- ----------
P884736        676 ---------- ---------- ---------- ---------- ----------

alignment position 851....... 861....... 871....... 881....... 891.......
P884734        817 tatacaggtc gacccccgga ggtcccctcc gcagctttgg gagtcgcctc
P884735        674 ---------- ---------- ---------- ---------- ----------
P884736        676 ---------- ---------- ---------- ---------- ----------

alignment position 901....... 911....... 921....... 931....... 941.......
P884734        867 cCCTCTCTAC CCCACCCTGT CGCATCTTGC AGTGGCTCTA Gaatcctccc
P884735        674 -CCTCTGCGA CCTGCATGGT CACATCTCGC CTTGGCTCCA GCCATTCCTG
P884736        676 -CCTCTGCGA CCTGCACGGT CACATCCCGC CTt-GCTCCA GACATTCTTG
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alignment position 951....... 961....... 971....... 981....... 991.......
P884734        917 cctttcgccc tcCACAGCGA CCTATTCTCC CTTCCGTGAA TaataGTGAT
P884735        723 TGCG------ --CACTGCGA CCGGCCTCTC TTCTTGTGAA TCGG-GTGAT
P884736        724 TGCG------ --CACCGAGA CCGACCTCTC CTCTTATGAA TCGG-GTGGT
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alignment position 1001...... 1011...... 1021...... 1031...... 1041......
P884734        967 ACATTTTATT Aagcaccaac cagtcatttt actta----- ----------
P884735        764 ACTTTCCATT AGCATCACCT AGCCCCTTGC TCTCCCTCCC GGTGAGGCGA
P884736        765 ACTTTCCGTT AGTATCACCT AGCCCCTTGC TCTCCCTCCC CGTGAGGCGA
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alignment position 1051...... 1061...... 1071...... 1081...... 1091......
P884734       1002 ---------- ---------- ---------- ---------- ----------
P884735        814 GCCTGCCTCC tcttggtgct caccttccCC TTCCAAGTCT GTCAAAATCT
P884736        815 GTCTGCCTCC ccaaatgctc a-------CC TTCCAAGTCT GTCAAAACCT
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alignment position 1101...... 1111...... 1121...... 1131...... 1141......
P884734       1002 ---------- ---------- ---------- ---------- ----------
P884735        864 CGGTGCAGAG CAGGCCTGgg tGCCGCGGCA GCACACAGTA CGTGTTGGAC
P884736        858 CGGTGCAGAG CAGGCCTGga aGCCGCGGCA GCACACAGTG TGTGTTGGAC
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alignment position 1151...... 1161...... 1171...... 1181...... 1191......
P884734       1002 ---------- ---------- ---------- ---------- ----------
P884735        914 AGTGAGTCTG GcaTGGGCCA GGGTGTTTTG GTAATGGGAC ACAAgTAAAG
P884736        908 AATGAGTCTG GtgTGGGCCA GGTTGTTTTG GTAATGGGAC ACAAtTAAAG
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alignment position 1201...... 1211...... 1221...... 1231...... 1241
P884734       1002 ---------- ---------- ---------- ---------- ----
P884735        964 CATTTACTTC TTCGAGAGAC ATTTAAGTAT TTgttatg-- ----
P884736        958 CATTTACTTC TTCAAGAGGC ATTTAAGTAT TTtgttatgt gcac
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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.

	P884735 (1001 bp)	**P884736 (1001 bp)**
P884734 (1001 bp)	0.242 43 %	0.251 38 %
P884735 (1001 bp)		1.000 80 %

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

Extract alignment region	
Positions in alignment	from: to:
Output file	dialign.seq

Extract aligned sequences

For comments, questions or bug reports, please contact support@genomatix.de

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License Agreement

GEMS Launcher 4.1.1

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Genomatix Main GEMS ElDorado Gene2Promoter BiblioSphere
Frequently asked questions Your Results Your Sequences Your Protocol Help

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

[Alignment] [Pairwise similarities]

DiAlign professional TF Release 3.1 December 2004 **Tue Jun 7 00:50:41 2005**

Solution parameters:

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

Aligned Sequences:

No.	Sequence Name	Sequence Description	Length
1	P921928	sym=NDUFA9|loc=Loc4704|taxid=9606|spec=Homo sapiens|chr=12| ctg=NT_009759|str=(+)|start=4612044|end=4613044|len=1001| tss=501| comm=NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 9, 39kDa; (NM_005002/503/bronze;)	1001 bp
2	P921929	sym=Ndufa9|loc=Loc66108|taxid=10090|spec=Mus musculus|chr=6| ctg=NT_039356|str=(-)|start=2341012|end=2342012|len=1001| tss=501| comm=NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 9; (NM_025358/501/bronze;)	1001 bp
3	P921930	sym=nalloc=Loc362440|taxid=10116|spec=Rattus norvegicus| chr=4|ctg=NW_047696|str=(-)|start=16340910|end=16341910| len=1001|tss=501| comm=similar to NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 9; (XM_342761/501/bronze;)	1001 bp

Alignment (DiAlign format):

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

V$YY1F V$BRNF V$OCT1 V$AP1F V$STAT V$NRF1 U$NRF1 V$STAF V$BRAC V$CREB V$HIFF V$TEAF
V$VBPF

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alignment position 1.........  11.........  21.........  31.........  41.........
P921928          1 ttggga----  ----------  ----------  ----------  ----------
P921929          1 ggatgttcct  ggcGGCGTTG  GCGT------  ---------G  CGAGGGGCTT
P921930          1 ttttgat---  ---GGCGTTG  GCGTgcactt  actttggcgG  CGAGGGGCTT
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alignment position 51........ 61........ 71........ 81........ 91........
P921928          7 ---------- ---------- ---------- ---------- ----------
P921929         36 agGGTGGGGG CGCCTCTGCA TTTCTATTTA ACTCCCCCac ttgtacactg
P921930         45 gaGGTGGGGG CGCCTCTGCA TTTCTATTTA ACTCCCCCca ctgtaat---
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alignment position 101....... 111....... 121....... 131....... 141.......
P921928          7 ----CACACC CTATTt---- TGGTTTCTCT TCTCCACTTt tcccctcgtt
P921929         86 tacGCAGACC CTATTACACC TTTTTCCTCc gTGCAACTCC TT--------
P921930         92 ---GCAGATC CTATTACACC TGTTTTCTCT TTGCAACTTC TT--------
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alignment position 151....... 161....... 171....... 181....... 191.......
P921928         49 cttgtccccc cttttctctc tcctgggccc tggatctcct gaGCGCGGAG
P921929        128 ---------- ---------- ---------- ---------- --GAGTGCAG
P921930        131 ---------- ---------- ---------- ---------- --GAGTGCAG
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alignment position 201....... 211....... 221....... 231....... 241.......
P921928         99 GGCTACGCCT CCTTCTTCCT CCGGActcac cAGGGCTGCC AGCTTAGCTT
P921929        136 GGGCACCCTT CCTTCTTACC CCTGC----- -AGAGCTGTC TGACTCTTTT
P921930        139 GGACACCCTT CCTCCTTACC CCTGA----- -AGAGCTGTC AGACCCTTTC
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alignment position 251....... 261....... 271....... 281....... 291.......
P921928        149 ACATTTTCAG GGAACAGGAA Actgagagtc aggaaaggtg agctcttcta
P921929        180 TGGTAATTAG CCCATAGAAA AAGgGTCTTT GAAAG----- ----------
P921930        183 TGGcca-TCG CCCCTAGAAT GAGcGTCTTT GAAAG----- ----------
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alignment position 301....... 311....... 321....... 331....... 341.......
P921928        199 cctcgggtCT TGCCATTTTG CATGTCCT-G AGTCAGTCAC TGGTTAACTC
P921929        215 --------CT GGCCATTTTG CATGCCCTTG AGTCAGTCCT TGGTTAACTC
P921930        217 --------CT GGCCATTTTG CATGCCCTTt AGTCAGTCCC TGGTTAACTC
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alignment position 351....... 361....... 371....... 381....... 391.......
P921928        248 TGAACTTCAG GTTCCTCGGc aattagagat tataaaTAGC CTATACAGCC
P921929        257 TGAAATGCAG ATTCCCCGGA AATATCAGG- ------TGGT CTTCACAACC
P921930        259 TGAAATGCAG ATTCCCCaGA AATATCAGA- ------CGGC CTTCACAACC
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alignment position  401....... 411....... 421....... 431....... 441.......
P921928         298 TATTCCAGAT CTGAGATTCC aacagccaaa gt------CT TTTCACTTCC
P921929         300 CATTCCAAAA CCGGGACTgt aTTTTCCCCT GCCTTCTCCT CCTCTTTTTC
P921930         302 CATTACAGAT CCCGGATTCT gTTTTCCCCT GCCTTCTCTC CCTCTCTTTT
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alignment position  451....... 461....... 471....... 481....... 491.......
P921928         342 TTTCT--TCC CCCTCTCCTT CACTTTCCCA GCTTTCTTCT TAACCAACAA
P921929         350 TTTTT--CTC TCCTCTGCTT TTACTCCCAG GCTCTCTTAT CAACCATCAA
P921930         352 TCTTTtcTCT ACCTCTGCTT TCACTCCCAG TCTCTCTGAT CAACCtgggc
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alignment position  501....... 511....... 521....... 531....... 541.......
P921928         390 TCTACCcgaa accgtcgtTT CTTGGTTAGC GCTTGCGCAG ACAGGcgaga
P921929         398 CCTGCCACTT CCG-----TT CCCAGTTGGC GTTTGCGCAG AGAGGTCCtt
P921930         402 cccGCCACTT CCG-----TT CTCAGTTGGC GTCTGCGCAG AGAGGTCCat
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alignment position  551....... 561....... 571....... 581....... 591.......
P921928         440 aAGGTAAGTT TTGACCCAGC TTAGCAGCCG TAGTCAGCCG ggagtgctgt
P921929         443 gAGATACCAT TTGACCCCGC GTTGTTGCCG TAGTTGGCGG AAGCACCGGC
P921930         447 gaga----TT TTGGCCCTGC GTAATTGCCG TAGTTGGCGG AAGCGCCGGC
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alignment position  601....... 611....... 621....... 631....... 641.......
P921928         490 CGTGGGGGAT TGTGGGAAAA GATGGCGGCT GCCGcacaat ccCGGGTTGT
P921929         493 CGTGAGGCAT TGTGGGAGAA GATGGCGGCC GCCGTCCGCT TTCGGGTTGT
P921930         493 CGTGAGGCAT TGTGGGAGAA GATGGCGGCC GCCGTCCGCT TTCaGGTTGT
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alignment position  651....... 661....... 671....... 681....... 691.......
P921928         540 ccgggtcctg tCAATGTCAC GTAAGTGTTA CCGGGAACgg cGGCCCCTGG
P921929         543 TAGAGCGCTT CCAATGTCAC GTAAGTGTCA CCGGGGACCG -GGTCTTGGG
P921930         543 TAGAGCGCTT CCAATGTCAC GTAAGTGTCA CCGGGTACCG -GGTCTTGGA
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alignment position 701....... 711....... 721....... 731....... 741.......
P921928        590 TCGGGATTCC GAGACGGGGA TTTA-AGGTT Ttggaagtgg caccgtgctg
P921929        592 GTTGCATTCG GCGACGGGAA CATG-ACCTT TCTTCCTCAT AC--------
P921930        592 GCTGCATTCC GCGACGGGAA CAaaaACCTT TCTTCCTCAT AC--------
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alignment position 751....... 761....... 771....... 781....... 791.......
P921928        639 cagcggtcac gccaacttcc taggcacact ctggtttctc taggtttgga
P921929        633 ---------- ---------- ---------- ---------- ----------
P921930        634 ---------- ---------- ---------- ---------- ----------

alignment position 801....... 811....... 821....... 831....... 841.......
P921928        689 gctgcctcag tctggtttct cctttcgctt tccgcttCCC CGGCTCACAT
P921929        633 ---------- ---------- ---------- -------TCT TGGCTCATGT
P921930        634 ---------- ---------- ---------- -------CCT TGGCGCATGT
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alignment position 851....... 861....... 871....... 881....... 891.......
P921928        739 ATTCAATTGT GCACcacctt GGGAGGGGAC aaaAGATCTT AAGCAGCTGT
P921929        646 GTGAAACTG- -CACTCG--- GCAAGGGGAC GG-AGAGCTG GAGGAGCTGG
P921930        647 GTGAAACTGT GCACTCG--- GGGAGGAGAC GG-AGAGCTG GAGTAGTTGG
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alignment position 901....... 911....... 921....... 931....... 941.......
P921928        789 AAGCGAAGAG GAGAATGCGG gg---GAC-A CGTTAGGGAT cgagagaatc
P921929        690 GAGGGACGAG GAGAACCCGG ACACTGAC-A GGTTCGAGAT ----------
P921930        693 GTGAGACGAG GAGGACCTGG ACACTtaaaA GGCTCGAGAT ----------
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alignment position 951....... 961....... 971....... 981....... 991.......
P921928        835 agAATTCTGA TATGGTTGTA AGGGTTTAGG Gttat----- ----------
P921929        729 --AGTGCGTG GATTGTGGGG AAGGTTGCGG tccaagagag tacttatcca
P921930        733 --AATGCGGA GATTGTTGGG AAGGTTGAGG Gcaaaggaac tacttaggga
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alignment position 1001...... 1011...... 1021...... 1031...... 1041......
P921928        870 ---------- ---------- ---------- ---------- ----------
P921929        777 ggGGAAAGGG GGCTTGGACG GCAGGACATC GATTGACTTC ATGGTGGTGA
P921930        781 --GGAAAAGG GGTTTGGACA GCTGGACATC GATTGGCTTC ATGGTAGTAA
                     ******** ********** ********** ********** **********
                     ******** ********** ********** ********** **********
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alignment position 1051...... 1061...... 1071...... 1081...... 1091......
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P921928        870 ---------- ---------- ---------- ---------- ----------
P921929        827 TCGCACTGGA AATCAGAATC CGCGCCACAG A-------TG TCAGGTTGTG
P921930        829 TTGCAATGGA AATCATAATC CGCTCCACGG AtggagtcTG TCAGGTTGTG
                   ********** ********** ********** *       ** **********
                   ********** ********** ********** *       ** **********
                   ********** ********** ********** *       ** **********
                                                            ** **********

alignment position 1101...... 1111...... 1121...... 1131...... 1141......
P921928        870 ---------- --------GA GAAATATTTG TATGGGGCGG GGGGAGAAAT
P921929        870 GCGGTAGGGA CTGCAGCAGC GAGAGATGGT TGTGGAGAGT CGGGAGCTGG
P921930        879 GCGCTAGGGT CTGCAGCAGA GAAAGATGTT TGTGGAGAAT TGGGAGCTGG
                   ********** ********** ********** ********** **********
                   ********** ********** ******** * ********** **********
                   ********** ********** ******** * ********** **********
                   ********** ********** ******** * ********** **********

alignment position 1151...... 1161...... 1171...... 1181...... 1191......
P921928        902 GTGTAAGGga gggaaaaaag gctagtggcg agaggttttc ttAGATTGAT
P921929        920 GTGGAAAGAA AAGTGAAGGa CCGCTTAGAA TTTGTCA--- --GCGTTGTT
P921930        929 GTGGAAAGAA AAGCGAAGG- CCGCTTAGAA TTTGTCA--- --ACATTGTT
                   ********** *********  ********** *******      ********
                   ********** *********  ********** *******      ********
                   ********** *********  ********** *******      ********
                   ********** *********  ********** *******      ********
                                         ********** *******      ********

alignment position 1201...... 1211...... 1221...... 1231...... 1241......
P921928        952 TTTATGACCT TGTGCAAACC CTTAATgggt ctcaattcat atgagcacaa
P921929        965 TATTTACTCT TCTGtcGTGA TTGAATGTGt tcacagc--- ----------
P921930        973 TATTTACTCT TCTGCTGTGC TTGAATCTG- ---------- ----------
                   ********** ********** *********
                   ********** ****
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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.

	P921929 (1001 bp)	P921930 (1001 bp)
P921928 (1001 bp)	0.156 40 %	0.156 34 %
P921929 (1001 bp)		1.000 79 %

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

Extract alignment region	
Positions in alignment	from: ☐ to: ☐
Output file	dialign.seq

Extract aligned sequences

For comments, questions or bug reports, please contact support@genomatix.de

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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 Jun 7 01:08:06 2005**

Solution parameters:

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

Aligned Sequences:

No.	Sequence Name	Sequence Description	Length
1	P982079	sym=NDUFA10|loc=Loc4705|taxid=9606|spec=Homo sapiens|chr=2|ctg=NT_005416|str=(-)|start=138902|end=139902|len=1001| tss=501| comm=NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 10, 42kDa; (NM_004544/501/silver;)	1001 bp
2	P982083	sym=Ndufa10|loc=Loc67273|taxid=10090|spec=Mus musculus|chr=1|ctg=NT_039173|str=(-)|start=6870406|end=6871447| len=1042|tss=501,506,542| comm=NADH dehydrogenase (ubiquinone) 1 alpha subcomplex 10; (AK013675/517/gold;AK005339/522/gold;NM_024197/558/silver;)	1042 bp
3	P982085	sym=Ndufa10|loc=Loc314071|taxid=10116| spec=Rattus norvegicus|chr=9|ctg=NW_047817|str=(-)|start=7820309|end=7821309|len=1001|tss=501| comm=NADH dehydrogenase (ubiquinone) 1 alpha subcomplex 10; (XM_234089/558/bronze;)	1001 bp

Alignment (DiAlign format):

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

V$MAZF V$CREB V$E4FF V$HESF V$MOKF V$EREF V$SF1F V$REBV V$EBOX

```
alignment position 1.........  11.........  21.........  31.........  41.........
P982079          1 tggatgagac  cacttagcct  tcagctccgg  aggcga----  ----------
P982083          1 ttctctcaga  aacctaggca  gggagaatgt  gacgccccta  gaactcagat
P982085          1 ----------  ----------  ----------  ----------  ----------
```

```
alignment position 51........ 61........ 71........ 81........ 91........
P982079         37 ---------- ---------- ---------- ---------- ----------
P982083         51 ggggaatgga ctctctcctc agcgaccaga aggGCGGGGA GCGGATCCTC
P982085          1 ---------- ---------- ---------- ---GCAGTGA GCAGATCCTC
                                                       ******* **********

alignment position 101....... 111....... 121....... 131....... 141.......
P982079         37 ---------- ---------- ---------- ---------- ----------
P982083        101 CCTACAGaac tcaaa----- ---------- CAGAAAGTGG GTCtacgttt
P982085         18 CCCTCAGact gggagtgggt ccatgcaacc CAGGAAGTGG ATCctcttgt
                   *******                          ********** ***

alignment position 151....... 161....... 171....... 181....... 191.......
P982079         37 ---------- ---------- ---------- ---------- ----------
P982083        136 gg-------- GCGTGGAGCA GGGAGACAGC A--------- --CAGATTCT
P982085         68 cagagctcga GCGTGGAGCA GAGAGGCAGC Aggttctcac tgCAGAATCT
                              ********** ********** *            ********
                                                                 ********
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alignment position 201....... 211....... 221....... 231....... 241.......
P982079         37 ---------- ---------- ---------- ---------- ----------
P982083        167 GGGGAGCGAG AGGATTCACC CCACAGAACA CCtgggagtg gggg------
P982085        118 GGGGAGCGAG CGGATCCACC CCACAGAATA CCcagagaga ggaggggtga
                   ********** ********** ********** **
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                   ********** ********** ********** **

alignment position 251....... 261....... 271....... 281....... 291.......
P982079         37 ---------- ---------- ---------- ---------- ----------
P982083        211 GTCACACTTT TGTCACACAA CTCAAGCATC TGCGAGA-AC CCGAGCTCAA
P982085        168 GTCACACTTT TGTCACACAA CTCCAGCATC TGCGAGAaAC CCGAACTCAA
                   ********** ********** ********** ******* ** **********
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alignment position 301....... 311....... 321....... 331....... 341.......
P982079         37 ---------- -------CCC A--------- ----GGCCGG CCTTgccagg
P982083        260 AGCTGGGAGC CTCaaggCCC A--------- ----GGCAGG ACTTCTAGCC
P982085        218 GACTGGCAGC CTCcgtgcaa ttcacaaggc tcagGGTGGG TCTTTTCGCC
                   ********** ***    *** *              ****** **********

alignment position 351....... 361....... 371....... 381....... 391.......
P982079         57 tccctctccc tgacaggcgc cccgcgacag gggtcccacc ccgtccctcC
P982083        297 CTTTGCCACT TTCATACTAT Aacttgtcta ggatctagGC G--------C
P982085        268 CTTCCCCAGA CTTGTACTGT Atgggtcgag gaagta--GC A--------C
                   ********** ********** *                  ** *        *
                                                            ** *        *
                                                                        *

alignment position 401....... 411....... 421....... 431....... 441.......
P982079        107 GCTCCTCGCC Ccctcttttt ccactttccc tccccagcga gaacgttctg
P982083        339 GCTCCTCGCC CAAACAATCT AAgctcaagc aactagagcg tcgacaa---
P982085        308 GCTCCCCGCC CAAACAATCT AAaccccggc ccagagccgc aatctaga--
                   ********** ********** **
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alignment position 451....... 461....... 471....... 481....... 491.......
P982079        157 agagctagga atgttctcta ggaggtcgct ttgacgtcca caccgcgcct
P982083        386 ---------- ---------- ---------- ---------- ----------
P982085        356 ---------- ---------- ---------- ---------- ----------
```

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alignment position 501....... 511....... 521....... 531....... 541.......
P982079        207 gggggattct gcggggagca caggaccctg ggacgagacg cagaagtcgc
P982083        386 ---------- ---------- ---------- ---------- ----------
P982085        356 ---------- ---------- ---------- ---------- ----------

alignment position 551....... 561....... 571....... 581....... 591.......
P982079        257 tccacgccct gggcgGCCTC AGCTCCcgcg acaccgcagc aactcagaac
P982083        386 ---------- -----GCCTA AGCTCCGCCC CTTCCCTCT- ----------
P982085        356 ---------- ------CCTA AGCCCCGCCC CTTCCCTCT- ----------
                              ***** ********** *********
                               **** ********** *********
                               **** ********** *********

alignment position 601....... 611....... 621....... 631....... 641.......
P982079        307 ccaggcaggg gccgggcagc cagcatgctg cccccacgtt cacctccaac
P982083        410 ---------- ---------- ---------- ---------- ----------
P982085        379 ---------- ---------- ---------- ---------- ----------

alignment position 651....... 661....... 671....... 681....... 691.......
P982079        357 tcccacctct cggccctcgc cccaacccgc aggaccctgg cagcgcactg
P982083        410 ---------- ---------- ---------- ---------- ----------
P982085        379 ---------- ---------- ---------- ---------- ----------

alignment position 701....... 711....... 721....... 731....... 741.......
P982079        407 gctgtctccg cggaagcccc cgagggcctc ggcgcGGCCC CGCCCCctgg
P982083        410 ---------- ---------- ---------- -----GGCCC CGCCCCGTCc
P982085        379 ---------- ---------- ---------- -----GGCTC TGCCCCATCt
                                                          ***** *********
                                                          ***** *********
                                                          ***** *********
                                                          ***** ******

alignment position 751....... 761....... 771....... 781....... 791.......
P982079        457 aagg------ ---------- TTCCCGACAG GCGCCGCGGG CACCCCGgcc
P982083        425 cagttccgga atattttcTT TTTTCGACAG GCGCCGCGAA CACTCAGTG-
P982085        394 cgggtagt-- --------TT TTTCCGACAG GCGCCGCGGA CACTCGGTT-
                                       ** ********** ********** *********
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alignment position 801....... 811....... 821....... 831....... 841.......
P982079        491 GTGACGTCAC GGCAGCGCGC CGgccgCGAG AGAGGGCCCC GTCGCGACCG
P982083        474 GTGACGTCAT GGCAGCGCGC CGCGGACGAG CTAGGACCCC GTCGCGTTCA
P982085        433 GTGACGTCAT GTCAGCGCGC CGCGGACAAG ATAGGACCCT GTCGCGTTCA
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alignment position 851....... 861....... 871....... 881....... 891.......
P982079        541 CGTCCCcttg GGTCCTTGAT CCTGAGCTGA CCGGGTAGCC ATGGCCTTGc
P982083        524 TGTCCCTCT- GGTCCTTGAG CCGGCGCAGA CGGCGAAGTC ATGGCCTTGA
P982085        483 CGTCCCTCT- GGTCCTTGAG CCGGCGCAGG CAGCGAAGCA ATGGCCTTGA
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alignment position 901....... 911....... 921....... 931....... 941.......
P982079        591 GGCTCCTGAA GCTGGCAGCG ACGTCCGCGT CCGCCCGGGt cgtgGCGGCG
P982083        573 GGTTGCTGAG ACTCGTCCCG GCGTCGGCTC CCGCGCGCGG CCTCGCGGCC
P982085        532 GGTTGCTGAG ACTTGTCCCG GCGTCGGCGT CCGCGCGCGG CCTCGCGGCC
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                                                                   ******
alignment position 951....... 961....... 971....... 981....... 991.......
P982079        641 GGCGCCCAGC GCGTGGTGAG CGGgcggcgg ggtggcaggg tggcggggtg
P982083        623 GGAGCCCAGC GCGTGGTGAG CGGCGGGTGG CTCTCCTTGC TTGGATC-TC
P982085        582 GGAGCCCAGC GCGTGGTGAG CGGCGGGTGG CTTTCCTCGC TTGGATCcTC
                   ********** ********** ********** ********** ******* **
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                   ********** **********
alignment position 1001...... 1011...... 1021...... 1031...... 1041......
P982079        691 gcagggtggc ---------- ---------- ---------- ----------
P982083        672 GGCCTGtcgg cTCCGAGCCC TGACGCTCCG GCggcgtctg TCAGACCCGT
P982085        632 GGCCTG---- -TCCGAGACC TGACACTCCG GCattgttga TCAGACCCTT
                   ******      ********* ********** **         **********
                                                              **********
                                                              **********
alignment position 1051...... 1061...... 1071...... 1081...... 1091......
P982079        701 ---------- ---------- ---------- ---------- ----------
P982083        722 GAGCCGCGAG CTCCTGAGGC CTCCgctcac agcacc-GGT GCAGCGGGAC
P982085        677 GAGCTACGAG CTCTTGAGGC CTCCacctac agctcagGGT GCAGCGGGAC
                   ********** ********** ****              *** **********
                   ********** ********** ****              *** **********
                   ********** ********** ****              *** **********
alignment position 1101...... 1111...... 1121...... 1131...... 1141......
P982079        701 ---------- ---------- ---------- ---------- ----------
P982083        771 TCACTTTCCC GGCTGCAtac GGAGAGCCGA GATGCCGGAG CtccGGAGCC
P982085        727 TCACATTCCC GGTTGCActt GGGGAACCGA GATGCCAGAG CcgtGGAGCC
                   ********** *******    ********** ********** *   ******
                   ********** *******                              ******
                   ********** *******                              ******
alignment position 1151...... 1161...... 1171...... 1181...... 1191......
P982079        701 ---------- ---------- ---------- ---------- ----------
P982083        821 TGGGCCCGCA TGCTCATCGG TTCAG----- ----AAACTG CTTTGTGGAA
P982085        777 TGGGCCCGCG TGCTCATCCG TTCAGtgatt ggtgAAGCTG CTTTGTCGAA
                   ********** ********** *****          ****** **********
                   ********** ********** *****          ****** **********
                   ********** ********** *****          ****** **********
alignment position 1201...... 1211...... 1221...... 1231...... 1241......
P982079        701 ---------- -----GGGGT GGCGGGGTGG GGAGCAGttc cacatctccc
P982083        862 CGCCTTGTAG ACTCTGGGGT GACGTGATGT GGAGCAGCAA CAGAGATTTG
P982085        827 CGCCTTGTAG ACTCGGGTGT --CGTGACGT GGAGCAGGAA CAGCGATTTG
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alignment position 1251...... 1261...... 1271...... 1281...... 1291......
P982079        736 ccggcctctg gcggcggctc ccaggtcgct ctccgggtgg gtTTGGGGGA
P982083        912 GGGTAGA--- ---------- ---------- ---------- --TTGGGgag
P982085        875 GGGTAGA--- ---------- ---------- ---------- --TTGGGGGA
                   *******                                       ********
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alignment position 1301...... 1311...... 1321...... 1331...... 1341......
P982079        786 cccctcctgc ctccggaatt gtttggtctt tggtcgtgga cagacctcag
P982083        927 gattAGGACC TTTTAGGGTG CATGCAG--- ---------- ----------
P982085        890 ggagAGGACT TCCTAAGATG CATGCAG--- ---------- ----------
                       ****** ********** *******
                       ****** ********** *******
                       ****** ********** *******

alignment position 1351...... 1361...... 1371...... 1381...... 1391......
P982079        836 ggggccacga gcttctccag gccattttat ctcagcttta agcaAAACGC
P982083        954 ---------- ---------- ---------- ---------- ----AATAAT
P982085        917 ---------- ---------- ---------- ---------- ----AATAGT
                                                                   ******
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                                                                   ******

alignment position 1401...... 1411...... 1421...... 1431...... 1441......
P982079        886 TGGAGCGCGG AGGTGATCAG GGCCCCGAGG CTGccctgat gcgggaggcc
P982083        960 GGGTGACAGT AGGTGCTTAG GGGACCGTGG CTGGAAACAG GACACGTcTT
P982085        923 GGGTGATAGT AAATGCCTAG GGGACCGTGA CTGGAAACAG GACACGTtTT
                   ********** ********** ********** ********** ******* **
                   ********** *  ******* ********** ********** ******* **
                   ********** *  ******* ********** ********** ******* **
                                 ******* ********** ********** *******

alignment position 1451...... 1461...... 1471...... 1481...... 1491......
P982079        936 cgtgtgcagg tggcaggccg ggggcacacg cgcttgtcat tagataattc
P982083       1010 ATGACGGCAT CATAACTTCT TTGCTTTata gta------- ----------
P982085        973 ATGACGACAT CATAGCTTCT TTGCTTTct- ---------- ----------
                   ********** ********** *******
                   ********** ********** *******
                   ********** ********** *******

alignment position 1501...... 1511..
P982079        986 acgtagcagc cctgtc
P982083       1043 ---------- ------
P982085       1002 ---------- ------
```

Pairwise similarities:

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

	P982083 (1042 bp)	**P982085 (1001 bp)**
P982079 (1001 bp)	0.150 22 %	0.136 25 %
P982083 (1042 bp)		1.000 71 %

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

Extract alignment region	
Positions in alignment	from: ☐ to: ☐
Output file	dialign.seq

Extract aligned sequences

For comments, questions or bug reports, please contact support@genomatix.de

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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 Jun 7 02:18:19 2005**

Solution parameters:

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

Aligned Sequences:

No.	Sequence Name	Sequence Description	Length
1	P865912	sym=NDUFAF1|loc=Loc51103|taxid=9606|spec=Homo sapiens| chr=15|ctg=NT_010194|str=(-)|start=12484677|end=12485677| len=1001|tss=501| comm=NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, assembly factor 1; (NM_016013/501/bronze;)	1001 bp
2	P865914	sym=Ndufaf1|loc=Loc69702|taxid=10090|spec=Mus musculus| chr=2|ctg=NT_039207|str=(-)|start=60384597|end=60385597| len=1001|tss=501| comm=NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, assembly factor 1; (AK010328/501/gold;NM_027175/501/bronze;)	1001 bp
3	P865917	sym=na|loc=Loc296086|taxid=10116|spec=Rattus norvegicus| chr=3|ctg=NW_047657|str=(-)|start=47582514|end=47583514| len=1001|tss=501| comm=similar to NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, assembly factor 1; (XM_215814/501/bronze;)	1001 bp

Alignment (DiAlign format):

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

Warning: No common TF matches found.

```
alignment position 1.........  11........  21........  31........  41........
P865912          1 ccgtctctac  taaaaataca  aaaattagtc  gggcatgatg  gcgcgcacct
P865914          1 gtgtgcacaa  gctctgttgt  gtggattaca  taGGGGCACG  ACTGAGGAAA
P865917          1 ggattatgtg  g---------  ----------  --GGGGCACG  ATTGAGGAAA
```

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                                                     ******** **********

alignment position 51........ 61........ 71........ 81........ 91........
P865912         51 gtaatcccag ctactcggga ggctgaggca ggagaatcgc ttgaatct--
P865914         51 GCCAGGATTG ATAGCTATCT AGGTGTACAG TGGCTCTCCA AAGGCAGTTA
P865917         30 GCCTGGATTG GTTGCTATCT AGGTGTACAG TGGCTCTCCA GAAGCAGTTA
                   ********** ********** ********** ********** **********
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                                          ********* ********** **********

alignment position 101....... 111....... 121....... 131....... 141.......
P865912         99 ---------- ---------- ---------- ---------- ----------
P865914        101 AGTGGCTTTC TaAAGTCACG CAGCAGACAG TTCTCAAGGG ACTACAGGGA
P865917         80 AGTGGATTTC TgAAGTCACA CAGCAGACAG TTCTCAAGGG ACTACAGGGA
                   ********** * ******** ********** ********** **********
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alignment position 151....... 161....... 171....... 181....... 191.......
P865912         99 ---------- ---------- ---------- -GGGAGGCAG AGGTTGTAGT
P865914        151 AGaagaggcc CAAGCGGCCA GGCatctagA AGTGAAGAGG CGATAGCAGT
P865917        130 AGacaca--- CAAGTGGCCA GGC------A AGTGAAGAGG AGTTAGTAGT
                   **         ********** ***      * ********** **********
                   **                             * ********** **********
                   **                             * ********** **********
                   **                             * ********** **********
                   **
                   **
                   **

alignment position 201....... 211....... 221....... 231....... 241.......
P865912        118 GAGCCGAgat cgcgccactg cactccagcc tgggcgacag agcgagaatc
P865914        201 GCAGAGATCC TGTTTAAAAg ---------- ---------- ----------
P865917        171 GCGGAGATCC TGCTTGAAAa ataggggttg gggatttagc tcagtggtag
                   ********** *********
                   ********** *********
                   ********** *********
                   ********** *********

alignment position 251....... 261....... 271....... 281....... 291.......
P865912        168 cg-------- ---------- ---------- ---------- ----TCTCAA
P865914        221 ---------- ---------- ---------- ---------- ----------
P865917        221 agcgcttgcc taggaagcgc aaggccctgg gttcggtccc aagcTCCGAA
                                                                   ******
                                                                   ******

alignment position 301....... 311....... 321....... 331....... 341.......
P865912        176 AAAAAAAAAA AAAAAAAAAG Acgcagggat ggagtttgcc gcctgaaa-G
P865914        221 ---------- ---------- ---AGGATTG GTATTTACAT ACGGGGGCGG
P865917        271 AAAAAGAAAA AGGAAAAAAT AaaAGGATTG ATATTTACAT ATGAGGGCGG
                   ********** ********** *  ******* ********** **********
                   ********** ********** *  ******* ********** **********
                                            ******* ********** **********
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alignment position 351....... 361....... 371....... 381....... 391.......
P865912        225 GATACAGGAA GGAGAGgcga aaaacttatc tgaattctca ctgcttcctt
P865914        248 GGTACAAGAA GCTGAGCGAA GAGCTGGCTC ACAAATGACA GGAcATTTCA
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P865917        321 ATTACAAGAA GTAGAGCGAA GAGCTCGCTC ACAAAGGACA GGAaATTTCA
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alignment position 401....... 411....... 421....... 431....... 441.......
P865912        275 acaactggcg accaagtgga ccaaaaacct CCAAAAACCT CAGttggctg
P865914        298 GAAAGCGACC CCGCTGGGGA ATTTTGAggA CCTGAAGCCT CCGGTTGTCT
P865917        371 GAAAGCGAAC CCGCTGGGGA ACTTTGAatA CCAAAAGCCT CAGGTTGTCC
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alignment position 451....... 461....... 471....... 481....... 491.......
P865912        325 g--GCTACGG GGTCCTTGCT GTCCTTCCTG GGCTtctgta ctcggccgga
P865914        348 TACGCTTTAG GATACTTTCC GTTACTCTTG AACTATCTGA AGCTCTTgtt
P865917        421 CATGCTTTAG GATACCTTtt GGTACTCTTG TACGACCTGA AACTCTA---
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alignment position 501....... 511....... 521....... 531....... 541.......
P865912        373 actttggtgt tctgACGCCT TGTTTGGCAT CGGAAGGGAA AAGCAGATGG
P865914        398 tactgT---- ----ACACCT AGTTTGATGT CGGACAGGAA AAGTAGCGGG
P865917        468 -----T---- ----ACACCT AGTTTGGTGC CGGACGGGAA AAATAGATGG
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alignment position 551....... 561....... 571....... 581....... 591.......
P865912        423 ACCTatacgg gtaaagtggc tt-------- ---------- -----CTGGG
P865914        440 ACCacaACCG GAAGCGTGGC GAACCGGGCG AGAAAAGTAG AAGGACtatt
P865917        505 ACCTgcACCG GAAGCGTGGA GAACCGGGCG GAGAAAACAG AAGGACTGGC
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alignment position 601....... 611....... 621....... 631....... 641.......
P865912        450 C---GGAAGg tac------- ---------- ---------- ----------
P865914        490 cgggGGAAGC CGAATGTG-- GGGTCTGAGA AGGTGAGCGG AACCTTCTCA
P865917        555 C---GGAAGC CATATGTGgg GGGTCTGAGA AGGTAAGCTG ACCCTTCTCC
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alignment position 651....... 661....... 671....... 681....... 691.......
P865912        460 ---------A CTATAGGCTC GGGGAGGTaa gcggcggcag gccggcggtt
P865914        538 TAGGTGGGAA CTGCAGGGAC GAGGAGGTCG GGA------- ----------
P865917        602 TAGATGGGAA actCAGGGAC AAGGAGGCGG GGA------- ----------
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alignment position 701....... 711....... 721....... 731....... 741.......
P865912        501 ggtgtgtccc gggtgtgggg aggcgacAGA GCCCTGGC-- ---ACTTGAG
P865914        571 ---------- ---------- -------AGA GTCCTGGCgg gtgAGGTGAG
P865917        635 ---------- ---------- -------AGA GTCCTGGC-- ---AGGTGAG
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alignment position 751....... 761....... 771....... 781....... 791.......
P865912        546 GGTTGAGGGG GCCTCcccag cgcggcgaac CGTCTAGCCT CCGGAGGCCA
P865914        594 GGTCGAGGGG CtgcCACTCC TCGGGAG--- CGCCTAGCTT CAGGAGGCTG
P865917        653 GGTTGAGGGG CCGTCACTCC TCGGGAG--- CGCCTAGCTT CCGGAGGCTG
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alignment position 801....... 811....... 821....... 831....... 841.......
P865912        596 GGCCGTGagt g--------- ----CGGGAG GTATACGCCA AGGCGGAAGA
P865914        641 GGACGTGacc aaccccgCGC CTGCCGAGAG GTGAACGCCT GGTCTTCAGA
P865917        700 GGgacgtggt taactc-CGC CAGCCGAGAG GTGAACGCCT GGTCTTCAGA
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alignment position 851....... 861....... 871....... 881....... 891.......
P865912        633 ATtttgccac tcactaccTG TGTGACCTCG GGTAAattag ccttggaacg
P865914        691 GTGAgTTTGG TCTCTGG-TG TGTGACCTCG AATAAttATT TAATTGTGGA
P865917        749 GTGAcTTTTG TCTCTGG-TT TGTGATCTCG AATA---ATT TAATTGTGGA
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alignment position 901....... 911....... 921....... 931....... 941.......
P865912        683 tcag----TT TCTTCGTCTC TATAATTGAA ATAATAATAG tacctctc--
P865914        740 ATCTCCTTTT TTTTAGTCTT TGTAATTGGA ATAATACTAG AAGT-ACCTG
P865917        795 GTCTCCTTTT cgTTAGTCTT TGTCATTGGA ATAATACTAG AAGTtACCCG
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alignment position 951....... 961....... 971....... 981....... 991.......
P865912        727 --------TC AGGATTGTTG TGAGCCGTCA GTGAA---AC ACTTAGAGCA
P865914        789 TCTCAGGGTC AGGATTATCG TGAGAAGTCA GTAAAAACAC ACGGAGAATA
P865917        845 TCTCAGGATC AGGATTATTG TGAGAAATCA ATAAAAACAC ACGGAGAATA
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alignment position 1001...... 1011...... 1021...... 1031...... 1041......
P865912        766 GTTTCTGGCA CATGGTAAGG CATGGATAGc tttactaatt ctactcactt
P865914        839 GTTGCTGGCA CATGGGAAGC CCTAGGTTGA ACAGTCGTTT CTGTACTCAG
P865917        895 GTTTCTGGCA CATGGTAAGC CCTAGATt-A ACAGTCGTTT CTGTACATAG
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alignment position 1051...... 1061...... 1071...... 1081...... 1091......
P865912        816 ct-------- ---------- -AGCTGCGTG GATTGTGTTG TCAAAACCCA
P865914        889 TAGTACAGTC ATActgCTAG GAGCGGTGTG AATATCTTAT TAAAAACTCA
P865917        944 TAGTACAGTC ATAgtaCTAG GAGCGATGTG AACACCCTAT TAAAAACTCA
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alignment position 1101...... 1111...... 1121...... 1131...... 1141......
P865912        847 CCGTCAACCT Cagggcggta ttgtccagtt aatagtttag attttctgtt
P865914        939 CAGTTAGCTT Cggaccgacg tcacccggtt actgagtttg accgagtttc
P865917        994 CCGTTAgc-- ---------- ---------- ---------- ----------
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alignment position 1151...... 1161...... 1171...... 1181...... 1191......
P865912        897 tactggtaga aaaaaaaaaa tgaaacaaag catttataat taaagttata
P865914        989 ttgtaagaaa tta------- ---------- ---------- ----------
P865917       1002 ---------- ---------- ---------- ---------- ----------

alignment position 1201...... 1211...... 1221...... 1231...... 1241......
P865912        947 ttattagaga agtaacacta cggagggttt ggaaaacatt ttatgagcta
P865914       1002 ---------- ---------- ---------- ---------- ----------
P865917       1002 ---------- ---------- ---------- ---------- ----------

alignment position 1251.
P865912        997 tcatt
P865914       1002 -----
P865917       1002 -----
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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.

	P865914	P865917

	(1001 bp)	(1001 bp)
P865912 (1001 bp)	0.097 28 %	0.143 28 %
P865914 (1001 bp)		1.000 74 %

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

Extract alignment region	
Positions in alignment	from: ☐ to: ☐
Output file	dialign.seq

Extract aligned sequences

For comments, questions or bug reports, please contact support@genomatix.de

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License Agreement

GEMS Launcher 4.1.1

GEMS Launcher Task: *DiAlign TF*: Multiple alignment plus TF sites
working on C1-NDUFB1 (3 seq.)

[Alignment] [Pairwise similarities]

DiAlign professional TF Release 3.1 December 2004 **Tue Jun 7 14:05:14 2005**

Solution parameters:

Sequence file:	C1-NDUFB1 (3 seq.)
Type of sequences:	nucleotide sequences
Threshold T:	0.00
'*' signs below alignment denote:	diagonal similarity (max. similarity is represented by 10 '*' signs)
Alignment output:	complete alignment is shown # nucleic acids per line: 50
TF output:	common TF matches located in aligned regions (common to 3 (100.0 %) sequences)
Family matches:	yes
MatInspector library:	Matrix Family Library Version 5.0 (February 2005)
Selected groups (core/matrix sim):	• ALL user_defined.lib (0.75/Optimized) • ALL vertebrates.lib (0.75/Optimized)

Aligned Sequences:

No.	Sequence Name	Sequence Description	Length
1	P303789	P303789 sym=NDUFB1|loc=Loc4707|taxid=9606|spec=Homo sapiens|chr=14|ctg=NT_026437|str=(-)|start=73587406|end=73588406|len=1001|tss=501|comm=NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 1, 7kDa; (NM_004545/501/bronze;)	1001 bp
2	mNDUFB1	mNDUFB1 m5_dna range=chr12:96654325-96656324 5'pad=0 3'pad=0 revComp=TRUE strand=? repeatMasking=none	2000 bp
3	rNDUFB1	rNDUFB1 n3_dna range=chr6:126249139-126250606 5'pad=0 3'pad=0 revComp=TRUE strand=? repeatMasking=none	1468 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$STAT V$IKRS V$YY1F V$NRF1 V$EREF V$RREB

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alignment position 1.........  11.........  21.........  31.........  41.........
P303789          1 gtca------  ----------  ----------  ----------  ----------
mNDUFB1          1 gaaactagGA  ATGGGATCTT  GGGAAacgtg  GTGATTGTGG  tagcgccgag
rNDUFB1          1 --------GA  ATGGGATCTT  GGGAAtca--  GTGATTGTGG  aggcactaag
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alignment position 51.........  61.........  71.........  81.........  91.........
P303789          5 ----------  ----------  ----------  ----------  ----------
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mNDUFB1         51 a--GAAGTTA ATTCTATCAA GGCGTGGCAT gagCCTCTCA AGGGTCTTTG
rNDUFB1         41 cgcGACGTTA ATTCTAGCAA GGCGTGGCAT aaaCCTCTCA AGGGTCTTTG
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alignment position 101....... 111....... 121....... 131....... 141.......
P303789          5 ---------- ---------- ---------- ---------- ----------
mNDUFB1         99 GAATTAAGGA GCTACGAAGG CACctgCTGG CCTCGTGTTC TCTGAGCCCA
rNDUFB1         91 AAGTTAAGGA GCTAGGAGGG CAC---CTGG CCTCGTGGTC TCTGAACCCA
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alignment position 151....... 161....... 171....... 181....... 191.......
P303789          5 ---------- ---------- ---------- ---------- ----------
mNDUFB1        149 AGATGGGAAA GGCAgAGATG GGGAGGCTTG GGGAGTACGG CGGTACAAGG
rNDUFB1        138 AGATGGGAAA GGCAcAGATG GGGAGGCTTG GGGAGTAAAG CGGCAACAGG
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alignment position 201....... 211....... 221....... 231....... 241.......
P303789          5 ---------- ---------- ---------- ---------- ----------
mNDUFB1        199 GGAAaGAGCC CAGGCTGGAC GCGGATTAAC TTTTAGCTCC AGctGATGAA
rNDUFB1        188 GGAA-GAGCC CAAGCAGGAC TCCGATTAAC TTTTAGTTCC AGagGATGAA
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alignment position 251....... 261....... 271....... 281....... 291.......
P303789          5 ---------- ---------- ---------- ---------- ----------
mNDUFB1        249 AGCTCAGAGG AACTAGACAG GAGGgagggc -------AAG GAGGAAGCAT
rNDUFB1        237 AGATCAGAGG AAATGGACAG AAGGagggca aggggcaAAG GAGGAACCAT
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alignment position 301....... 311....... 321....... 331....... 341.......
P303789          5 ---------- ---------- ---------- -CTTCTCTT- ----------
mNDUFB1        292 AGGCGCGCCC C-AACACCCC GAGGTTTCAG CCcggggaaa agtcacttct
rNDUFB1        287 AGGAGCGCTC CaAACACCCC GAGGCTTCAG CCTTCTCTT- ----------
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alignment position 351....... 361....... 371....... 381....... 391.......
P303789         13 ----TCCCTC GCTGACCACT TCTGCCGGGA ACGACCGGGA CAGTCGCAGC
mNDUFB1        341 cttcCCCCTT GCGGAACGCT TGTTCCAGGA ACCACGGAGA CTGTCACAAC
rNDUFB1        326 ----CCCCTT GCGGAACGCT TGTTCCAGGA ACCACGGAGA CGGACACAAC
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alignment position 401....... 411....... 421....... 431....... 441.......
P303789         59 CGAAGCGGCG GGGGCGAGTC CtcGGGGGAG ACCGGGTCGG AGTCGGGGCC
mNDUFB1        391 CGAAACCGCG GGAGCGCGTC C--GGGCGAC ACCGGGCCGA CGCGGGAACC
rNDUFB1        372 CGAAACCGCG GGAGCGCGTC C--GGGCGAC ACCGGGCCGa tGCGGGAACC
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alignment position      451....... 461....... 471....... 481....... 491.......
P303789            109  CcgtGCTCCC GGAGGGCCaa tgacgccgcC TTCCCCAGCC CG--AGGCTC
mNDUFB1            439  CA--TCCCCT TGAGGGCCT- ---------C CTCCCAACCC GA--AGGCTC
rNDUFB1            420  CA--GCTCCT TGAGGGCCT- ---------C CTCCCAACCC GAgaAGGCTC
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alignment position      501....... 511....... 521....... 531....... 541.......
P303789            157  GCTCCTTTCT CCCGCCCTCA CTTGCCTCGT CAGgcCTCCC CCAACG-CCG
mNDUFB1            475  CTTTCCGTCT CCCGTCCTCA CCTGCCAGGC CAAT-CTCCC CCcggcaCCG
rNDUFB1            458  CTTTC-TTCT CCCATCCTCA CCTGCCAGGT CAAT-CTCCC CCGGTA-CCG
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alignment position      551....... 561....... 571....... 581....... 591.......
P303789            206  TCCACAGCCC TTCCCAACCC CTAGGCGAAT CCAGGTTCAA GACGTAGAAA
mNDUFB1            524  TCCGCCGCCC TTCCCAACCC CTAGTGGAAC GCAGGTCGGA GAGCGAGCAG
rNDUFB1            505  ACCGCTGCCC TTCCCAACCC CTAGTGGAAC GCAAGTCGGA GAGCGAGTAG
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alignment position      601....... 611....... 621....... 631....... 641.......
P303789            256  AGCCGATGCT GGGTCAGCAG CGccagggac taccgGCCGG CAGAAGCCCC
mNDUFB1            574  AGCTAGCGCG CGCTCAGCGG CGGAGAGCA- -----GCCGG CAGGAGCCCC
rNDUFB1            555  ACCTAGCGCG CGCTCAGCGG CGGAGAACA- -----GCCGG CAGGAGCCTC
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alignment position      651....... 661....... 671....... 681....... 691.......
P303789            306  ACAGTGGCAG CCGCCATTTT GGaGCTGGAG ACTAGCGGCG GAGACGAGGA
mNDUFB1            618  TGTGTGGTGG CCGCCATCTT GG-GCCTGAG CAGAGCGGCT GAGGCGGGGA
rNDUFB1            599  TGTGTGGTGG CCGCCATCTT GG-GCCTGAG CAGCGCGGCT GAGGCGGGCA
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alignment position 701....... 711....... 721....... 731....... 741.......
P303789        356 GGAaCCAGGG CGAGACCATC TCCGGGGGgt gggcacggtg ctgtc--GGA
mNDUFB1        667 CGA-CCCGGG CGACACCATC TGTAGGGGTG GTGACGAACC GGGTCAGGGA
rNDUFB1        648 CGA-CCCGGG CGACACCATC TGTAGGGGTG GCGAGGAACC GGTTCAGGGA
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alignment position 751....... 761....... 771....... 781....... 791.......
P303789        404 AGGCGACGGC Ggtcacgcct GCACGCCTCG TCTGTCTGGA GCGAAATTTT
mNDUFB1        716 AGAGGACAGC GCaaAAGCTC GCAAACCTTG TCAGCCTGGA TCCACGTCTT
rNDUFB1        697 AAGTGACGGC GCc-AAGCTC GCAAACCTTG TCAGCTTGGA TCCAAGTTTT
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alignment position 801....... 811....... 821....... 831....... 841.......
P303789        454 ATTCAGAAat tattggtaat gtttggaagc taaaaaaaaa AAAAATGAGA
mNDUFB1        766 ATTCAaaacg tgtcgcgatc ATTCACAGCT T--------- AAGATGTACG
rNDUFB1        746 ATCCAGAAcc tatcacgat- ATTTAAAGCT C--------- AAAATGTAGA
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alignment position 851....... 861....... 871....... 881....... 891.......
P303789        504 GGAGTCAACC CTGAGGAGGA AAAagtagta tgatttgctg gcgt--CA-C
mNDUFB1        807 GGATTCGCGC GTGAGAAGGG AGAGAGAAGC GCCGGTTTGC CGACGCCAcC
rNDUFB1        786 GGACTCACTC GTGAGAAGGG AGAGAGAGGC GTCGATTGGC CATCGCCA-C
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alignment position 901....... 911....... 921....... 931....... 941.......
P303789        551 CCCTCTGCTC CGTGCGGGCG CGGCGAATGG CAGGTCCcgA GGTCGCAGCT
mNDUFB1        857 CCCTCTCATC AGGGCTGGCG CGGCGAGTGG CAGCTCCTTA GGTCACGGCT
rNDUFB1        835 CCCTCTCCTC AGGGCGGGCG CGGCGAGTGG CAGCTCCTTg GGTCACGGCT
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alignment position 951....... 961....... 971....... 981....... 991.......
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P303789        601 TCCACTGGCG CGGGTTGagt tcc------C TGTTGCCCTT GGTCTCGGGG
mNDUFB1        907 TCCGCCGGCG CCAGTGGCCT AGCTCCCTGC GGCTGTCCTT GGTCGCCTTG
rNDUFB1        885 TCCGCCGTCG CCAGTGGCCT AGCTCCCTGC GGCTGTCCTT GGTCGCGctt
                   ********** ********** ********** ********** **********
                   ******* ** ********** ********** ********** ******
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                           ** *******

alignment position 1001...... 1011...... 1021...... 1031...... 1041......
P303789        645 T-CGCtgtag gcgctgAGGC TGCAGGTGGG TTTGGGGAGC CCGGggggcc
mNDUFB1        957 T-CACC---- ------AGGC TGAAGGTGGG TCTGGGGACC CCGGCGCCAC
rNDUFB1        935 gaCACC---- ------GGGC TGAAGGTGGG TCTGGGGACC CCAGTGCCAC
                   * ****           **** ********** ********** **********
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                     ****           **** ********** ********** **********
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                                     *** ********** ********** **

alignment position 1051...... 1061...... 1071...... 1081...... 1091......
P303789        694 gccgcgacga ggatcacggc gacggtggcg GGGAGGGTTC TAGGCAAgcc
mNDUFB1        996 CC---GTGGT GGTGatgcgG GC-------- GGGAGGGTTC TGGGGAACGC
rNDUFB1        975 CCtctGTGGT GGTGca---G GC-------- GGGAGGGTTC TGGGGAACGC
                   **   ***** ****     * **         ********** **********
                   **                  * **         ********** **********
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alignment position 1101...... 1111...... 1121...... 1131...... 1141......
P303789        744 ctcggtgctg tgcatgtgtg gaggggtggt ctgggcttcc ccggggcttc
mNDUFB1       1035 TCGCAT---- ---------- ---------- ---------- ----------
rNDUFB1       1014 TCTCAT---- ---------- ---------- ---------- ----------
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alignment position 1151...... 1161...... 1171...... 1181...... 1191......
P303789        794 cgaacgaagg tgacgGGAAA GGAAAATGGG GTTTTCTTCG GGTGgaggat
mNDUFB1       1041 ---------- -----GGAGG GGAAAca-GG GTCGCCTTCG G-TGACCCCT
rNDUFB1       1020 ---------- -----GGAGG GGAAATCGGG GTCGCCTTCG GGTGACCTCT
                                   ***** ********** ********** **********
                                   ***** *****                    *******
                                   ***** *****                    **
                                   ***** *****
                                   ***** *****
                                   ***** *****

alignment position 1201...... 1211...... 1221...... 1231...... 1241......
P303789        844 gg--GATTTC CGGGCCGGAG CTTTTGGAAA GGGTT----- ----------
mNDUFB1       1074 GCGCGCTGCC CGCCCCACGC CTTTTACAAA GACTG----- ----------
rNDUFB1       1055 GCGCGCTGTC AGCTTCACAC CTTTCACAGA GAattcgcta tgctagctta
                   ********** ********** ********** *****
                   ********** ********** ********** **

alignment position 1251...... 1261...... 1271...... 1281...... 1291......
P303789        877 ---------- TTCTGAGGct gtcataacag gaaaacgtcc gtagagatgt
mNDUFB1       1109 ---------- CTCTGGGGAC ---------- ---------- ----------
rNDUFB1       1105 atcaaagcgt CTTTGGGGAC ---------- ---------- ----------
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alignment position 1301...... 1311...... 1321...... 1331...... 1341......
P303789        917 GACCCAGTGA CCGCCCGCTA ACCGGACTGG AGAGaagacc ggccc-----
mNDUFB1       1119 GATCTGATGG CCTGGCTCTC GGGGGACTcG GAAGGGTTCT CAAGGATCCG
rNDUFB1       1125 GATCCGATGG CCTCGCTCTC GAGGGACTAG GAAGGGCTCT CAAGGATCCC
                   ********** ********** ********** ********** **********
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                   ********** ********** ********

alignment position 1351...... 1361...... 1371...... 1381...... 1391......
P303789        962 ---------- ---------- GGATCCCACG CCTGGCCTGA AGCAGGGAAg
mNDUFB1       1169 ACTCTTGAGC CCACAaTAGG GAATGCAGCT CCTATCCAGA AGCGGGGcgc
rNDUFB1       1175 ATTCTTGAAC CCACAgTAGG GAATGCAGCT CCTATCCAGA AGCAGGGAAc
                   ********** ***** **** ********** ********** *********
                   ********** ***** **** ********** ********** *******
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                                    **** ********** ********** *******

alignment position 1401...... 1411...... 1421...... 1431...... 1441......
P303789        992 acgctgcctc ---------- ---------- ---------- ----------
mNDUFB1       1219 ggTCGCCCAG GCGTCTGTCT CCTCGTCCAA CTCTCCTgat tGTGAAACCC
rNDUFB1       1225 atTCGCCCAG GCATCCGCCT CCTGGTTCAA CTCTCCTaaa cGTGAAACCC
                     ******** ********** ********** ********    *********
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alignment position 1451...... 1461...... 1471...... 1481...... 1491......
P303789       1002 ---------- ---------- ---------- ---------- ----------
mNDUFB1       1269 GCACGTAGCC ATTTGCCTTT TAAAAACAaG GCTTTCTGCT TGGTTTCCAG
rNDUFB1       1275 GCACTTACCC ATTTGCCTTT TAAAAACAtG GCTTTCTGCG TGGTTTCCAG
                   ********** ********** ******** * ********** **********
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alignment position 1501...... 1511...... 1521...... 1531...... 1541......
P303789       1002 ---------- ---------- ---------- ---------- ----------
mNDUFB1       1319 tccg----TG TTATGATCTC AACGGTTTCg gttttgctcc atcca-----
rNDUFB1       1325 cgtgtgtaTG TCGTGTTCGC AAAGGTTTCa tagctccatg cattcacttg
                           ** ********** *********

alignment position 1551...... 1561...... 1571...... 1581...... 1591......
P303789       1002 ---------- ---------- ---------- ---------- ----------
mNDUFB1       1360 --TTCCATAT CTTAGGTGAC ACTTTGTAAT AATT-ATAAA GAACTGTGGG
rNDUFB1       1375 ttTTCCTTGG CTTAGGTGAT ACTTTGTAAT ACTTaATAAG GAACTGTGGG
                     ******** ********** ********** **** ***** **********
                     ******** ********** ********** **** ***** **********
                                                         ***** **********
                                                         ***** **********

alignment position 1601...... 1611...... 1621...... 1631...... 1641......
P303789       1002 ---------- ---------- ---------- ---------- ----------
mNDUFB1       1407 GTCCAGTCCA ACACAAGGTA TTatCTCTTA AAAAGTCTAC ATGTgcctgc
rNDUFB1       1425 GTCCAGTCGG ACACAAGGTA TTgcCTCTTA AAAAGTCTAC ATGT------
                   ********** ********** **  ****** ********** ****
                   ********** ********** **  ****** ********** ****
                   ********** ********** **
                   ********** ********** **

alignment position 1651...... 1661...... 1671...... 1681...... 1691......
P303789       1002 ---------- ---------- ---------- ---------- ----------
```

```
mNDUFB1     1457 agtggtggtg gcgcatgcct ttaatcccag cacttggaaa gcagaggcag
rNDUFB1     1469 ---------- ---------- ---------- ---------- ----------

alignment position 1701...... 1711...... 1721...... 1731...... 1741......
P303789     1002 ---------- ---------- ---------- ---------- ----------
mNDUFB1     1507 gtggatttct gagttcaagg ccaggctggt ctacagagtg agttccaggg
rNDUFB1     1469 ---------- ---------- ---------- ---------- ----------

alignment position 1751...... 1761...... 1771...... 1781...... 1791......
P303789     1002 ---------- ---------- ---------- ---------- ----------
mNDUFB1     1557 cagccagggc tttaaagaga acccctgtct tgaaaaacaa aacaacaaaa
rNDUFB1     1469 ---------- ---------- ---------- ---------- ----------

alignment position 1801...... 1811...... 1821...... 1831...... 1841......
P303789     1002 ---------- ---------- ---------- ---------- ----------
mNDUFB1     1607 aaagtctaca tgtttccagc atgaatccag atagaagact cagcaaaata
rNDUFB1     1469 ---------- ---------- ---------- ---------- ----------

alignment position 1851...... 1861...... 1871...... 1881...... 1891......
P303789     1002 ---------- ---------- ---------- ---------- ----------
mNDUFB1     1657 agactcacag cagtgtctgt tattcttgaa aagggaaaga aactttaatc
rNDUFB1     1469 ---------- ---------- ---------- ---------- ----------

alignment position 1901...... 1911...... 1921...... 1931...... 1941......
P303789     1002 ---------- ---------- ---------- ---------- ----------
mNDUFB1     1707 ccagcacttg gaaagcagag gcaggtggta tttaagggaa ataccttgtg
rNDUFB1     1469 ---------- ---------- ---------- ---------- ----------

alignment position 1951...... 1961...... 1971...... 1981...... 1991......
P303789     1002 ---------- ---------- ---------- ---------- ----------
mNDUFB1     1757 ttagagaaaa atattaagaa atatgtggga tgtggggtta gttgtttttt
rNDUFB1     1469 ---------- ---------- ---------- ---------- ----------

alignment position 2001...... 2011...... 2021...... 2031...... 2041......
P303789     1002 ---------- ---------- ---------- ---------- ----------
mNDUFB1     1807 gttttttaaaa agtctcacac acacacacat ggagagagag agagagagag
rNDUFB1     1469 ---------- ---------- ---------- ---------- ----------

alignment position 2051...... 2061...... 2071...... 2081...... 2091......
P303789     1002 ---------- ---------- ---------- ---------- ----------
mNDUFB1     1857 agagagagag agagagagag agagagagag gctctgcaaa gaagaaaaga
rNDUFB1     1469 ---------- ---------- ---------- ---------- ----------

alignment position 2101...... 2111...... 2121...... 2131...... 2141......
P303789     1002 ---------- ---------- ---------- ---------- ----------
mNDUFB1     1907 gaggaggagt tatttaactg tttacctccg tacacaggag agagagtaga
rNDUFB1     1469 ---------- ---------- ---------- ---------- ----------

alignment position 2151...... 2161...... 2171...... 2181...... 2191
P303789     1002 ---------- ---------- ---------- ---------- ----
mNDUFB1     1957 acaaaagagc ttaagcctga tcaggataca gattgtctgg ggac
rNDUFB1     1469 ---------- ---------- ---------- ---------- ----
```

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.

	mNDUFB1 (2000 bp)	**rNDUFB1 (1468 bp)**
P303789 (1001 bp)	0.123 42 %	0.134 44 %
mNDUFB1 (2000 bp)		1.000 80 %

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

Extract alignment region	
Positions in alignment	from: to:
Output file	dialign.seq

Extract aligned sequences

For comments, questions or bug reports, please contact support@genomatix.de

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GEMS Launcher 4.1.1

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

[Alignment] [Pairwise similarities]

DiAlign professional TF Release 3.1 December 2004 **Tue Jun 7 14:28:13 2005**

Solution parameters:

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

Aligned Sequences:

No.	Sequence Name	Sequence Description	Length
1	P914132	sym=NDUFB2|loc=Loc4708|taxid=9606|spec=Homo sapiens|chr=7|ctg=NT_007914|str=(+)|start=987533|end=988533|len=1001| tss=501| comm=NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 2, 8kDa; (NM_004546/501/bronze;)	1001 bp
2	P914133	sym=Ndufb2|loc=Loc68198|taxid=10090|spec=Mus musculus|chr=6|ctg=NT_039341|str=(+)|start=8838279|end=8839314|len=1036| tss=501,503,510,536| comm=NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 2; (AK028334/501/gold;AK007495/536/gold;AK010642/503/gold; NM_026612/510/bronze;)	1036 bp
3	P914135	sym=na|loc=Loc362344|taxid=10116|spec=Rattus norvegicus|chr=4|ctg=NW_047690|str=(+)|start=309516|end=310516| len=1001|tss=501| comm=similar to NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 2; (XM_342664/532/bronze;)	1001 bp

Alignment (DiAlign format):

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

V$CREB V$E4FF V$ETSF V$EGRF V$WHZF V$SF1F V$STAF V$P53F

```
alignment
position        1.........  11.........  21.........  31.........  41.........
P914132       1 cctgagccta  tgccaaccca  gccttaaagc  cagtggatcg  aatcaagcca
P914133       1 aCCTCGAATT  GGCTAAGGCT  CGAGGCGTTA  GGAACTTTcc  ccCATGTTCC
P914135       1 -CCCCGAATG  GTCTAAGGAT  TAAGGCGTTA  GAAACCTTta  ctCATATTCC
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              ********* ********** ********** ********     ********
              ********* ********** ********** ********     ********

alignment
position     51........ 61........ 71........ 81........ 91........
P914132   51 tttgtggcat tatct----- ---------- ---------- ----------
P914133   51 TGGCCGACTT ATTCCGAGtg tGCCGGGTTG GGTTCCTCAG GTGATTCccg
P914135   50 TGGCCGCCTT ATTCCAAGga gGCAGGGTTG GGTTCCTCAG GTGACTCtga
             ********** ********    ********* ********** *******
             ********** ********    ********* ********** *******

alignment
position     101....... 111....... 121....... 131....... 141.......
P914132   66 ---------- ---------- ---------- ---------- ----------
P914133  101 TGCCACCAGT CCAGGTTCTG AAATTTAACA CCctggctga ttagtca---
P914135  100 TGCCAGCGGT CCACGTTCTG AGATTTAACA CCtggctgct ggtgaatcat
             ********** ********** ********** **
             ********** ********** ********** **

alignment
position     151....... 161....... 171....... 181....... 191.......
P914132   66 ---------- ---------- ---------- ---------- ----------
P914133  148 -----TTCAG AACAATGCTG AAACAACGAt gctataaaat aaacattgcg
P914135  150 caggtTTCAG AACAGTACTG GAACAACGA- ---------- ----------
                  ***** ********** *********
                  ***** ********** *********

alignment
position     201....... 211....... 221....... 231....... 241.......
P914132   66 ---------- ---------- -ATTGCTGCG TACGAACTTA -GCCTGGCAC
P914133  193 aTGTTATAAA ATAAACATTG CGTGGTTCAG AAAGGGCTTA gGCCTTTAAC
P914135  179 -TGTTATAAA CTAAACATGG CATGGTTCAG AAAGGACTTA -GCCTTTAAC
              ********* ********** ********** **********  *********
              ********* ********** ********** **********  *********
              ********* ********** ********** **********  *********
                                    ********* **********  *********

alignment
position     251....... 261....... 271....... 281....... 291.......
P914132   94 AATGCCtgta atcccagcta ctcgggaagt tgaggcagga gaatcgcttg
P914133  243 AAGGGCCCAC AGTGGCA--- ---------- ---------- ----------
P914135  227 AAGGGCCCAC AGTGGCA--- ---------- ---------- ----------
             ********** *******
             ********** *******
             ********** *******
             ********** *******

alignment
position     301....... 311....... 321....... 331....... 341.......
P914132  144 agcctgggag gcagaggttg cagtgagccg agatggtgtc actgcactcc
P914133  260 ---------- ---------- ---------- ---------- ----------
P914135  244 ---------- ---------- ---------- ---------- ----------

alignment
position     351....... 361....... 371....... 381....... 391.......
P914132  194 agcctgggtg acagagcaag gccttgtctc aaaaagaaaa aaaaaaaaaa
P914133  260 ---------- ---------- ---------- ---------- ----------
P914135  244 ---------- ---------- ---------- ---------- ----------

alignment
position     401....... 411....... 421....... 431....... 441.......
P914132  244 aaaagaatta tacaccactc agttttagga ggggcAGAAC ACGgggagag
P914133  260 ---------- ---------- ---------- -----AGAAC AtGCATGAAA
P914135  244 ---------- ---------- ---------- -----AGAAC ACGCACGAAA
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                                                         *****  *
                                                         *****  *
alignment
position        451....... 461....... 471....... 481....... 491.......
P914132     294 ccctacagga tcagaggggc aaccaacaag ctgtttcagA AGGCATGGGG
P914133     275 GCACCGTCTA TATGAGCC-- ---------- ---------A AAGCAGGGAG
P914135     259 GCACCGTTCA TATAAGCC-- ---------- ---------G AAGCAa----
                ********** ********                        * **********
                ********** ********                        * *****
alignment
position        501....... 511....... 521....... 531....... 541.......
P914132     344 CAGCtcagca accataagtt atgcgtgggc tttgctctcg ggagagaggt
P914133     304 CAGCagTAAG GTCAG----- ---------- ---------- ----------
P914135     284 ------TAAG GTCAG----- ---------- ---------- ----------
                ****  **** *****
                      **** *****
                      **** *****
alignment
position        551....... 561....... 571....... 581....... 591.......
P914132     394 ttcctgcagc CGAAGGACTC ACAGCTAATC TGGGTCAGGA GCGGCTGCCG
P914133     319 ---------- CCAAGAGCAC CTTGCCAGGC TGTGCCACGA GGCAGCCAGG
P914135     293 ---------- CTAAGAGCAC CTTGCCACGC TGCGTCACGA GACAGCCAGA
                           ********** ********** ********** **********
                           ********** ******* ** ********** **********
                           ********** ******* ** ********** **********
alignment
position        601....... 611....... 621....... 631....... 641.......
P914132     444 GCTCCCCCac tcctg----- ---------- ---------- ----------
P914133     359 GCTCCTCCTG AAGGACGAcC TATCTGCCCG TTAACCTGGA GCCTCTAAGG
P914135     333 GCTCCTCCCA AAGGACGAtC TATCTGCCCG TTAACCCGGA GCCTCTAAGG
                ********** ******** * ********** ********** **********
                ********** ******** * ********** ********** **********
                ********** ******** * ********** ********** **********
                                    * ********** ********** **********
                                    * ********** ********** **********
alignment
position        651....... 661....... 671....... 681....... 691.......
P914132     459 ---------- ---------- ---------- ---------- ----------
P914133     409 TCCGCCAATg gcttgaaCTT GTCCCCTGTG GCCTACCATC AGCCCGGGTA
P914135     383 TCCGCCAATa gtctgagCTT GTCCGCTGTG GCCTACCATC AGCCCCGATA
                *********         *** ********** ********** **********
                *********         *** ********** ********** **********
                *********         *** ********** ********** **********
                *********         *** ********** ********** **********
                *********
alignment
position        701....... 711....... 721....... 731....... 741.......
P914132     459 GAGATGA--- GCGACTCTGT GACGTCACGG Gaggcgcggg cggagcgcCG
P914133     459 GAGACGCagt GCGACGCAGT GACGTCACGG GCCGGGACT- --------CG
P914135     433 GAGACGC--- GCGACGCAGT GACGTCACGt tCCAGGACT- --------CG
                *******    ********** ********** *********          **
                *******    ********** *********   ********          **
                *******    ********** *********   ********          **
                *******    ********** *********   ********          **
                *******
alignment
position        751....... 761....... 771....... 781....... 791.......
P914132     506 GGGAAGCGAA GTAGGCAGGG GCGAGGCGGC Tggggaccgc ggggcggacg
P914133     500 GGGAAGTGAC GCATCAGGGG TGGGAACTGC agtctt---- ----------
P914135     471 GGGAAGTGAC GCATCAGGGG TGGGGACTGC Tctccc---- ----------
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alignment
position         801....... 811....... 821....... 831....... 841.......
P914132      556 ggaGCGAGTA TGTCCGCTCT GACTCGGCTG GCGTCTTTCG cTCGCGTTGG
P914133      536 ---GCTAGTA TGTCTGCGCT CACCCGTCTG GTACCTTTCG GcCGCGTCGG
P914135      507 ---GCTAGGA TGTCTGCGCT GGCCCGCCTG GCACCTTTCG GTCGCGTTGG
                    ******* ********** ********** ********** **********
                    ******* ********** ********** ********** **********
                    ******* ********** ********** ********** * ********
                    ******* ********** ********** **********   ********
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alignment
position         851....... 861....... 871....... 881....... 891.......
P914132      606 AGGCCGCCTT TTCAGAAGCG GCTGCGCACG GactGCTGGA GATGGTGGAG
P914133      583 AGGCCGCCTG CTCCGGGGCT GCCGCGCGCG GGcgGCTGGA GACAGTGGAG
P914135      554 AGGCCGCCTG CTTCGGGGCT GCCGCGCGCG GGcaGCTGGA GACGGTGGAG
                 ********** ********** ********** **  ****** **********
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alignment
position         901....... 911....... 921....... 931....... 941.......
P914132      656 TCCGTCAGTG AGTGTGGGGC TGGGgatgGG GGCCTCGCCG GCCTGTAGCG
P914133      633 TCCGTCAGTG AGTGTCGGGC GGGGgc--GA GGGTTCGGCC GGCTTGAACA
P914135      604 TCCGTCAGTG AGTGTCGGGT GGGGacc--A GGGCTCGGCC GGCTCGAACA
                 ********** ********** ****    ** ********** **********
                 ********** ********** ****     * ********** **********
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alignment
position         951....... 961....... 971....... 981....... 991.......
P914132      706 GACAGCGCGG gtccctgGGA CGCTCTCACC TTGACTGGGG CGCCTGAaga
P914133      681 GGCAGCGCTG CCATCC-GGA CGCTGTCACC TTGAAGCAGT CGCCCGGGAG
P914135      652 GGCAGCGCTG CCATCCc-GA CGCTGTCACC TTGAAGCAGT CGCCCGAGCG
                 ********** ****** *** ********** ********** **********
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                 ********** ******  ** ********** ********** **********
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                                    ** ********** ****

alignment
position         1001...... 1011...... 1021...... 1031...... 1041......
P914132      756 g--------- -----GCCGC GTCCCGAGGC ATGCTGGGAC CTGTAGTCC-
P914133      730 GGTGCGTGaa actccGCTGC CGCCCGAGGC ATGCTGGGTC TTGTAGTttt
P914135      701 AGTGCATGac actttGCTGC CGCCTGAGGC ATGCTGGGTC TTGTAGTCG-
                 ********        ***** ********** ********** *********
                 ********        ***** ********** ********** *********
                 ********        ***** ********** ********** *******
                 ********        ***** ********** ********** *******
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                                    ******** ********** *******

alignment
position        1051...... 1061...... 1071...... 1081...... 1091......
P914132     791 GCGTGtctcc tgaagccgcg actcgaggag ---------- ----------
P914133     780 GCCTGGACCG AGAC--TGGC CTTTTAGTCG GCTTGGTGGG CTAGAGGTga
P914135     750 GCCTGGACGG AGACtgTGGC TTTTTGGTCG GATTGGTGGG GTAGAGGTt-
                ********** ****  **** ********** ********** ********
                *****            **** ********** ********** ********

alignment
position        1101...... 1111...... 1121...... 1131...... 1141......
P914132     821 AGGGACCCCG CTGGCCGGAG GGAGAGGGag agacttcgct gggcagatgg
P914133     828 AGGGATGGCG CAGGGTTGCG GGAGAGAGGC GTTAACTAAG ACccgagtga
P914135     799 --GGATGGCA CAGGGTTAGG GGAGAGAGGC GTTAACTAGG ACttgagtgc
                ********** ********** ********** ********** **
                  ******** ********** ********** ********** **
                  ******** ********** ********** ********** **
                  ******** ********** ********** ********** **

alignment
position        1151...... 1161...... 1171...... 1181...... 1191......
P914132     871 gacaccgtgt gcagggccgt catggtagta ggggccgcct gccctcggga
P914133     878 tAAGAATCCA GTCCCGCACA GTCTCC---- ---------- ----------
P914135     847 aAAGAATCCA GCCGTGCACA GTCTCC---- ---------- ----------
                 ********* ********** ******
                 ********* ********** ******
                 ********* ********** ******

alignment
position        1201...... 1211...... 1221...... 1231...... 1241......
P914132     921 gacgcacgcg tgaatgcgga gCGGGCTGAG CCagtcggcg ccggcgc---
P914133     904 ---------- ---------- -CGGACTGAG CCTTCCAAGC AGCTGGCTAG
P914135     873 ---------- ---------- -GGGCCTGAA CCTTCCAAGT CGCTGGCTAG
                                       ********* ********** **********
                                       ********* ********** **********
                                       ********* ********** **********

alignment
position        1251...... 1261...... 1271...... 1281...... 1291......
P914132     968 ---------- ---------- ---------- ---------- --------GG
P914133     933 TGGAGGTCCC GAGCGCATGG AGACggGTGG AGATGGGCTC AGAGACAAGA
P914135     902 TGTAGGTCCG GAGCGCAAGG AGACcaGTGG AGATGGGCTC TGAGACCAGA
                ********** ********** ****  **** ********** **********
                ********** ********** ****  **** ********** **********
                ********** ********** ****  **** ********** **********

alignment
position        1301...... 1311...... 1321...... 1331...... 1341......
P914132     970 GCGGTCCAGG CGGAGGAAGC agcgtgcgcg gc-------- ----------
P914133     983 CGGGTCCAGG CAGGGcagac acggagacct tgagtcagta aggtagtata
P914135     952 GTGGGCCAGG CAGGGAATGC cttggaggac tgaggatttt tccatcagtc
                ********** **********
                ********** *****
                ********** *****

alignment
position        1351
P914132    1002 ----
P914133    1033 gtct
P914135    1002 ----
```

Pairwise similarities:

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

	P914133 (1036 bp)	**P914135 (1001 bp)**
P914132 (1001 bp)	0.133 25 %	0.139 27 %
P914133 (1036 bp)		1.000 79 %

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

Extract alignment region	
Positions in alignment	from: ☐ to: ☐
Output file	dialign.seq

Extract aligned sequences

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

[Alignment] [Pairwise similarities]

DiAlign professional TF Release 3.1 December 2004 **Tue Jun 7 14:48:40 2005**

Solution parameters:

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

Aligned Sequences:

No.	Sequence Name	Sequence Description	Length
1	P876211	sym=NDUFB3|loc=Loc4709|taxid=9606|spec=Homo sapiens|chr=2| ctg=NT_005403|str=(+)|start=52145450|end=52146450|len=1001| tss=501| comm=NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 3, 12kDa; (NM_002491/572/bronze;)	1001 bp
2	P876212	sym=Ndufb3|loc=Loc66495|taxid=10090|spec=Mus musculus|chr=1| ctg=NT_039170|str=(+)|start=36282125|end=36283164|len=1040| tss=501,506,518,540| comm=NADH dehydrogenase (ubiquinone) 1 beta subcomplex 3; (AK013608/761/gold;AK009008/783/gold;AK007930/749/gold; NM_025597/744/bronze;)	1040 bp
3	P876213	sym=na|loc=Loc301427|taxid=10116|spec=Rattus norvegicus| chr=9|ctg=NW_047816|str=(+)|start=681579|end=682579| len=1001|tss=501| comm=similar to NADH dehydrogenase (ubiquinone) 1 beta subcomplex 3; (XM_217400/645/bronze;)	1001 bp

Alignment (DiAlign format):

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

V$HOXH V$TALE V$CMYB V$EGRF V$NF1F V$NEUR V$ECAT V$PCAT V$AREB V$ETSF U$NRF2 V$RORA
V$CREB V$HOXF

```
alignment position 1.........  11.........  21.........  31.........  41.........
P876211         1 cttgctcccg cctctcctcc ctctctgctg gcgccaccgc agcccccacg
P876212         1 ---------- ---------- ---------- ---------- ----------
P876213         1 c--------- ---------- ---------- ---------- ----------
```

```
alignment position 51........ 61........ 71........ 81........ 91........
P876211         51 ccctaggtgg gcccccacgt cgccccacaa gGCTCGGCTT CCACCCGCCT
P876212          1 ---------- ---------- ---------- ---------- ----------
P876213          2 ---------- ---------- ---------- -GCTCATCCT CAAGCCACCT
                                                     ********* **********

alignment position 101....... 111....... 121....... 131....... 141.......
P876211        101 CGGCTGCCGC CTTctcctcC TCACGACCCT CCCAAGatgc tacctggttt
P876212          1 ---------- ---------- ---------- ---------- ----------
P876213         21 CAGCAGTCGC CTT------C TCACGACCCT CCCGAGcttg ctctcaggtc
                   ********** ***      * ********** ******

alignment position 151....... 161....... 171....... 181....... 191.......
P876211        151 acgagaGGTT CCGGGACCAC CAACACACCG GCTACCGCCT TTCCAgacCA
P876212          1 ---------- ---------- ---------- ---------- -------TCA
P876213         65 tgcag-GGTT TCGGATCCGC CAACATTCCT GCTGCCGCCA CCCCAccTCA
                         **** ********** ********** ********** *****  ***
                                                                      ***
                                                                       **

alignment position 201....... 211....... 221....... 231....... 241.......
P876211        201 CCCTCGCCAG CTCCCGTCTG TAGTTTCCGC GGCCGAAGGA GAAgaaaacC
P876212          4 CCTTCGTCAG CTCCCGACTA CGGCGTCCGA AGCCGGAGGA GAAAT----T
P876213        114 CCTTCGTCAG CTCCCGGCTA CCATGTCCGC AGCCGGAGAA GAAAA----C
                   ********** ********** ********** ********** *****    *
                   ********** ********** ********** ********** *****    *
                   ********** ********** *   ****** ********** ***
                      ******* ********** *   ****** ****

alignment position 251....... 261....... 271....... 281....... 291.......
P876211        251 CCTCTTCATC T--AGCACTT TGCct----- ---------- CCCCCAAAGA
P876212         50 CCTCTTCACC C--GGCACCG TGCGcccccc cccccgcaac CCCCCCAAGA
P876213        160 CCTCTTCACC CcgGGCACCG TGCGttgtcg cccttccta- CCCCCCAAGA
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alignment position 301....... 311....... 321....... 331....... 341.......
P876211        284 CAGCACCGCC GCCTACCTGT CACCCTGCtg tCTCCGGCTT CCTACCGCCG
P876212         98 CAGCACCGCC GCCTACCTGT CACCCCGCAG CCTCAGGCTT CCTACCGCCA
P876213        209 CAGCACCGCC GCCTACCTGT CACCCCGCAG CCTCAGGCTT CCTACCGCCA
                   ********** ********** ********** ********** **********
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                                   ***** ********

alignment position 351....... 361....... 371....... 381....... 391.......
P876211        334 ---------- --CCGCCTCC CGCAGCAGCC TGCCAACTGC AGCGCAACAA
P876212        148 ccgccaccgc caCCGCCTCC CGCAGCAGCC TGCCAACTGC AGCATAACAA
P876213        259 ---------- --CCGCCTCC CGCAGCAGCC TGCCAACTGC AGCATAACAA
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                                     *** ********** ***
alignment position 401....... 411....... 421....... 431....... 441.......
P876211        372 CCAACCCTCT CATTGGGTGa gaaCACGCTC TCAACAACAG CCTCCCTTAT
P876212        198 CCAGCCTTCT CATTGAGTGG GCCCACGCGC TTAATAACAA CCGCTCTCAT
P876213        297 CCAGCCTTCT CATTGAGTGG GTCCACGTGC TTAATAACAA CCGCTCTCAT
                   ********** ********** ********** ********** **********
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                   ********** *********     ******* ********** **********
                   *******                                 *** **********
                   *******
alignment position 451....... 461....... 471....... 481....... 491.......
P876211        422 TGGCTGCAGT ATGccggcag ccccgccctg tGTGCGGTGT CTAAGGATTC
P876212        248 TGGCTGCGCT ATGACTTTGG CCCGCCTcTC GGTGCTCCGC CTAAAGATTC
P876213        347 TGGCTGCGCT ATGGCTTTGG CCCGCCTtTC GGTGCACCTC TTACAGATTC
                   ********** ********** ******* ** ********** **********
                   ********** ********** ******* ** ********** **********
                   ********** ********** *******     ********* **********
                   ********** ********** *******                    *****
                   ********** ***
                   ********** ***
alignment position 501....... 511....... 521....... 531....... 541.......
P876211        472 CGTCCCCAAG CAAGGACAAC Atattatctt ccccgccctt ctCTTTTCTA
P876212        298 CGTCCTGGAG CAAGACAAAC ACGGCTTTAT CGTC------ --CTTCTCCT
P876213        397 CGTCCGGGAG CAAGGAGAAC AAGGCTTCAT CGTC------ --CTCCTCCT
                   ********** ********** ********** ****         ********
                   ********** ********** ********** ****         ********
                   ********** ****   *** *                       ********
                   ********** ****   *** *
alignment position 551....... 561....... 571....... 581....... 591.......
P876211        522 CAGTATCTGT TACCTCAGTC AGATTGAGGA TGCAcatata ctgggAAAAT
P876212        340 CAATATCTTC TACCTCAAGC AGACTCCAGC TGCAAAGTGT GGGA-AATAA
P876213        439 CCGTGTCTCC TACCGCAGTC AAACTCCAGC TGCAAAGAGT AGAA-AACAA
                   ********** ********** ********** ********** **** *****
                   ********** ****         ******** ********** **** *****
                   ********** ****         ******** ****            *****
alignment position 601....... 611....... 621....... 631....... 641.......
P876211        572 AATCGACTTC CAGCGTCCCT CATGTAGTCT CTACctgatt caggaatctc
P876212        389 TCTCTACTTC CAGGCTCCTT CATGTCATCT CTACGTTGTC TGGGAGCCTT
P876213        488 TATCGACTTC CAGGCTTTTT CATGTCATCT CTGTCTTGTC TGGGAGCCTT
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                     ******** ***     ** ********** ****
                                      ** ********** **
alignment position 651....... 661....... 671....... 681....... 691.......
P876211        622 taacCCAGTA TCGGAACGTT AAGCGGCTTC TCCGCTTTCC TGCCGTgAGA
P876212        439 GCG-CCAGTA CCGGAACGTT TACCATCTCC CCCATTTTCC TGTCGTAAGA
P876213        538 GCG-CTAGTC CCGGAACGTT TACTATCTCC TCCACTTTCC TGTCGTAAGA
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alignment position 701....... 711....... 721....... 731....... 741.......
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P876211        672 AACTCGAGGT GACAACCTCC GTTTCCGGTT GGCTCCGgtt gcagag----
P876212        488 AACTAGAGGA AACAACGTCC GTTTCCGGTT GTCTCCGGCT GTAAGGTTGA
P876213        587 AACTAGAGGA AACAACGTCC GTTTCCGGTT GGCTCCaGCT GGAAGGTTGA
                   ********** ********** ********** ********** **********
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alignment position 751....... 761....... 771....... 781....... 791.......
P876211        718 ---TTGAGTG TCCTGAGAGG TCAGATTGCT GTCAGGTAAA TTAGGGAGTT
P876212        538 ATATTGAGTG TCCCGGGAGG TCAGATTGCT GTCAGGTAAT TTAGGGAGCT
P876213        637 ATATTGAGTG TCCTGGGAGG TCACATTGCT GTCAGGTAAT TTAGGGAGTT
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                      ******* ********** *** ****** *********  **********
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alignment position 801....... 811....... 821....... 831....... 841.......
P876211        765 GGTGGGAGGC CCGTTGATTA GGATTAAgag ctagactctA TTCTGGGGAG
P876212        588 GGTGGGAGAC TTCTGGATTA CGCATAAtct aaacttt--- ATCCAGGGAA
P876213        687 GATGGGAGAC TTCTGGAta- ---------- ---------A ATCTGGGAAA
                   ********** ********** *******             * **********
                   ********** *******                          **********
                   ********** *******                           *********
                   ********** *******
                   ********** *******
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                   ********

alignment position 851....... 861....... 871....... 881....... 891.......
P876211        815 TGCAGAAAAG GAGAGActaa atggagaagg atgggaggct gGGAGGGAGA
P876212        635 TGCAGAAGTG GAGAGGGCTG AAGGGAtccg ataAGACC-- -GGGAGAAGA
P876213        717 TGCAGAAGTG GAGAGTGTTG AGAGGAcgag ctcAGACC-- -GGGAGGAGA
                   ********** ********** ******        *****    *********
                   ********** ********** ******        *****    *********
                   ********** *****                    *****    *********

alignment position 901....... 911....... 921....... 931....... 941.......
P876211        865 TCAAAGAACT AGCAGGCGAG AACTAATGaa gtcCTAGTTT AGAGTTGGGG
P876212        682 TCCGGGATCT AGCTTGGGAG CGCCGCtg-- ---CAAGGTT CTTGCTGGGC
P876213        764 TCCGGGACCT AGCTAGGGAG CCCTGCTGcc tagtacagct ggacgaggg-
                   ********** ********** ********      ******* **********
                   ********** ********** ******
                   ********** ********** ******

alignment position 951....... 961....... 971....... 981....... 991.......
P876211        915 TAGGAAGAGG TGGTTGGAGG ATTCAGTGAT CATTACTGTA GTTGTTAAAT
P876212        727 TGTGTTGAGG CGGATGAAGG ATgtctTGAG AATTACGATG GTTGTTAAAT
P876213        813 ------GAGG CGGATGAAGG ATACTGTGAG AATTACTGTG GTGGTTAAAT
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                                  ****** **    **** ********** **********
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alignment position 1001...... 1011...... 1021...... 1031...... 1041......
P876211        965 CCA---GGTG CTTGTTCCCG CTTCTGCCAC ACGCAAaatt ----------
P876212        777 CCCAGAGATG TTTTAAACCG CCGCTACCAG ATGCAATGTA CTCCTCGCCT
P876213        857 CCCAGAGATG TTTTAACACG CCGCTGCCAG ATGCAATTTA CTCCTCGCCT
```

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                   **

alignment position 1051...... 1061...... 1071...... 1081...... 1091......
P876211       1002 ---------- ---------- ---------- ---------- ----------
P876212        827 CCTGGCTTTT TGGGTTGTAT TTGAATAGGG TAAAGAACAG CTCatacttt
P876213        907 CCTGGCTTTT GGGGTTGTGT TTGAATAGGG TAAAGAAGAA CTCtgtcccg
                   ********** ********** ********** ********** ***
                   ********** ********** ********** ********** ***
                   ********
                   ********

alignment position 1101...... 1111...... 1121...... 1131...... 1141......
P876211       1002 ---------- ---------- ---------- ---------- ----------
P876212        877 tAAATACTTA AAACTAGAAG AAATAATTGC AACGGTTGct tcacaagctt
P876213        957 aAAATACTTA AAACTAGAAG AAATAATTGC AACGGTTGtt tcaca-----
                    ********* ********** ********** ********
                    ********* ********** ********** ********
                    ********* ********** ********** ********
                    ********* ********** ********** ********

alignment position 1151...... 1161...... 1171...... 1181...... 1191......
P876211       1002 ---------- ---------- ---------- ---------- ----------
P876212        927 gtattttaag tacggtttcc caaatataag tgtttacgac acagtgctta
P876213       1002 ---------- ---------- ---------- ---------- ----------

alignment position 1201...... 1211...... 1221...... 1231...... 1241......
P876211       1002 ---------- ---------- ---------- ---------- ----------
P876212        977 agtgaaaaag agcaagtcac aaaatcaaga ctactgcata atcctaggat
P876213       1002 ---------- ---------- ---------- ---------- ----------

alignment position 1251...... 1261
P876211       1002 ---------- ----
P876212       1027 taaggattgg atac
P876213       1002 ---------- ----
```

Pairwise similarities:

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

	P876212 (1040 bp)	**P876213 (1001 bp)**
P876211 (1001 bp)	0.364 48 %	0.419 52 %
P876212 (1040 bp)		1.000 73 %

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

Extract alignment region	
Positions in alignment	from: to:

Output file	dialign.seq

Extract aligned sequences

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

[Alignment] [Pairwise similarities]

DiAlign professional TF Release 3.1 December 2004 **Tue Jun 7 15:09:12 2005**

Solution parameters:

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

Aligned Sequences:

No.	Sequence Name	Sequence Description	Length
1	P914161	sym=NDUFB4|loc=Loc4710|taxid=9606|spec=Homo sapiens|chr=3|ctg=NT_005612|str=(+)|start=26809774|end=26810774|len=1001| tss=501| comm=NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 4, 15kDa; (NM_004547/501/silver;)	1001 bp
2	P914163	sym=Ndufb4|loc=Loc68194|taxid=10090|spec=Mus musculus|chr=16|ctg=NT_096987|str=(-)|start=2776611|end=2777611| len=1001|tss=501| comm=NADH dehydrogenase (ubiquinone) 1 beta subcomplex 4; (AK009807/571/gold;NM_026610/571/bronze;)	1001 bp
3	P914164	sym=na|loc=Loc288088|taxid=10116|spec=Rattus norvegicus|chr=11|ctg=NW_047356|str=(+)|start=18247379|end=18248379| len=1001|tss=501| comm=similar to NADH:ubiquinone oxidoreductase B15 subunit; (XM_213619/569/silver;)	1001 bp

Alignment (DiAlign format):

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

V$IRFF V$NRF1 U$NRF1 V$ETSF U$NRF2 V$EREF U$EREF V$RORA V$TBPF

```
alignment position  1.........  11.........  21.........  31.........  41.........
P914161           1 ttaatgttgt  atgaatctag  catggtaaag  tacagaaaag  cttattctct
P914163           1 a---------  ----------  ----------  ----------  ----------
P914164           1 tg--------  ----------  ----------  ----------  ----------

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

```
P914161         51 tcttcttggg tagggaattc tgtTTTGCAA AGCACTTTgt gaTCTATTTG
P914163          2 ---------- ---------- --------AA AGCAATTTCA T-TGTTTTCA
P914164          3 ---------- ---------- ---TTTGGAA AGCAATTTCA T-TGTTTTCG
                                            ******* ********** * ********
                                                 ** ********** * ********
                                                 ** ********** * ********
                                                 ** ********

alignment position 101....... 111....... 121....... 131....... 141.......
P914161        101 TTAGCTTATT TAAtcCTCAC AACAACTTTG CTAGGTGGAC AGgagtcatt
P914163         23 ATGTCTCATT TAA--TTCC- AACAACCTTG CTAGGAGTGC AGAGTCAAGG
P914164         29 TTGTCTCATT TAA--CTCCC AACAACTTTG CTAGGAGTGC GGGGTCAAAG
                   ********** ***  ***** ********** ********** **********
                   ********** ***  ***** ********** ********** **********
                   ********** ***  ****  ********** ********** **********
                                   ****  ********** ********** **
                                   ****  ********** *****

alignment position 151....... 161....... 171....... 181....... 191.......
P914161        151 a----TCTCC AGGATAAGGA AAAGGAAAct ca-GAGACTT TAAGTGACTT
P914163         70 TCATTTCTCC AGGGTAAGAA AAAGGAAATT TGGGAGACAC TAATGACCTT
P914164         77 TCATTTCTCC AGGATAAGAA AAAGGAAATT TGGGAGACAT TAATGACCTT
                   ********** ********** ********** ********** **********
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                        ***** ********** ********
                              ********** ********

alignment position 201....... 211....... 221....... 231....... 241.......
P914161        196 AT------CC AAGGTGACAC AGcacggtta gACCCACAAT GAAAACCCGG
P914163        120 gactaatgAC AAGGTCACCC AGGTTGGAAG AACCCACCCT GGACTGTAGG
P914164        127 CT------AC AAGGTCACCC ACTTTGGAAG AACGCACCCT GAACTGTAGA
                   **      ** ********** ********** ********** **********
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                           ** ********** ********** ********** ********
                           ** ********** *           ********* ********

alignment position 251....... 261....... 271....... 281....... 291.......
P914161        240 ACTTCTGACT CCACAGCCAg tcccacaca- ---------- ------GCTC
P914163        170 ACTTCAGGAG TCACAGACAA CCCAGTTTCC CAGTCTCcTC TAGTCTACTC
P914164        171 CCTTCAGGAG CCACAGACAA CCCAGTTTCC CAGTCTCgTC TAGTCTGCTC
                   ********** ********** ********** ******* ** **********
                    ********* ********** ********** ******* ** **********
                    ********* ********** ********** *******
                    ********* ********** ********** *******

alignment position 301....... 311....... 321....... 331....... 341.......
P914161        273 AACTTTACAT AATAAGccct ggttatgtca gtagagacaa ggCTGCTAGG
P914163        220 AACTTCAGGA AATCAGTT-- ---------- ---------- --CTGCAAAC
P914164        221 AACTTCAGGA AAcCAGTT-- ---------- ---------- --CTGCAAGC
                   ********** ********                           ********
                   ********** ** *****                           ********
                                 *****                           ********

alignment position 351....... 361....... 371....... 381....... 391.......
P914161        323 AAGAAGCAGC GCGGTGACAG A-TGAGtagg tggggagcgg cggtggg---
P914163        246 AAGTAGTAGC ACAGAGAGAA AaGGAGTTTA CCACCAGACA AGAGGAGGCA
P914164        247 AAGCAGTAGC ACAGAAAGAA A-GGAGCTTA ACACCAAACA AAAGGAGACA
                   ********** ********** * ******** ********** **********
                   ********** ********** * ******** ********** **********
                   ********** ********** *

alignment position 401....... 411....... 421....... 431....... 441.......
P914161        369 ---------G CAGGGCGCAC TGCGAGAAGA gcacttcgcg catgcgcata
P914163        296 AAacGAGAAG CAGTGCGCAC GCGCAGAATA CG-------- ----------
P914164        296 AAcaGAGAAA CAGTACGCGT GCGCAGACTA CG-------- ----------
```

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                   **  ****** ********** ********** **
                   **  ****** ********** ********** **

alignment position 451....... 461....... 471....... 481....... 491.......
P914161        410 tcaccgagcg aaCGCGCCGT GTTCGG--GA AGGtaggaga aagaggcg--
P914163        328 ---------- --CGGGACGA GGGCGT--GA AGGAGGATTG GCAAAGGCTC
P914164        328 ---------- --CATGACGA GaggcttgGA GGGAGCCTGG GTAAAGGCTC
                              ********** ******  ** ********** **********
                              ********** *

alignment position 501....... 511....... 521....... 531....... 541.......
P914161        456 ---------- ---------- ---------- ---------- ---GAGCTCC
P914163        364 CACCCaGCCT CGAACCCCAC CCCTCTCCCG CCCCTTCCTG CCAGAGCGCC
P914164        366 CGCCCcGCCT CGAACTCTAC CTCTTTTCCA CCTCTTCCTG CCAGAGcact
                   ***** **** ********** ********** ********** **********
                         **** ********** ********** ********** ******

alignment position 551....... 561....... 571....... 581....... 591.......
P914161        463 TTGTtaacga catccccaac ctctgctaaC GCGCAGGCGC ACTTCCTGAA
P914163        414 TTGTGCG--- ---------- ---------C GCGCAGGCGC ACTTCCTGAG
P914164        416 cTGTGCG--- ---------- ---------C GCGCAGGCGC ACTTCCTGAG
                   *******                        * ********** **********
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alignment position 601....... 611....... 621....... 631....... 641.......
P914161        513 GCTGAAGGTC AGcatagaca aag--GGCCT CAGAATCGCG CAGGCGCAAT
P914163        442 CCTGAAGGTC AGactcgAGA GGGCAGCCCT CATATCCGCG CAGGCGCAGA
P914164        444 TCTGAAGGTC AaactaaAGA GGGCAGCCCT TATATCCGCG CAGGCGCAAA
                   ********** **     *** ********** ********** **********
                   ********** **     *** ********** ********** **********
                   ********** **     *** ********** ********** ******** *
                   ********** *               ***** ********** ******** *
                   ********** *                 *** ********** ********
                   ********** *
                   ********** *
                   ********** *
                   ********** *

alignment position 651....... 661....... 671....... 681....... 691.......
P914161        561 TGTGCCCTGG ttcGCCAAGA TGTCGTTCCC AAAGTATAAG CCGTCGAGCC
P914163        492 TGTGCGCCGG GA-GTCAAGA TGTCGGGTTC CAAGTATAAG CCTGCGCCCC
P914164        494 TGTTCGCCGG GA-GCCAAGA TGTCGTTTTC CAAGTATAAG CCTGCACCCC
                   ********** ** ******* ********** ********** **********
                   ********** ** ******* ********** ********** **********
                   **********    ******* ********** ********** **********
                   **********    ******* *****  *** ********** **********
                                 ******* *****  *** ********** **********
                                                *** ********** **      **
                                                *** ********** **

alignment position 701....... 711....... 721....... 731....... 741.......
P914161        611 TGCGCACTCT GCCTGAGACC CTCGACCCAG CCGAATACAA CATATCTCCG
P914163        541 TGGCCACTCT CCCCAgTACC CTCGACCCTG CCGAGTATGA CGTGTCTCCG
P914164        543 TGGCCGCTCT CCCCAATACC CTCGACCCCG CCGAGTATGA CGTGTCTCCG
                   ********** ********** ********** ********** **********
                   ********** ********** ********** ********** **********
                   ********** ***** **** ********** ********** **********
                   ********** ***** **** ********** ********** **********
                   ********** ***** **** ********** ********** **********
                   **               **** ********** ********** **********
                                     *** ********** *******  * **********
                                     *** ********** *******  * **********
```

```
alignment position 751....... 761....... 771....... 781....... 791.......
P914161        661 GAAACCCGGC GGGCGCAAGC CGAGCGGTTG GCCATAAGAG CCCAGCTGAA
P914163        591 GAGACCaGAA GGGCGCAGGT CGAGCGCTTG AGCATAAGGG CCCGGCTTAA
P914164        593 GAGACCCGAA AGGCGCAGGT CGAGCGCATG AGCATAAGGG CCCGGCTTAA
                   ********** ********** ********** ********** **********
                   ********** ********** ********** ********** **********
                   ****** *** ********** ********** ********** **********
                   ****** *** ********** ********** ********** **********
                   ****** *** ********** ********** ********** **********
                   ******     ********** ********** ********** **********
                   ******     ********** *******      ******** **********
                   ******                             ******** **********
                                                                       **
                                                                       **

alignment position 801....... 811....... 821....... 831....... 841.......
P914161        711 ACGAGAGTAC CTGCTTCAGT ACAACGATCC CAACCGCCGA GGGCTCATCG
P914163        641 ACGGGAGTAT CTGCTTCAGT ACAACGACCC CAAACGCgtg tCGCACATCG
P914164        643 ACGGGAGTAT CTGCTTCAGT ACAACGACCC CAAACGCCAA ACGCACATCG
                   ********** ********** ********** ********** **********
                   ********** ********** ********** ********** **********
                   ********** ********** ********** *******     *********
                   ********** ********** ********** *******     *********
                   ********** ********** ********** *******     *********
                   ********** ********** ********** *******     *********
                   ********** ********** ********** *******     *********
                   ********** ********** ********** *******
                   ********** ********** ********** *******
                   ********** ********** **

alignment position 851....... 861....... 871....... 881....... 891.......
P914161        761 TGAGTGTGGg gcctcCCAGG CGGGAATAGG GCCCGAGTCc tgggagagac
P914163        691 TGAGTGGGG- -----CCGGG CGGGACTGTG GGCCGGGGCA GCCGCATCTC
P914164        693 TGAGTGGGG- -----CCGGG CGGGACTGTG GGCCGGGGCA GCCGCATCTC
                   *********       ***** ********** ********** **********
                   *********       ***** ********** ********** **********
                   *********       ***** ********** ********** **********
                   *********       ***** ********** ********** **********
                   *********       ***** ********** *******
                   *********
                   *********

alignment position 901....... 911....... 921....... 931....... 941.......
P914161        811 cgagag---- ---------- ----AGA-CC ACGCAAAGGG TCGGCCACCG
P914163        735 GCGTGGGCAC ACGCGGGGCC GCCCAGC-TC CCTCCGTGTG CTGGACACCG
P914164        737 GCGCGGGCAC ACGCGGGGTC ACCCAGCtCC AATCCGTGTG CTGGACACCG
                   ********** ********** ******* ** ********** **********
                   ********** ********** *******      ******** **********
                   ********** ********** *******      ******** **********
                   ********** ********** *******      ******** **********

alignment position 951....... 961....... 971....... 981....... 991.......
P914161        842 CTCCCGATCA GTAtctcaga cgcaggtcct cttccaggcc tagccaactc
P914163        784 GCCCCGAGCC GCA------- ---------- ---------- ----------
P914164        787 GCCCCTAGCT GCA------- ---------- ---------- ----------
                   ********** ***
                   ********** ***
                   ********** ***
                   ********** ***

alignment position 1001...... 1011...... 1021...... 1031...... 1041......
P914161        892 actacccttt tacctttgcC AGAGCTTGGC CCTcgagagg acc-------
P914163        797 ---------- ---------C AGCCCTTGGC CCTTCAACTT CGGCCTTCGG
P914164        800 ---------- ---------C AGCCCTTGGT CCTTCAACTT TAGCCTTATG
                                       * ********** ********** **********
                                       * ********   ********** **********
                                       * ********   ********** **********
                                       * ********
```

```
alignment position 1051...... 1061...... 1071...... 1081...... 1091......
P914161        935 ---------- ---------- GGCTCTGGAC TCAGACCTGG CTGGGTTTGA
P914163        828 CTCAGTGGTC AAAGGGATcg gacggcttcc cccttgg--- ----------
P914164        831 CTCAGTGGTC AAAGGGATtg GGCTCCGGCT GCAGACCCAG CTGGCCTTGC
                   ********** ********   ********** ********** **********
                   ********** ********   ********** ********** **********
                   ********** ********

alignment position 1101...... 1111...... 1121...... 1131...... 1141......
P914161        965 ATCCTGGCTt gatcacttcc tgcctgcgtg accttaa--- ----------
P914163        865 ---------- ---------- ----TTTAGA GAAACTTGTT ccACTCTGCA
P914164        881 GTCCTGGCTa gaccgttccc ccccaTTTGGA GAAAGTTGTT aaACTCTGCG
                   *********                 ****** **********   ********
                   *********                                     ********
                                                                 ********
                                                                 ********

alignment position 1151...... 1161...... 1171...... 1181...... 1191......
P914161       1002 ---------- ---------- ---------- ---------- ----------
P914163        891 TAGTCTCGGC TTTCTTGTCT GAAACATGGC CAtaATATGG TCCTTCATAT
P914164        931 TAGTCTCGGC TTTCTTATCT GAAACATGGC CAtgATATTG TCCTTCATAT
                   ********** ********** ********** **  ****** **********
                   ********** ********** ********** **  ****** **********
                   ********** ********** ********** **  ****** **********
                   ********** ********** ********** **

alignment position 1201...... 1211...... 1221...... 1231...... 1241......
P914161       1002 ---------- ---------- ---------- ---------- ----------
P914163        941 CTTTTGAGGC AGATTAacac atgactgact aatctagcac agtatcttcc
P914164        981 CTTCTGAAGC AGATTAcacg t--------- ---------- ----------
                   ********** ******
                   ********** ******
                   ********** ******

alignment position 1251...... 1261
P914161       1002 ---------- -
P914163        991 tcgaaaaggg c
P914164       1002 ---------- -
```

Pairwise similarities:

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

	P914163 (1001 bp)	P914164 (1001 bp)
P914161 (1001 bp)	0.188 39 %	0.233 40 %
P914163 (1001 bp)		1.000 81 %

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

Extract alignment region	
Positions in alignment	from: to:
Output file	dialign.seq

Extract aligned sequences

For comments, questions or bug reports, please contact support@genomatix.de

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

[Alignment] [Pairwise similarities]

DiAlign professional TF Release 3.1 December 2004 **Tue Jun 7 15:22:31 2005**

Solution parameters:

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

Aligned Sequences:

No.	Sequence Name	Sequence Description	Length
1	P862298	sym=NDUFB5|loc=Loc4711|taxid=9606|spec=Homo sapiens|chr=3|ctg=NT_005612|str=(+)|start=85817233|end=85818233|len=1001| tss=501| comm=NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 5, 16kDa; (NM_002492/553/bronze;)	1001 bp
2	P862299	sym=Ndufb5|loc=Loc66046|taxid=10090|spec=Mus musculus|chr=3|ctg=NT_039228|str=(+)|start=3823115|end=3824123|len=1009| tss=501,503,508,509| comm=NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 5; (AK013223/553/gold;AK088061/546/gold;AK002279/553/gold; AK005521/553/gold;AK018562/548/gold;NM_025316/554/bronze;)	1009 bp
3	P862300	sym=na|loc=Loc294964|taxid=10116|spec=Rattus norvegicus|chr=2|ctg=NW_047625|str=(+)|start=5303108|end=5304108| len=1001|tss=501| comm=similar to NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 5; NADH dehydrogenase (ubiquinone) 1 beta subcomplex 5; (XM_215544/501/bronze;)	1001 bp

Alignment (DiAlign format):

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

V$CREB V$YY1F V$PCAT V$SMAD V$RARF V$RORA V$EREF U$EREF V$SF1F

```
alignment position 1.........  11.........  21.........  31.........  41.........
P862298        1  catctacaaa  ccccatatac  tgtcttgtcc  acagcaggca  gcaacaaaat
P862299        1  ----------  ----------  ----------  ----------  ----------
P862300        1  tagaggaaga  acagggtgcg  ccagggtaga  cga-------  ----------
```

```
alignment position 51........ 61........ 71........ 81........ 91........
P862298       51 gaggaaggaa tagaaatgtc ggaggtgagc gacttCTCCA AGGTCACTCA
P862299        1 ---------- ---------- ---------- ---------- ----------
P862300       34 ---------- ---------- ---------- -----CTCCA AGGTCACGCT
                                                        ***** **********

alignment position 101....... 111....... 121....... 131....... 141.......
P862298      101 CTCctcacca aagtgggctc cggctctgcc atccaggcgg ccgttccatt
P862299        1 -----CCTCC GCGGTGGCCT GTctagagCT CTGTTGCATC CTGCAAGAAG
P862300       49 CTCtgCCTCC CTGGTGGTCT AT------CT CTATTGCACA CTGCAAGAAG
                   ***  ***** ********** **      ** ********** **********
                                                 ** ********** **********
                                                 ** ********** **********

alignment position 151....... 161....... 171....... 181....... 191.......
P862298      151 cttg------ ---------- -AGTTGTTCT Cggcatctcg gcatctcggc
P862299       46 CGCCCAAAGG CGGaGGCAGT CATTTCTTCT CT-------- ----------
P862300       93 CTCCCAAAGG CGGcGGCAGT CAGTTCTTCT CT-------- ----------
                   ********** *** ****** ********** **
                   ********** *** ****** ********** **
                   ********** *** ****** ********** **
                                  ****** ********** **
                                  ****** ********** **

alignment position 201....... 211....... 221....... 231....... 241.......
P862298      184 aaccaaacaa gatccaaagt tggagaggtg ggcaaaccta ctttataCAT
P862299       78 ---------- ---------- ---------- ---------- -------CAC
P862300      125 ---------- ---------- ---------- ---------- -------CAT
                                                                   ***
                                                                   ***
                                                                   ***
                                                                   ***
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                                                                   ***

alignment position 251....... 261....... 271....... 281....... 291.......
P862298      234 CACTTACCCT GTGCAGGCAG GGACCTGAGG AGTTATTaac gatcgggaag
P862299       81 CACTTACCCC GAGTGAGCAG CGTCCTTGGG ATTTACTAGG GAACAAGCTG
P862300      128 CACTTACCCG GAGTGAGCAG GGGTCTTGGG ATTTACTAGG GAACAAGCAG
                   ********** ********** ********** ********** **********
                   ********** ********** ********** ********** **********
                   ********** *********      ****** ********** **********
                   ********** *********      ****** ********** **********
                   ********** *********      ****** *******
                   ********** *********      ****** *****
                   ********** *********

alignment position 301....... 311....... 321....... 331....... 341.......
P862298      284 atttcagggc ggatgaaaCT CTCCTACAAA GAAGGGCCAA ACCGGCCGCA
P862299      131 CCTTcagGAA CGCTGAGGCT CTTCTACAAA TACCCACTAG ACTGGTCGCA
P862300      178 CCTTtaaGAA CGCTGAGGCT CTTCTACAAA TACCCACTAG ACTGGTGGCA
                   ****   *** ********** ********** ********** **********
                   ****   *** ********** ********** ********** **********
                   ****   *** ********** ********** ********** **********
                   ****   *** ********** ********** ********** ****** ***
                          *** ********** ********** ********** ****** ***
                          *** ********** ********** ********** ******
                                      ** ********** ********** ******
                                      ** ********** ********** ******
                                      ** ********** ********** ******

alignment position 351....... 361....... 371....... 381....... 391.......
P862298      334 GCCATGTTtt cgcataactg gcaaaa---- ---------- ----------
P862299      181 GCCATGTTTC TAATGgAGAC CCACAGTGTC GGTGTCCACG AGGTCACTTC
P862300      228 GCCATGTTTC TAATGcAGAC ACACTGTGCC GGTGTCCACT AGGTCACTTC
```

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                    ********** ***** **** ********** ********** **********
                    ********** ***** **** ********** ********** **********
                    ********         **** ********** ********** **********
                    ********         **** ********** ********** **********
                    ********

alignment  position 401....... 411....... 421....... 431....... 441.......
P862298         360 ---------- ---------- ---------- ---------- ----------
P862299         231 CGCtggcggc GTGAGGCAAG TGAAGCAAAC AGGAACAGGC TTTGCCCTTA
P862300         278 CGC------- GTGAGACGAA TGAAGCAAAC AAGAACAGGC TTTGCCCTTA
                    ***        ********** ********** ********** **********
                    ***        ********** ********** ********** **********
                    ***                                    **** **********
                    ***                                    **** **********
                                                           **** **********
                                                           **** **********

alignment  position 451....... 461....... 471....... 481....... 491.......
P862298         360 ---------- ---------- ---------- ---------- ----------
P862299         281 CTAAACATGG CCGCTCCCAC GGCTCTcgct tcaatctccc aa--------
P862300         321 CTAAACATGG TCGCTCCCAC GGCTCTttcc ctcactccct ccccccctcc
                    ********** ********** ******
                    ********** ********** ******
                    ********** ********** ******
                    ********** ********** ******
                    ********** ********** ******
                    ********** ********** ******

alignment  position 501....... 511....... 521....... 531....... 541.......
P862298         360 ---------- ---------- ---------- CGCGTTT-CC GCCAACGATA
P862299         323 -GTCTGCCAT AGAGTTTACA GGGCTCTCTT TGGGCgccCC ACCTACAATG
P862300         371 cGTATGCTAT AGAGTTTACG CGGCTCTCTT CGCGCAC-CC ACCTACAATG
                     ********* ********** ********** ******* ** **********
                     ********* ********** ********** *****    * **********
                                                              * **********
                                                              * **********
                                                              * **********

alignment  position 551....... 561....... 571....... 581....... 591.......
P862298         379 GCGTCACTTC CGGCGTCTCA AGCCGGCggt gaggagaata gaaaact---
P862299         372 TCGTCACTTT TGTCCGCCAG CGCCTGCCTg TGAAGCTCGC AGGAACGGGC
P862300         420 TCGTCACTGT TTTCCGCCAG CGCCTGCCTa TGAAGCTAGC AAGCACCCGT
                    ********** ********** *********  ********** **********
                    ********** ********** *********  ********** **********
                    ********** ********** *********  ********** **********
                    ********** ********** *********
                    ********** ********** *********

alignment  position 601....... 611....... 621....... 631....... 641.......
P862298         426 ---TGCCCTC ACTTAAGATG GCCACATCCT GCCTTTGTCC TCATTGGTAA
P862299         422 CGCTGCCCTC ACTCAATATG GCCTCCTCTA GCGTTCGCCC TCACTGGTGG
P862300         470 CGCTGCCCTC ACTCAACATG GCCttcccg- GCATTCGCCT TCACTGGTGG
                    ********** ********** ********** ********** **********
                    ********** ********** ********** ********** **********
                    ********** ********** ***        ********** **********
                       ******* **********            ********** **********
                       ******* **********            ********** **********
                       ******* **********            ********** **********
                                                     ********** ***

alignment  position 651....... 661....... 671....... 681....... 691.......
P862298         473 ATTGGCTCTC TCAGCTTCCG TGACCCGCCT CCCTtcttcc tccTGCCCGT
P862299         472 ATTGTCCCTC CCGGCTCCCT TAGCCCTCCC CACTTCCTTC CG-TGGCCGG
P862300         519 ATTGTCCCTC CCGGCTCCCG TtgcctaCCC TACTTCCTTC CG-TGGCTGT
                    ********** ********** ********** ********** ** *******
                    ********** ********** *      *** ********** ** *******
                    ********** *********         *** ********** ** *******
                    ********** *********         *** ********** ** *******
                    ********** *********                           *******
                    ********** *********                           *******
```

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.

	P862299 (1009 bp)	**P862300 (1001 bp)**
P862298 (1001 bp)	0.162 35 %	0.176 34 %
P862299 (1009 bp)		1.000 78 %

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

Extract alignment region	
Positions in alignment	from: ☐ to: ☐
Output file	dialign.seq

Extract aligned sequences

For comments, questions or bug reports, please contact support@genomatix.de

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GEMS Launcher Task: *DiAlign TF*: Multiple alignment plus TF sites
working on C1-NDUFB6 (3 seq.)

[Alignment] [Pairwise similarities]

DiAlign professional TF Release 3.1 December 2004 **Tue Jun 7 15:44:43 2005**

Solution parameters:

Sequence file:	C1-NDUFB6 (3 seq.)
Type of sequences:	nucleotide sequences
Threshold T:	0.00
'*' signs below alignment denote:	diagonal similarity (max. similarity is represented by 10 '*' signs)
Alignment output:	complete alignment is shown # nucleic acids per line: 50
TF output:	common TF matches located in aligned regions (common to 3 (100.0 %) sequences)
Family matches:	yes
MatInspector library:	Matrix Family Library Version 5.0 (February 2005)
Selected groups (core/matrix sim):	• ALL user_defined.lib (0.75/Optimized) • ALL vertebrates.lib (0.75/Optimized)

Aligned Sequences:

No.	Sequence Name	Sequence Description	Len
1	P855688	P855688 sym=NDUFB6|loc=Loc4712|taxid=9606|spec=Homo sapiens|chr=9|ctg=NT_008413|str=(-)|start=32562682|end=32563682|len=1001|tss=501|comm=NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 6, 17kDa; (NM_002493/501/silver;NM_182739/501/silver;)	1
2	mNDUFB6	mNDUFB6 m6_dna range=chr4:40417544-40418994 5'pad=0 3'pad=0 revComp=TRUE strand=? repeatMasking=none	1
3	P855691	P855691 sym=na|loc=Loc297990|taxid=10116|spec=Rattus norvegicus|chr=5|ctg=NW_047711|str=(-)|start=31999505|end=32000505|len=1001|tss=501|comm=similar to NADH dehydrogenase; (XM_216378/501/bronze;)	1

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$CREB V$CDEF V$RORA V$EVI1 V$HEN1 V$AP4R V$MYOD V$BEL1 V$EGRF V$BRNF

```
alignment
position       1.........  11........  21........  31........  41........

P855688      1 ggtgaaagca  tga-------  --ATTCATCT  ATGCAATTTT  GCTAGATATT
mNDUFB6      1 catacttggt  gtagttggtt  ttATTTACTT  ATTTATTTTT  TTAACTTATC
P855691      1 acca------  ----------  ----------  ----------  ----------
                                          ********  **********  **********
```

```
alignment
position        51........ 61........ 71........ 81........ 91........
P855688     42  AAgctact-- ---------- ---------- ---------- ----------
mNDUFB6     51  AAtagattgt agaagttact ccagttatga atagaaggct catttatggc
P855691      5  ---------- ---------- ---------- ---------- ----------
                **
alignment
position        101....... 111....... 121....... 131....... 141.......
P855688     50  ---------- ---------- ---------- ---------- ----------
mNDUFB6    101  agtagcatac caatgcttta cagtactata agctttccca ctaatcctct
P855691      5  ---------- ---------- ---------- ---------- ----------

alignment
position        151....... 161....... 171....... 181....... 191.......
P855688     50  ---------- ---------- ---------- ---------- ----------
mNDUFB6    151  attctgaaat ctgggaggtg atttttcaat gttttgctat tacatatcgt
P855691      5  ---------- ---------- ---------- ---------- ----------

alignment
position        201....... 211....... 221....... 231....... 241.......
P855688     50  ---------- ---------- ---------- ---------- ----------
mNDUFB6    201  gttgtgacga atattcgtgc acacccctac aaatttttac tgCCATACCT
P855691      5  ---------- ---------- ---------- ---------- --CCATACCT
                                                              ********
                                                              ********
alignment
position        251....... 261....... 271....... 281....... 291.......
P855688     50  ---------- ---------- ---------- ---------- ----------
mNDUFB6    251  TTGGGATGTC TTACAAAGTG GGcCGGCAGA ATCAAAGAGT GAGCGAGCCT
P855691     13  CTGGGATATC TTACAAAGTG GGaCGGCAGG ATCAAAGAGT GAGCCAGTCC
                ********** ********** ** ******* ********** **********
                ********** ********** ** ******* ********** **********
alignment
position        301....... 311....... 321....... 331....... 341.......
P855688     50  ---------- ---------- ---CTTTTCA CTATTCCTGT ACAGATGGAG
mNDUFB6    301  ATGGAAGCCT cCCAAATAAG GTGCTCTTTA TTTCTGCAGT ACAGAGaggg
P855691     63  ATGTAAGCCT -CCAAATAAG GTGCTCTTTA TTTCTGCAGT ACAGAGGAGG
                **********  ********* ********** ********** **********
                **********  ********* ********** ********** ******
                            ********* ********** ********** ******
                            ********* ********** ********** ******
alignment
position        351....... 361....... 371....... 381....... 391.......
P855688     77  GGACAGAtg- AGACAGCTGC CCAgggcact tcAGCAGTTA CTGGCATAGC
mNDUFB6    351  aagaAAACCG AGATAGGCGC TCAAGATTAC TtAGCGGGTT ACGAAAGAGG
P855691    112  GAAGAAACCC AGATAGCTGC TCAAAGTCAC Tt---GAGTT ACTAAAGGGC
                ********** ********** ********** * ******** **********
alignment
position        401....... 411....... 421....... 431....... 441.......
P855688    126  TGGGATTTGA ACTGGGATGT AActattttc atacacTCTC TAGGTCAttc
mNDUFB6    401  TGGGAGCCAA ATTCGGACGC AAGTG----- ------TCTC TCGGTCAAG-
P855691    159  TGGGAGCTGA ACTTGAATGC AATTG----- ------TCTC TAGGTCAAG-
                ********** ********** *****            **** *********
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alignment
position        451....... 461....... 471....... 481....... 491.......
P855688    176  cAAGGTGGGA gaggcaagca aataattttg aatctggcca gcatattcac
mNDUFB6    439  -AAGa---GA ATTCAAGGGG GCGAGGCAGA GGTTCGCT-- ----------
P855691    197  -AAGGTGGGA ATTCAAGCGG GCGGGGCAGA GGTTCCCT-- ----------
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alignment
position              501....... 511....... 521....... 531....... 541.......

P855688      226 tgAAACATTT ATGCTTATCC TTCCTCCTCC Cagca-TACA AGTTCTTCCT
mNDUFB6      473 --AAACCATC GTCCTTGTTC TTCCGGTCCC CTCCCCTACA AGTTCTTTCT
P855691      234 --AAACCCTT GTccttg--- ---CGGTCCC CTCCCCGACA AGTTCTTTCT
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alignment
position              551....... 561....... 571....... 581....... 591.......

P855688      275 Tagcaaaacc tccagtcctc taatttagca tactttcgtc taaTCTGTCA
mNDUFB6      521 CTGAACCCTA GCC--CCAGG ACT------- ---------- ---TCTCACA
P855691      276 TTGAACTCTA GCCccCCGGG ACT------- ---------- ---TCTCACA
                 ********** ***  ***** ***                     *******
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alignment
position              601....... 611....... 621....... 631....... 641.......

P855688      325 CTTTCCtcag gccccacaac tacgagtact cccttgtcccc acccggtcct
mNDUFB6      549 CTTTCCAACA CCGCCCACTT AgtTCTTAAC TCAGGGACCT TCCTGAGCTC
P855691      306 CTTTCTAACA CAGACCACTT AaaTCATAAC TAAAAGACCT TCCAGAGCTT
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alignment
position              651....... 661....... 671....... 681....... 691.......

P855688      375 aatttggtcg ggtatagcgg aggtgggcgt agagagaact ggaggtgGAG
mNDUFB6      599 aTACTTAACC CAGGTTGTTA AAACCCAGGG TCCAAGA--- -------GAG
P855691      356 gTACTTAATC CGGGTTCTTA AAACCCGGGG TCAGAGA--- -------GAG
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alignment
position              701....... 711....... 721....... 731....... 741.......

P855688      425 ACCTTTGTGC ATGCCCACAC ACTGCTTTCC TCGcgaggaa tctggggccc
mNDUFB6      639 GGCTTTGCGC ATGAGCAGAG CCTGCTTTCC GCGAAGGAGT CggcccgccC
P855691      396 GGCTTTGCGC ATGAGCAGAA CCTGCTTTCG GCGAAGGAAT CagctttgctC
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alignment
position              751....... 761....... 771....... 781....... 791.......

P855688      475 ttgCAGAGGC GGaaccagGA TGTGACGTAA TAACCGCGCG CGGCGC-TCG
mNDUFB6      689 C--CAGAGGC GGGGCT--GG TGTGGCGTCA TCACTCCGCG CCGCttcCAG
P855691      446 C--CAGAGGC TGGGCT--GC TGTGACGCCA TCACATCGCG CCGTTG-CAG
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alignment
position              801....... 811....... 821....... 831....... 841.......

P855688      524 GCGttcCCGC AAGGTCGCTT TGCAGAGCGG GAGCGCGC-T TAAGTaacta
mNDUFB6      735 GCG---CCTC AAGGTCGCTT TGCGGAGCGG GAGgggcagG TCAGTGACCG
P855691      491 GCG---CCTC AAGGTCGCTT TGCGGAGCGG GATCGCGC-G TAAGTGACCG
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alignment
position         851....... 861....... 871....... 881....... 891.......

P855688      573 gtccgtagtt cgaGGGTGCG CCGTGTCctt ttgcgttggt accagCGGCG
mNDUFB6      782 GTCCtgt--- ---------- ---------- -----GTAGG CTCGTCGGCA
P855691      537 GCCCcaggtt c--GGGTGCG CGCTGTCact ctctgGTAAG CTCGCCGGCG
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alignment
position         901....... 911....... 921....... 931....... 941.......

P855688      623 ACATGACGGG GTACACTCCG GATGAGAAAC TGCGGCTGCA GCAGCTGCGA
mNDUFB6      804 ACATGTCAGG GTACACGCCG GATGAGAAGC TGCGGCTGCA GCAGCTGCGG
P855691      585 ACATGTCGGG GTACACGCCC GATGAGAAGC TGCGGCTGCA GCAGCTGCGG
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alignment
position         951....... 961....... 971....... 981....... 991.......

P855688      673 GAGCTGAGAA GGCGATGGCT GAAGGACCAG GAGCTGAGCC CTCGGGAGCC
mNDUFB6      854 GAGCTAAGGA GACGATGGCT GAAGGACCAG GAGCTGAGTC CCCGGGAGCC
P855691      635 GAGCTGAGAA GGCGATGGCT GAAGGACCAA GAGCTGAGCC CCCGGGAGCC
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alignment
position         1001...... 1011...... 1021...... 1031...... 1041......

P855688      723 GGTGCTGCCC CCacagaaGA TGGGGCCTAT GGAGAAATTC TGGAATAAAT
mNDUFB6      904 CGTGTTGCCC CCGCGCAGGA TGTGGCCCCT GGAGCGATTC TGGGATAACT
P855691      685 CGTGTTGCCC CCGCGCAGGA TGTGGCCCCT GGAGCGATTC TGGAATAACT
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alignment
position          1051......  1061......  1071......  1081......  1091......
P855688       773 TTTTGgagaa  taaatCCCCT  TGGAGGAAAA  TGGTGAGTGA  CAGACCTCTC
mNDUFB6       954 TTTTGCGGGA  CgGGGCCGTG  TGGAAGAACA  TGGTGAGTGA  TGAGCCACAC
P855691       735 TTTTGCGGGA  CcGGGCCCTG  TGGAAGTACA  TGGTGAGTGA  TGTGCCACAC
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alignment
position          1101......  1111......  1121......  1131......  1141......
P855688       823 CGG--TCccc  ----------  ----------  -----CCCAA  CA---CATCC
mNDUFB6      1004 gggtgTCCGG  GTTCCCACCC  CGGGTCGCAG  CCTGGCCAAG  CCtccCAGCC
P855691       785 AGA--TCCGG  GTTCCCACTC  CGGGTCGCAA  CCCGGCCAAC  CC---CTTCC
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alignment
position          1151......  1161......  1171......  1181......  1191......
P855688       843 CACTGCTGCC  GGCAGCCTGA  ACACTGAACg  tccgctccct  gcagccacac
mNDUFB6      1054 CACTCCTCTC  AGTTCCATCA  AGGCCCAACC  CTGTCCAGAG  CCCGCATACC
P855691       830 CACTCCTCTC  AGTTCCATTA  AGGCCCGACC  CTCTCCAGAG  CCCGCACACC
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alignment
position          1201......  1211......  1221......  1231......  1241......
P855688       893 caaggactga  taacgctcag  tgct------  ----------  ----CTGGGA
mNDUFB6      1104 CGGGAGGGCC  CCAAGGGACA  ATCAGTCCAG  GGGCTCAGGT  TTAGCGGAGA
P855691       880 CGGGAGGGCC  CCAAGGGACA  ATCAGTCCAG  GCCCTCAGAT  TTAGCGGAGA
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alignment
position          1251......  1261......  1271......  1281......  1291......
P855688       923 CACTGGCCAG  TCCCGAGAGT  CCtcctggag  tctCGGGAGG  CAGGAGTCCA
mNDUFB6      1154 CGCTGTCAGG  TCGCTATTGT  TCAGGG----  ---CTGGGGT  CTGGAGTCCA
P855691       930 TGCTGTCACG  TCGCTAGAGT  TCAGGG----  ---CCGGGGT  CTGGAGTCCT
                  **********  **********  ******         *******  **********
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                  **********  ******  **  ******         *******  **********

alignment
position          1301......  1311......  1321......  1331......  1341......
P855688       973 GGAATATGTa  TGGCTTTGAG  AGAATCATg-  ----------  ----------
mNDUFB6      1197 GGAGCAGGTg  gctgtcaggt  gtactgagaa  gtcgggtctt  aggttttaca
P855691       973 GGAGCAGGT-  TGGCTTCGGG  AGGATGATcc  ----------  ----------
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alignment
position          1351......  1361......  1371......  1381......  1391......
P855688      1002 ----------  ----------  ----------  ----------  ----------
mNDUFB6      1247 agacgctcgc  cgcacatgca  gttctttcga  gtgtagatac  cttttctcgg
P855691      1002 ----------  ----------  ----------  ----------  ----------

alignment
position          1401......  1411......  1421......  1431......  1441......
```

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P855688   1002 ---------- ---------- ---------- ---------- ----------
mNDUFB6   1297 gttaaactgg tcagaattaa ctgagatcac aggctgtgat ttcagtattt
P855691   1002 ---------- ---------- ---------- ---------- ----------

alignment
position       1451...... 1461...... 1471...... 1481...... 1491......
P855688   1002 ---------- ---------- ---------- ---------- ----------
mNDUFB6   1347 gagaacactt acgcggtggg tagggttgag gtgccagaga ctggccagct
P855691   1002 ---------- ---------- ---------- ---------- ----------

alignment
position       1501...... 1511...... 1521...... 1531...... 1541......
P855688   1002 ---------- ---------- ---------- ---------- ----------
mNDUFB6   1397 ggtatagtac agccccatgg ggtcgcaaca gaagacaggg ttctatttgg
P855691   1002 ---------- ---------- ---------- ---------- ----------

alignment
position       1551.
P855688   1002 -----
mNDUFB6   1447 tatgc
P855691   1002 -----
```

Pairwise similarities:

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

	mNDUFB6 (1451 bp)	**P855691 (1001 bp)**
P855688 (1001 bp)	0.208 37 %	0.260 40 %
mNDUFB6 (1451 bp)		1.000 80 %

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

Extract alignment region	
Positions in alignment	from: ☐ to: ☐
Output file	dialign.seq

Extract aligned sequences

For comments, questions or bug reports, please contact support@genomatix.de

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

[Alignment] [Pairwise similarities]

DiAlign professional TF Release 3.1 December 2004 **Tue Jun 7 15:59:00 2005**

Solution parameters:

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

Aligned Sequences:

No.	Sequence Name	Sequence Description	Length
1	P906353	sym=NDUFB7|loc=Loc4713|taxid=9606|spec=Homo sapiens|chr=19|ctg=NT_011295|str=(-)|start=5945188|end=5946188|len=1001| tss=501| comm=NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 7, 18kDa; (NM_004146/501/bronze;)	1001 bp
2	P906354	sym=Ndufb7|loc=Loc66916|taxid=10090|spec=Mus musculus|chr=8|ctg=NT_078575|str=(+)|start=8532757|end=8533760|len=1004| tss=501,504| comm=NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 7; (AK002678/514/gold;NM_025843/511/bronze;)	1004 bp
3	P906355	sym=na|loc=Loc361385|taxid=10116|spec=Rattus norvegicus|chr=19|ctg=NW_047534|str=(-)|start=11544622|end=11545622| len=1001|tss=501| comm=similar to NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 7; (XM_341664/507/bronze;)	1001 bp

Alignment (DiAlign format):

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

V$ETSF U$NRF2 V$OAZF V$HEN1 V$MINI V$CP2F V$E2FF V$NRF1 U$NRF1

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alignment position 1.........  11........  21........  31........  41........
P906353          1 ----------  ----------  ----------  -------GGC  AAGAGAATTT
P906354          1 cacacctacg  tatgtgcact  CACACCGACA  AACCTAGGGA  AAGTGTTTGG
P906355          1 acatg-----  ----------  CACACCGACA  AACCTAAGGA  AAGTGTTTGG
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alignment position 51........ 61........ 71........ 81........ 91........
P906353         14 GAGCCCAGGA GGTGGAGGCT GCAGTGagcc gagatcgcgc caatacactc
P906354         51 AAGTTCGAGT GTTGGAAATG GTAGTGTATA TCTGTGGGAA AGCACTTATC
P906355         36 AGGTTGGAGa GTTGGAAGTG acAGTATATA TGCGTAGGAG AGCACTTATC
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alignment position 101....... 111....... 121....... 131....... 141.......
P906353         64 cagtctgggc gacaggtact gtgtct---- ----CCAAAA ACAAAAAATT
P906354        101 TACCATATGC TAggcctggG GGTCTATCCT AAAACCAGAA AAAAAAATTA
P906355         86 TGCCATGTGC TAt------G TGTCTATCCC AACGCCAttt tattattatt
                   ********** **       * ********** ********** **********
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alignment position 151....... 161....... 171....... 181....... 191.......
P906353        106 CTTAAAGtga ctttatgcaa aattacatac attaacgata taatagatat
P906354        151 ATTTAAGaaa aaaa------ ---------- ---------- ----------
P906355        130 attattatta ttattattat tat------- ---------- ----------
                   *******
alignment position 201....... 211....... 221....... 231....... 241.......
P906353        156 cgtgccTTTT TTAAGAGAAA TTTGAATGTT TTCAAAGAAA aaactt----
P906354        165 ---------- ---------- ---------- ----AAAAAA AGAGGAGGAG
P906355        153 ------TATT ATTATATTAT TATTATTATT TTAGAAGAAA GGAGGGGGAG
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alignment position 251....... 261....... 271....... 281....... 291.......
P906353        202 ---------- ---------- ------TTTG GAAAATGata tgaaaaataa
P906354        181 GAAGAGGAAC GCGGAAGATG GTTC------ ---------- ----------
P906355        197 GGGAAGGAAC GTGGAATATG GTTCagTTTG TAAAATGcct gccatgcgat
                   ********** ********** ****  **** *******
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alignment position 301....... 311....... 321....... 331....... 341.......
P906353        226 ttttaatatg tgctttagcc tcgggctacc agaagagccc cagatagGGT
P906354        205 ---------- ---------- ---------- ---------- -------GGT
P906355        247 cgtgctagtc a--------- ---------- ---------- ----------
                                                                      ***
alignment position 351....... 361....... 371....... 381....... 391.......
P906353        276 CGAGGGAGGC CTCAGTCCCa caccgtcccc ttctgccccg cccagatgga
P906354        208 CCAGGGTGTC CACAGTACCC ATGTAtacac atgtatACAG CAGGCTTGGT
P906355        258 -----GTGTC CACAGTACCC ATGTAa---- ------ACAG CAGGCTTGGT
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alignment position 401....... 411....... 421....... 431....... 441.......
P906353        326 tttccag--- ---------- ---------- --GCTCAGGG AAGTCC----
P906354        258 GGCACACATT TaTAATCCTA GCACTGGGCA GAGCACAGGG GACcctgcca
P906355        293 GGCACACATT TgTAATCCTA GGACTGGGTA GAGCATAGGG AACGCC----
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alignment position 451....... 461....... 471....... 481....... 491.......
P906353        347 ---------- ---------- -------CCT CTCGGGTCCA ACCATATCCT
P906354        308 cctccccgct tccacacccg cactcctCCC TGCAACTCCC TGGCCAGCCT
P906355        339 ---------- ---------- -------CCC TGCAGATCCC TGGCCAGCCT
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alignment position 501....... 511....... 521....... 531....... 541.......
P906353        370 Gcgaagagac aca------- ------GCAC CTGTCCCGCC TCCGCCTGTC
P906354        358 GGCCTTCTAG CCAACTGGCG TTCGCCGCAC CCGCTCTGTC TCCTCCACAC
P906355        362 GGCTTTCTAG CCAACTGGCG TTCGCCGCAG CCGCCCTGTC TCCTCCACGC
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alignment position 551....... 561....... 571....... 581....... 591.......
P906353        407 CGCGAGGTGA CGCCAGgcgg accggagcga tcctctggag tccTTCATCT
P906354        408 CGCCAGGGGG TGTCAGCGAG CCAGGAAGCG TTCCATCG-- ---TTCATCT
P906355        412 CACCAGGAGG TGCCAGCGGG CCAGGAAGTC TTCCACCG-- ---TTCgTCT
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alignment position 601....... 611....... 621....... 631....... 641.......
P906353        457 CTATGATCTC CGCAGCTGCC TAAATGACCC GGAAGctgtg tctgACTGAG
P906354        453 CTATGACCCC CGCCGCAGCC TAGATGACCC GGAAGaC--- ----ACTGAA
P906355        457 CTATGACCCC CGCTGCGGGC TAGATGACCC GGAAGtC--- ----ACTGAA
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alignment position 651....... 661....... 671....... 681....... 691.......
P906353        507 GGGTCAGTGG TTCCGGGTAG GAGCTAGGTG ACCCtCGGCT GCTgcaggga
P906354        496 GGGGCAGTGC TTCCAGGTGG GAGCGAGGTG ACCC-CGGCT ACTAAAGAAG
P906355        500 GGGGCAGTGC TTCCAGGTGG GAGCGAGGTG ACCC-CGGCT GCTAAAGAAA
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alignment position 701....... 711....... 721....... 731....... 741.......
P906353        557 tctgcagcga ctgcAGCCAT GGGGGCCCAC CTGGTCCGGC GCTACCTGGG
P906354        545 GGTAAGGCAG AGT-AGCCAT GGGGGCGCAC CTGACCCGGC GCTATCTGTG
P906355        549 GGTAGGGCAG AGT-AGCCAT GGGGGCGCAC CTGACCCGGC GCTATCTGTG
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alignment position 751....... 761....... 771....... 781....... 791.......
P906353        607 CGATGCCTCG GTGGAGCCCG ACCCCCTGCA GATGCCAACC TTCCCGCCAG
P906354        594 GGATGCCTCG GTGGAGCCTG ACCCCGAGAA GATACCCAGC TTCCCGCCGG
P906355        598 GGATGCCTCG GTGGAGCCTG ACCCTGAGAA GATGCCCAGC TTCCCGCCGA
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alignment position 801....... 811....... 821....... 831....... 841.......
P906353        657 ACTACGGCTT CCCCGAACGC AAGGAGCGCG GTGAGgccCA GTGCGCAGGC
P906354        644 ACCTCGGCTT TCCGGAGCGC AAGGAGCGAG GTGAGCT-CA GTGCGCAGGC
P906355        648 ACTACGGtcT TCCGGAGCGC AAGGAGCGAG GTGAGCT--- -TGCGCAGAC
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alignment position 851....... 861....... 871....... 881....... 891.......
P906353        707 GCagcc---- ---------- ---------- --AG------ ------AGGG
P906354        693 GCGACCGCAG ATCCCGCGGA ACTCAGCTGC ctgcttgcgg agggccGGGT
P906355        694 GCGACCGCCG ATCCCGCGGA ACTCGGCTGC agAG------ ------GGGT
                   ********** ********** **********   **             ****
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alignment position 901....... 911....... 921....... 931....... 941.......
P906353        719 CGTGGGGCGC GGGTGCCTGA acacctggca ccccagggct ggcaccccag
P906354        743 CGAGTCGGGA GGGCGacctc cttg------ ---------- ----------
P906355        732 CGGATCGCGA GGGCGCCTGA g--------- ---------- ----------
                   ********** **********

alignment position 951....... 961....... 971....... 981....... 991.......
P906353        769 ggctgggctc taacctcagg tgttgtatct gggtttgggt ctagactagg
P906354        767 ---------- ---------- ---------- ---------- ----------
P906355        753 ---------- ---------- ---------- ---------- ----------

alignment position 1001...... 1011...... 1021...... 1031...... 1041......
P906353        819 agtccacagg acgtgcatga ccccacctcA GTGTGGAGGC gttccagccc
P906354        767 ---------- ---------- ---------A GTGTGGAGGC tgtgc-----
P906355        753 ---------- ---------- ---------- ---------- ----------
                                                  * **********

alignment position 1051...... 1061...... 1071...... 1081...... 1091......
P906353        869 aaGGGCACGG CTTGAGCAAA AGCCAGGGAg caaaagtgag gcgacaa---
P906354        783 --GGGGATGG CTAAAGCAAA AGGCTGGGAC GAGACAGCAG AGAACGGGaa
P906355        753 ---------- -------AAA AGGCTGGGAC AAGACAGCAG AGAACGGGga
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alignment position 1101...... 1111...... 1121...... 1131...... 1141......
P906353        916 ---------- ---------- ---------- ---------- ----------
P906354        831 gat-GAGACT GCCCCGGTGC ACTTCGTCCT GGGCACAGCG CGGAgccta-
P906355        786 agacGAGACT GCCCCGGTGC ACTTCGTCCT GGACACAGCG CGGAgcctag
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alignment position 1151...... 1161...... 1171...... 1181...... 1191......
P906353        916 ---------- ---------- ---------- ---------- ----------
P906354        879 GGACATGTTC TTTGCATCTC CATACATTGT CACTagca-T TTGGTTACGT
P906355        836 GGACATGTTC TTTGCATCTC CATACAGTGT CACTcgtatT TTGGTTATGT
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                   ********** ********** ********** ****     * **********
                   ********** ********** ********** ****

alignment position 1201...... 1211...... 1221...... 1231...... 1241......
P906353        916 ---------- -------GTG GGGGTTCGGG CAGGAATGCG ACGCGCagag
P906354        928 ACAATAATAC AAGGTTGGGG GGc--TGGAG CGATCATGCt c----CTTGT
P906355        886 ACAATAATAC AAGGTCGGCG GGGGATGGGG CGGTCCTGCA GTGCACTTGT
                   ********** ********** ********** ********** **********
                   ********** ********** **                         *****
                   ********** ********** **                         *****
                                                                    *****

alignment position 1251...... 1261...... 1271...... 1281...... 1291......
P906353        949 ctgggtcgag tctttttttt ttttcttttg agacggagtc tcgctttttc
P906354        972 CCTGTCTAGT GTGATGGTGC TGGGGGAGGA ACC------- ----------
P906355        936 CCTGTCTAGT GTGATGGTGC TGGGGATGGA ACCcaaggcc tgtgtgtact
                   ********** ********** ********** ***
                   ********** ********** ********** ***
                   ********** ********** ********** ***
                   ********** ********** ********** ***

alignment position 1301...... 1311..
P906353        999 ttt------- ------
P906354       1005 ---------- ------
P906355        986 cgcacggttc ttgttc
```

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.

	P906354 (1004 bp)	P906355 (1001 bp)
P906353 (1001 bp)	0.217 31 %	0.177 28 %
P906354 (1004 bp)		1.000 72 %

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

Extract alignment region	
Positions in alignment	from: to:
Output file	dialign.seq

Extract aligned sequences

For comments, questions or bug reports, please contact support@genomatix.de

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

[Alignment] [Pairwise similarities]

DiAlign professional TF Release 3.1 December 2004 **Tue Jun 7 16:10:54 2005**

Solution parameters:

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

Aligned Sequences:

No.	Sequence Name	Sequence Description	Length
1	P927722	sym=NDUFB8|loc=Loc4714|taxid=9606|spec=Homo sapiens|chr=10|ctg=NT_030059|str=(-)|start=21037647|end=21038647|len=1001| tss=501| comm=NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 8, 19kDa; (NM_005004/510/bronze;)	1001 bp
2	P927731	sym=Ndufb8|loc=Loc67264|taxid=10090|spec=Mus musculus|chr=19|ctg=NT_039692|str=(-)|start=4936006|end=4937027| len=1022|tss=501,512,522|comm=NADH dehydrogenase (ubiquinone) 1 beta subcomplex 8;(AK028070/501/gold;AK010177/522/gold;NM_026061/512/bronze;)	1022 bp
3	P927735	sym=na|loc=Loc293991|taxid=10116|spec=Rattus norvegicus|chr=1|ctg=NW_047567|str=(-)|start=293982|end=294982| len=1001|tss=501| comm=similar to NADH dehydrogenase (ubiquinone) 1 beta subcomplex 8; (XM_215269/529/bronze;)	1001 bp

Alignment (DiAlign format):

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

V$MEF2 V$TBPF V$NRF1 U$NRF1 V$EVI1 V$YY1F V$RBPF V$AP1R V$EREF U$EREF V$ZF35 V$NKXH
V$EBOX

```
alignment position 1.........  11.........  21.........  31.........  41.........
P927722          1 cag-------  ----------  ----------  ----------  ----------
P927731          1 tttttttttt  cctgaaaaat  gGGAGGTTTG  GGGCTGGGTC  AGGCGAGCCG
P927735          1 at--------  ----------  -GGGGGTTTG  GGGCTGTGTC  AGGAGAGCCG
```

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alignment position 51........ 61........ 71........ 81........ 91........
P927722          4 ---------- --GGCCGAAT TGTGTGTTGC ACTGGCGTCT AAGTGA----
P927731         51 CCTCCAGTAA TcGGCTTGGT TTTTGTATTT GTTGGGTt-G AGGTGATTGA
P927735         32 CCTCCAGTAA TaGGCTTGGT TTTGTATTTC GTTGGATGCG AGGTGACTGA
                   ********** * ******** ********** ********** **********
                   ********** *                              * **********
                   ********** *                              * **********

alignment position 101....... 111....... 121....... 131....... 141.......
P927722         38 ---------- ---------- ---------- ---------- ----------
P927731        100 GACATTTAGA TGAACTGAGA ---------C AACTTTGAGT ATATAAGGAA
P927735         82 GACATTTAGA TGAACCGAGA ctaaggagcC AACTTTGAGT ATATAAGGAA
                   ********** **********          * ********** **********
                   ********** **********          * ********** **********
                   ********** **********          * ********** **********

alignment position 151....... 161....... 171....... 181....... 191.......
P927722         38 --AGATCAAC CCATTTGGAG aacAGAACAA CAAGCAAGAC CAACAGGTGA
P927731        141 AGAG------ --ATTTGGAG ---AAAGGAT CAAACAAAAC CAAGAGCTAA
P927735        132 AGAGGTGAGC CTATTTGGAG ---AGAGGAT CAAACAAAAC CAAGAGCTAA
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alignment position 201....... 211....... 221....... 231....... 241.......
P927722         86 ATTTGAAGAA TGATCATGTt tggggatgga aggaagtgcc cgtgaaggag
P927731        180 ATGTGAAAAA GGACTGTGT- ---------- ---------- ----------
P927735        179 ATGTGAAAAA TGAGTGCGT- ---------- ---------- ----------
                   ********** *********
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alignment position 251....... 261....... 271....... 281....... 291.......
P927722        136 aggaaagcaa gcagccagag aaGAGAGTAA GACAGGCTCA TTTCACTagt
P927731        199 ---------- ---------- --GTGAGGAC AGAAGGCTGG TTTTACTTTG
P927735        198 ---------- ---------- --GTGAGGAC AGACGCCTGA TTTTACTTTG
                                           ******** ********** **********
                                           ******** ********** **********
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alignment position 301....... 311....... 321....... 331....... 341.......
P927722        186 acagctcctg ggggaggtgg ttaAGCTGTC Tacctgagtt gctcaggttc
P927731        227 CAC------- ---------- ---AGCGGTC TGAGATATTC GGCTGGCG--
P927735        226 CTC------- ---------- ---AGCTGTC TGAGATATTC GGCGGGAG--
                   ***                      ******* ********** ********
                   ***                      ******* ********** ********
                   ***                      ******* ********** ********

alignment position 351....... 361....... 371....... 381....... 391.......
P927722        236 cgagttccca tCATCCCTGG ATGGGTCTAA GTCAGCTCAG GGAGAAAAAG
P927731        255 ---------- -CAGCCCCGA AAGGGCCTCA GTCGGTTGAA GGCGAAAAGG
P927735        254 ---------- -CAGCCCTGA A--------- ---------- ----AAAAGA
                               ********* ********** ********** **********
                               ********* *                         ****
                               ********* *

alignment position 401....... 411....... 421....... 431....... 441.......
P927722        286 GACACAACAT TCTGAAATGT CAGAgacct- ---GCCTGGT TTTCCCTTCT
P927731        294 AATACAGTAA CTTGCAATAT CAAGTAAGcA GTAGCTTTGT TTTCTCTCCT
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P927735          270 AACACTATAA CTCGAAATAT CAAATGAGtA GTAGCTTTGT TTTCTCTCCT
                     ********** ********** ******** * ********** **********
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                                                    * ********** **********

alignment position   451....... 461....... 471....... 481....... 491.......
P927722          332 TCCCGCTTAT CCTTCccagc ctctatccaa cccttggctt ------CCCA
P927731          344 TGCTGTCTGT CCTggcacc- ---TCATCAG CCGCTCACCG TCCAGGCTCT
P927735          320 TGCTGGCTGT CTATCttggc actTCACCAG CCACTCACTG CGCAGGCTCT
                     ********** *****         ******* ********** **********
                     ********** *             ******* ********** **********
                     ********** *                                      ****

alignment position   501....... 511....... 521....... 531....... 541.......
P927722          376 ACTGCGTATT TAA----ACC CCGCCCCTGT TGAACCCttc ggcttttCTT
P927731          390 ACAGCATATT TAAataaAGC CCGCCCAGCT TGATGCCGGG A------CTT
P927735          370 ACAGCGTATT TAA----AGC CCGTCCAGCT TGACACCCGG A------CTT
                     ********** ***    *** ********** ********** *      ***
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                     ********** ***    *** ********** *******           ***

alignment position   551....... 561....... 571....... 581....... 591.......
P927722          422 CACTCCCGGC TTCCTCCGTC A-CGTTTGGC CCGGCTCAGC CGCCGTGACA
P927731          434 CTGCGCTGGC TTCggagatc gcCGTTTGGC CCGACTCAGC CACCGTGACC
P927735          410 CAGCGCTAGC TTCAACGATC G-CGTTTGTC CCcGCTCAGC CACCGTGACC
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alignment position   601....... 611....... 621....... 631....... 641.......
P927722          471 GGCCTTTGCG CATGTGCAGA aggGAAACGT GAAGAAGGTG AAGATGGCGG
P927731          484 CGCTTTTGCG CATGTGCAGA gt-GAACCGC GGAGAAGGTG AAGATGGCTG
P927735          459 CGCCTTTGCG CATGTGCAcg gcgagcgt-C GGAGAAGGTG AAGATGGCGG
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alignment position   651....... 661....... 671....... 681....... 691.......
P927722          521 TGGCCAGGGC CGGGGTCTTG GGAGTCCAGT GGCTGCAAAG GGCATCCCGG
P927731          533 CCGCCCGGGC TGCGGCCCTG GGAGTCCGAT GGCTGCAGAG GACAACCCGG
P927735          508 CGTCCCGGGC TGCGGCCCTG GGAGTCCGGT GGCTGCAAAG GACATCCCGc
                     ********** ********** ********** ********** **********
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alignment position   701....... 711....... 721....... 731....... 741.......
P927722          571 aaCGTGATGC CGCTGGGCGC ACGGACAGGT CCGCgagaac gggcgagacc
P927731          583 gGCGTGGTGC CACTGGAGGC ACGGAGAGGT CTGCACG--- ----------
P927735          558 tGCGTGGTGC CACTTGAGGC ACGGAGAGGT CTGCACG--- ----------
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alignment position   751....... 761....... 771....... 781....... 791.......
P927722          621 tcaGTGTGGG AAGGGGGTAC CTGAAATTTG GTGTATCGGG AGGggggatc
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P927731         620 ---GTGTGGG AAGCGGGTGC CTGAAGTTTA CTGCTTCGGG ATGGAGGCAT
P927735         595 ---GTGTGGG AAGCGGGTGC CTGATGTTTG CTGCTTCGGG AGGGAGGCAT
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alignment position  801....... 811....... 821....... 831....... 841.......
P927722         671 gtagatgccg cggcggcagc ctccgggtag GGAGTGGAGG TGGCGTTGAT
P927731         667 CCTT------ ---------- ---------- GGGACGGTGG CGGAGGTGTC
P927735         642 CCTT------ ---------- ---------- GGAATGGTGG CGTCGGTGTT
                    ****                             ********** **********
                    ****                             ********** **********

alignment position  851....... 861....... 871....... 881....... 891.......
P927722         721 ATATCCAGAA A-ATGGGGTG GAGGATCGCA CTGatcct-- ----------
P927731         691 CTGGCTGGGG gtAAGGGGTG GGAGGTCGCG GTGGATTCGT GTGCCCAAAG
P927735         666 CTGCCTGGGG C-TGGGGGTG Gtacagt--- -TGAATTACT GAGTCCAAAG
                    ********** *  ******** ********** ********** **********
                    **********                         ********* **********

alignment position  901....... 911....... 921....... 931....... 941.......
P927722         758 ---------- ---------- ------GCGA AGTCCCGGGC TCGGACCTCT
P927731         741 AAGGGATACA GGGTTGCTgt aGTCCGGCAA GGTGCGAAAC gaCAGCCTCT
P927735         711 AAGGAATACA AGGTTGCTat -GTTCGGCCA GGTGCGGAAC AGCAACCTCT
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alignment position  951....... 961....... 971....... 981....... 991.......
P927722         782 GCAGCCCCTG CGACTTGAAG CCTT-CGGag cggctggaga gcgggct---
P927731         791 GCAGTCACTG CGGCTTAGTC CTTT-CTGGG TGGGCGCCTA AAGCACCGTG
P927735         760 GCAGTTACTG CAGCTTAGTC CTTTtCTGGG TGGGTGTCTA AAGAACCGTA
                    ********** ********** **** ***** ********** **********
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alignment position  1001...... 1011...... 1021...... 1031...... 1041......
P927722         828 CGCTTCTGAC CTGTTCTCTT CTGCGtTCTA GCCTCCCACA TGACCAAGGA
P927731         840 TCCATCTGAC CTGCATCCCT CTGCG-TCCA GCCTTCCATA TGACCAAGGA
P927735         810 CCCATCTAAC CTGCTTCCCT CTGTG-TCCA GCCTTCCACA TGACCAAGGA
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alignment position  1051...... 1061...... 1071...... 1081...... 1091......
P927722         878 CATGTTCCCG GGGcccTATC CTAGGACCCC AGAAGAACGG GCCGCcGCCG
P927731         889 CATGTTGCCG GGGTCATATC CTAGGACCCC AGAGGAACGC GCCGCGGCCG
P927735         859 CATGATGCCG GGGTCATATC CTAGGACCCC AGAAGAACGG GCCGCGGCCG
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alignment position  1101...... 1111...... 1121...... 1131...... 1141......
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P927722       928 CCAAGAAGTA TAATATGCGT GTGGAAGACT ACGAaCCTTA CCCGGATGAT
P927731       939 CCAAGAAGTA TAACATGCGA GTGGAAGACT ACGAGCCATA CCCCGATGAT
P927735       909 CCAAGAAGTA TAATATGCGT GTGGAAGACT ACGAGCCGTA CCCAGATGAT
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alignment position 1151...... 1161...... 1171...... 1181...... 1191
P927722       978 GGCATGGGGT GAGAcagaga gggt------ ---------- ---
P927731       989 GGCATGGGGT GAGtg--AGG TAGAGGACTC GGGTCA---- ---
P927735       959 GGCATGGGGT GAGAtgaAGG AAGTCTACTC GCATCAgggg cag
                  ********** ****   *** ********** ******
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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.

	P927731 (1022 bp)	**P927735 (1001 bp)**
P927722 (1001 bp)	0.340 50 %	0.384 50 %
P927731 (1022 bp)		1.000 78 %

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

Extract alignment region	
Positions in alignment	from: ☐ to: ☐
Output file	dialign.seq

Extract aligned sequences

For comments, questions or bug reports, please contact support@genomatix.de

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

[Alignment] [Pairwise similarities]

DiAlign professional TF Release 3.1 December 2004 **Tue Jun 7 17:05:45 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)
Selected groups (core/matrix sim):	• ALL user_defined.lib (0.75/Optimized) • ALL vertebrates.lib (0.75/Optimized)

Aligned Sequences:

No.	Sequence Name	Sequence Description	Length
1	P922003	sym=NDUFB9|loc=Loc4715|taxid=9606|spec=Homo sapiens|chr=8|ctg=NT_008046|str=(+)|start=38769028|end=38770040|len=1013| tss=501,513| comm=NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 9, 22kDa; (AK026538/513/gold;NM_005005/501/silver;)	1013 bp
2	P922004	sym=Ndufb9|loc=Loc66218|taxid=10090|spec=Mus musculus|chr=15|ctg=NT_039621|str=(+)|start=20271682|end=20272682| len=1001|tss=501| comm=NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 9; (AK003540/601/gold;NM_023172/601/bronze;)	1001 bp
3	P922005	sym=na|loc=Loc299954|taxid=10116|spec=Rattus norvegicus|chr=7|ctg=NW_047779|str=(-)|start=13034523|end=13035523| len=1001|tss=501| comm=similar to NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 9, 22kDa; NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 9 (22kD, B22); (XM_216929/577/bronze;)	1001 bp

Alignment (DiAlign format):

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

V$ECAT V$ETSF U$NRF2 V$STAF V$TBPF V$ZF5F V$OCT1

```
alignment position 1.........  11........  21........  31........  41........
P922003          1 gatatgaacg  aatgaatgct  tgagtgaatt  ggtccccaga  agcggtcagc
P922004          1 taga------  ----------  ----------  ----------  ----------
P922005          1 ----------  ----------  ----------  ----------  ----------
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```
alignment position 51........ 61........ 71........ 81........ 91........
P922003         51 ctctccgcca aggcagaggG GAAGGGCCGG GAGGTGCACG tgggatgaat
P922004          5 ---------- ---------- ---------- AGAGTTCACG AAAGACA---
P922005          1 ---------- ---------G GGAGGGAGGG AGGGTTCACG AAATACC---
                              * ********** ********** *******
                                           ********** *******

alignment position 101....... 111....... 121....... 131....... 141.......
P922003        101 gGAAACATAG TGATTGGCct ttttggag-- -------TTT TCTTCTTaaa
P922004         22 -GAAGAAAAG TGATTGGCtT GGGGGGCGGT GCTTTttgag aga-------
P922005         29 -GGAGAATAG TGATTAGC-T GGGGGGCGGT GCTTTctTTT TCTTTTTtgg
                    ********* ******** * ********** *****  *** *******
                    ********* ******** * ********** *****

alignment position 151....... 161....... 171....... 181....... 191.......
P922003        142 aaactgaata cattacagat gt-------- ---------- ----------
P922004         64 ----TGGGAG GACTCGGGGA CTAGCCCATG CTAGGCgatc AGTCTACGGC
P922005         77 gtggTGGGAG GACTCGGGGA TTAGCCCATG CTAGGC---- AGTCTACCGC
                       ****** ********** ********** ******     **********
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                       ****** ********** ********** ******

alignment position 201....... 211....... 221....... 231....... 241.......
P922003        164 ---------- ---------- ---------- ---------- ----------
P922004        110 TGaaGCACAC CCCACACCTA TTCCTCTCTT TCCAGTTGAA TTaaacACAC
P922005        123 TGtcGCACAT CCCACACCTA TACCTCTATT TTCAGTTGAA TT----ACAC
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alignment position 251....... 261....... 271....... 281....... 291.......
P922003        164 -TGAAAACAG CACAAaaatc ataactgtac gGCTTGTTAA TTTTTACAAA
P922004        160 ACAAAAAAAG CACAAGTCac aatgattcat TGCCCGGGAA TGCTCATAAA
P922005        169 ATAAAAAATG CACAAGTCca atta------ TGCTCGTGAA TTCTCATAAA
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alignment position 301....... 311....... 321....... 331....... 341.......
P922003        213 TAAATACACC CTCGTGAATC CAgaaCCTAG ATCAAGAACC AGAGCA----
P922004        210 TGAACATGCA CTAGGGAAAC CAT--CCTCC AGCAAGAACC AGATCAGTCA
P922005        213 TCAATATGCA TTCGGGAAct CAT--CCTCG AGCAAAAACC AGATCAATCA
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alignment position 351....... 361....... 371....... 381....... 391.......
P922003        259 TTACCAGCAC ccagaaacct ccccgcgccc tcctccactg agcggcCCTT
P922004        258 TTGCCAGCAC gCGAGGCCTC CGGGCAT--- ---------- ------CTTC
P922005        261 TCGCCAGCAC tCGAGGCCTC CGGGAAT--- ---------- ------CTTC
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alignment position 401....... 411....... 421....... 431....... 441.......
P922003        309 TCAACCCTTA CAATGCCGGA GGGCGCAAtt cctgggtcct gtgaccttgg
P922004        289 CGTGCCCTGG AAAgGCCATG CCGCGAAAAG GG-------- ----------
P922005        292 TGTACCCTGG AAAAGCCAAG CCGCGAAAAG GG-------- ----------
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alignment position 451....... 461....... 471....... 481....... 491.......
P922003        359 tgaccgacGC CCGGGACAAG TCAGAAAGAC CCAAGGGCGT GGAAAACgCT
P922004        321 --------GA CCCGGGACTG TCAGCGAGGC TCACGACCAA GACAAAC-CT
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P922005        324 --------GG CCCGGGACAG CCAGCAAAAC CCATGGCCAA GGAAAtC-CT
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alignment position 501....... 511....... 521....... 531....... 541.......
P922003        409 CCTCTTACCG ATAAACTTGA AGCGACTCAT GACTGCGCAt ggaggacctc
P922004        362 GCCCTTACCC ACGAACTTGA AGAGACTCAT GACGGCGCGG CAGGCTCCTC
P922005        365 GCCCTTACCC ACGAACTTGA AGAGACTCAT GATAGCGCAG CAGACTCCTC
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alignment position 551....... 561....... 571....... 581....... 591.......
P922003        459 cccagcggAA GCGGAAGTGG CCGCCGGCAA CTCCGCCCTT CCGGCTggcc
P922004        412 CCAGGGAAAA GCGGAAGTGG CTCAGAGCAC GCTCGTCCTT CCGGTTCCGC
P922005        415 CCAGGAAAAG GCGGAAATGG CGTAGAGCAC GCTCATTCTT CCGGCTCCGT
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alignment position 601....... 611....... 621....... 631....... 641.......
P922003        509 ccgctcagtc acccgCAGCA GGCGTGCAGT TTCCCGGCTC TCCGCGCGGC
P922004        462 CTCACAA--- -----CCGCC CGCTTCCGGG TTCCCGGCAG CCCCCGCGGC
P922005        465 CTCGCAA--- -----CCGCC TGCTTCCGGG TTCCCGGCAG CCCCCGCGGC
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alignment position 651....... 661....... 671....... 681....... 691.......
P922003        559 CGgg---GAA GGTCAGCgcc gta--ATGGC GTTCTtggcg tcgggacCCT
P922004        504 GGCCGCTGAA GGTGAGCCGG ACGCTATGGC GTTCTGCGCT CCCCCGGCCT
P922005        507 AGCCGCTGAA GGTGAGCCGG GCGCTATGGC GTTCTGTGCT CCCCCGGCCT
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alignment position 701....... 711....... 721....... 731....... 741.......
P922003        604 ACCTGACCCA TCAGCAAAAG GTGTTGCGGC TTTATAAGCG GGCGCTACGC
P922004        554 ACCTGACCCA CCAGCAGAAG GTGCTGCGGC TGTATAAGCG CGCGCTGCGC
P922005        557 ACTTAACCCA CCGGCAGAAG GTGCTGCGGC TGTATAAGCG CGCGCTGCGC
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alignment position 751....... 761....... 771....... 781....... 791.......
P922003        654 CACCTCGAGT CGTGGTGCGT CCAGAGGTAa gggatGGGGA CCCAGGACTC
P922004        604 CACCTCGAGT CATGGTGTAT CCACAGGTGG GGAGAGGGGA CCCGGGGCTC
P922005        607 CACCTCGAGT CATGGTGTGT CCACAGGTAG GGAGAggaga -CCTGGTCTC
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alignment position 801....... 811....... 821....... 831....... 841.......
P922003        704 GGGGAGGTGA CCCTCGGGGC CCCATGgagg tggagaggcc cctgggtaCC
P922004        654 GGGGACGGAA GCCGAGGGGC CCCGTGGG-- ---------- --------CC
P922005        656 GGGGACGGAA GCCGAGGGGC CCTGTGGGtt gat------- ----------
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alignment position 851....... 861....... 871....... 881....... 891.......
P922003        754 TGGAGGTTCA AGGACTTC-G GGAacggaat tggaaggtgg cctctcgctt
P922004        684 AGGCTGATCA AGGACTTggG GGACACAGTG AAGGGAGCCC GCCCTTGA--
P922005        689 ---CTGATCA AGGACTTA-G GGACACAGTG AAGGGAGCCC GCCCTTGA--
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alignment position 901....... 911....... 921....... 931....... 941.......
P922003        803 cacagaatcc tatggtagAC CCGGGTTCAA ATCCAGGCTT CGCCA-----
P922004        732 ---------- --------AC CCGGGTCCCG ATGCAGTCCT CTCTG-----
P922005        733 ---------- --------AC CTGGGTCCTG ATGCAGTCCT CTCTcttgcc
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alignment position 951....... 961....... 971....... 981....... 991.......
P922003        848 -CTTatggcc gggaGACCTT GTAGAGTTGC TTGTCGGGtc tgggcgtcag
P922004        759 -CTT------ ----GATCTG GCGGAGATGA TTGTGTGGGG CGca------
P922005        765 tCTT------ ----TATCTG GCAGAGATGA TTATGTGGAG CG--------
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alignment position 1001...... 1011...... 1021...... 1031...... 1041......
P922003        897 ctttttgttt agtaaaacgg acGCACGACC AGCGCAGAGG GTCGCAGGAa
P922004        792 ---------- ---------- -------ACC AGGACCCAGC GTAGAAAGTT
P922005        797 ---------- ---------- --GCGCGACC AGGACACAGC GTAGAAGGAT
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alignment position 1051...... 1061...... 1071...... 1081...... 1091......
P922003        947 aattaagtga aataaaggAA AGTGCCTAAA ATTGTAATTG TCATGGGTCC
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P922004        815 GCATGAAGAA ATAA----AA AGTACCTAGG ACTGTCATTG TCATGGATCT
P922005        825 GCATGAAGAA ATAA----AA AATACCCAGG ACTGTCATTG TCATGAATCT
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alignment position 1101...... 1111...... 1121...... 1131...... 1141......
P922003        997 AGCGCTcgct caatcgt--- ---------- ---------- ----------
P922004        861 AAAGCTAACG TTTTTATgac tctgtcGTCC CTAACCTTAA CAGTAATTTG
P922005        871 AACGCTAATG TTTTTATaac tctt--GTCC CTAACCTTAA CAGTAATTTG
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alignment position 1151...... 1161...... 1171...... 1181...... 1191......
P922003       1014 ---------- ---------- ---------- ---------- ----------
P922004        911 TCCATtATCT TTAGTTTGCA GAGTAACTCA GatatTAGTG ATTATTTTAG
P922005        919 TCCATgATCT TTAGTTTGCA GATTAACTGA GgaacTAGTG ATTATTTTAG
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alignment position 1201...... 1211...... 1221...... 1231...... 1241
P922003       1014 ---------- ---------- ---------- ---------- -
P922004        961 CCTGATTTTA CAGATAAGCa ggctcattct attccacctc c
P922005        969 CCTCATTTTA TAGGTAAGCt caggattgac ttg------- -
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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.

	P922004 (1001 bp)	P922005 (1001 bp)
P922003 (1013 bp)	0.188 38 %	0.161 38 %
P922004 (1001 bp)		1.000 80 %

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

Extract alignment region	
Positions in alignment	from: to:
Output file	dialign.seq

Extract aligned sequences

For comments, questions or bug reports, please contact support@genomatix.de

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Frequently asked questionsYour ResultsYour SequencesYour ProtocolHelp

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 Jun 7 17:18:57 2005**

Solution parameters:

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

Aligned Sequences:

No.	Sequence Name	Sequence Description	Length
1	P914197	sym=NDUFB10|loc=Loc4716|taxid=9606|spec=Homo sapiens|chr=16|ctg=NT_037887|str=(+)|start=1949020|end=1950020|len=1001| tss=501| comm=NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 10, 22kDa; (NM_004548/526/silver;)	1001 bp
2	P914198	sym=Ndufb10|loc=Loc68342|taxid=10090|spec=Mus musculus|chr=17|ctg=NT_039649|str=(-)|start=1254142|end=1255239| len=1098|tss=501,598| comm=NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 10; (AK002517/598/gold;XM_128594/501/bronze;)	1098 bp
3	P914199	sym=na|loc=Loc287121|taxid=10116|spec=Rattus norvegicus|chr=10|ctg=NW_047334|str=(-)|start=802694|end=803694| len=1001|tss=501| comm=similar to NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 10, 22kDa; NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 10 (22kD, PDSW); (XM_213242/534/bronze;)	1001 bp

Alignment (DiAlign format):

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

V$OAZF V$STAF V$NRF1 U$NRF1 V$PAX5 V$TEAF V$EBOX V$HESF V$HIFF V$PAX1

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alignment position 1.........  11.........  21.........  31.........  41.........
P914197          1 cctcccc---  ----------   ----------   ----------   ----------
P914198          1 gctgtttctt  agcccctaac   tctggcagga   ggtgaccagc   acctagatga
P914199          1 ----------  ----------   ----------   ----------   ----------
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alignment position 51........ 61........ 71........ 81........ 91........
P914197          8 ---------- ---------- ---------- ---------- ----------
P914198         51 cacataagtg aggatttcca ggttgcaaaa ccaggtttta aacacataaa
P914199          1 ---------- ---------- ---------- ---------- ----------

alignment position 101....... 111....... 121....... 131....... 141.......
P914197          8 ---------- ---------- ---------- ---------- ----------
P914198        101 ctcaagagtt ttggcagtgc agtcctggac agTGAACAAT TCAGGACACA
P914199          1 ---------- ---------- ---------- --TGGGCAAC TCGGGGCACA
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alignment position 151....... 161....... 171....... 181....... 191.......
P914197          8 ---------- ---------- ---------- ---------- ----------
P914198        151 AgtGCTCAGG ACCAGAACCA CcagaaGCAG GGCGAAGCAC TGTG--CCTA
P914199         19 A--GCTCAGG ACCAGAACCA Ctctt-GCAG AGCAAAGCAC TGTGtgCCTA
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alignment position 201....... 211....... 221....... 231....... 241.......
P914197          8 ---------- ---------- ---------- ---------- ---CAGACAG
P914198        199 GGGTGGCGGA CCCTTTtcct ccaaggattg catc------ -TTCAGAGAA
P914199         66 GGGTAGGAAA TCCTTTatgg acacgagaca agccctgcct aTTCAGAGAA
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alignment position 251....... 261....... 271....... 281....... 291.......
P914197         15 GCTCCCAAGT TAACTGGCAC CAGCCAGTCC atgaggggcc cttgtagaGA
P914198        242 GTCCCGAGGT TCACTGGGAC CCACCAGCCC Cag-GGAACC T-------AG
P914199        116 GTCCCGAGGT TTACAGGGAC CCACCAGCCC CcaaGGGACC T-------GA
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alignment position 301....... 311....... 321....... 331....... 341.......
P914197         65 GCGGGGCCCA GAGAAGTctg tagggactag gcaatccagg aaagcttcct
P914198        284 GCAGAGTCTA GAGCAGTTGT TGACTggtg- ---------- ----------
P914199        159 GCAGAGTCTA GAGCAGTTGT TGACTtatat gtactcttt- ----------
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alignment position 351....... 361....... 371....... 381....... 391.......
P914197        115 ggaggagtag ggtgtttgga atcgcgtgcT ATTTGTTCAC TTTGTCGtgt
P914198        313 ---------- ---------- ---------- ---------- ----------
P914199        198 ---------- ---------- ---------T ATTTATTTTT TTTTTCGgag
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alignment position 401....... 411....... 421....... 431....... 441.......
P914197        165 gcgctctaac ggcctgtgtt ctccatcaca ---------- ----------
P914198        313 ---------- ---------- ---------- ---------- ----------
P914199        219 ctgggaaccg aacccagggc cttgccaagc gcactctacc actgagctaa

alignment position 451....... 461....... 471....... 481....... 491.......
P914197        195 ---------- ---------- ---------- ---------G TTTATCTTAT
P914198        313 ---------- --------TG TGTACTCTT- CCAAGCCATG TTCACCATAT
P914199        269 atccccaacc ccgactctTG TGTACTCTTg CCAAGCCATG TTCACtgcAT
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alignment position 501....... 511....... 521....... 531....... 541.......
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P914197         206 TCCCTGCTgc actcagcaca gtgcctggcg cgcagtggga accgaatgac
P914198         344 TCCCTGCTAT CTTAGCTGGT AGGTCAGGGC AAAGCATTtc cagccatt--
P914199         319 TCCCTGCTAT CTTAGCTGGT AGGTCAGGGC AAAGCATTtc cgtgcacttg
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alignment position  551....... 561....... 571....... 581....... 591.......
P914197         256 cccctcctat tccttatgtc agttgccttt tgtctgtttc tttcatcgta
P914198         392 -TGGTGATCT TTGTCCAACT ---------- ---------- ----------
P914199         369 gTGATGATCT CTGTCCAACT ---------- ---------- ----------
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alignment position  601....... 611....... 621....... 631....... 641.......
P914197         306 agcaggaatc tgtccggttc gcggctgctt cccaggcgcc cagaccagcg
P914198         411 ---------- ---------- ---------- ---------- ----------
P914199         389 ---------- ---------- ---------- ---------- ----------

alignment position  651....... 661....... 671....... 681....... 691.......
P914197         356 accagcaccg cgtaggcgct cggcacAGAC CGAGAACGGA ----------
P914198         411 ---------- ---------- ------AAAa acaggatgcc tcagagcgct
P914199         389 ---------- ---------- ------AAAC CAGGTGCGCG ----------
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alignment position  701....... 711....... 721....... 731....... 741.......
P914197         396 -GGCCCCACG CGGGGGCGCC Ctgcggcgag gcgggtcccg gccgcgcccg
P914198         435 gGGGACCACA AGGGGGTGCT CGAGA----- ---------- ----------
P914199         403 -GAAACCACA AGGGGGTGCC aGAGA----- ---------- ----------
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alignment position  751....... 761....... 771....... 781....... 791.......
P914197         445 gcggagccGG GGAACTACAA gTCCCATGGT GCATCGCGGC -G-CCAGCGC
P914198         460 --------GG CGAACCACTA -TCCCATGGT GCCTCGCGGC TGcCCACTAC
P914199         427 --------GG CGAACCACAA -TCCCATGGT ACCTCGCGGC TG-CCACTAC
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alignment position  801....... 811....... 821....... 831....... 841.......
P914197         493 GCAGACGCAG CCGCCCTCGg cgtcctctg- ---------- ---------T
P914198         501 GCAGGCGCAG CTGtcacCTT TCTGCGCAGG CGTAGAGGTC CCGCGTCCTT
P914199         467 GCAGGCGCAG CTGCCGTCTT TCTGCGCAGG CGTAGAGGTC CCGCGTCCTT
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alignment position  851....... 861....... 871....... 881....... 891.......
P914197         523 AGCGGGCgac ctaggccgcg ggacccggac ggaggtagag gccagggCAG
P914198         551 AGCGGGCC-- ---------- ---------- ---------- -------CAG
P914199         517 AGCaGGCC-- ---------- ---------- ---------- -------GAG
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alignment position  901....... 911....... 921....... 931....... 941.......
P914197         573 CGCGTCCGGG AGCGGAGtcc gcgcccgccg cc-------- ----------
P914198         562 CGGATCCGGA CGTGGAGCGA GTAGAAGGTC GGtggggaga GTTTGCTTAA
P914199         528 CCGACCCAGA CACAGAACGA GTGGAAGGTC CGcaggg--- GTTCGCTTAA
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alignment position 951....... 961....... 971....... 981....... 991.......
P914197        605 GCCATGCCGG ACagcTGGGA CAAGGATGTG TACCCTGAGC CCCCGCGCCG
P914198        612 GCCATGCCAG ATTCTTGGGA CAAGGATGTG TACCCGGAGC CCCCGAGCCG
P914199        575 ACCATGCCGG ACTCTTGGGA CAAGGATGTG TACCCGGAGC CCCCGCGCCG
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alignment position 1001...... 1011...... 1021...... 1031...... 1041......
P914197        655 CACGCcggtg cag------- ---------- -CCCAATCCC ATCGTCTACA
P914198        662 CACGCCTGCT CCCTCGCCGC AGACCTCGCT CCCTAACCCC ATCACCTACT
P914199        625 CACGCCTGCT CCCTCGCCGC AGACCTCGAT CCCTAACCCC ATCACCTACT
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alignment position 1051...... 1061...... 1071...... 1081...... 1091......
P914197        687 TGATGAAAGC GTTCGACCTC aTCGTGGACC GACCCGTGAC CCTCGTGAGA
P914198        712 TGACGAAGGC CTACGACCTC GTCGTGGACT GGCCCGTGAC CCTCGTGAGA
P914199        675 TGACGAAGGC CTACGACCTC GTCGTGGACT GGCCCGTGAC CCTCGTGAGA
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alignment position 1101...... 1111...... 1121...... 1131...... 1141......
P914197        737 GGTACgaagc cccagcccgg ggctccctcg ccggcctctg ggga--CCCC
P914198        762 GGTACAGGGT CTAGAATTTC GCCCGCTTAG TGGAGATCCC cccTACCCCG
P914199        725 GGTACAGGGT CTAGAATTGC TCCTGCTTAG TGGAGATCCC gg-TACCCCA
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alignment position 1151...... 1161...... 1171...... 1181...... 1191......
P914197        785 TGGATCCCAC ACCCtgcctg gatcctccaa tgcctccggg gtcccgtctg
P914198        812 CGGATCCCAC ATCCAGTTTC CGCCC----- ---------- ----------
P914199        774 CGGATCCCAC AGCCAGGTTC CGCCC----- ---------- ----------
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alignment position 1201...... 1211...... 1221...... 1231...... 1241......
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P914197        835 CCTGAGACCG CCCCCCGCTG CACCCCGggg acaa-CTCCC CACCCCCGGA
P914198        837 CCTGAAACCA CCACCCGCTG CATGCCGCTG TCCCGCACCC TGAATC----
P914199        799 CCTagaa--- -------CTG CATGCCGCTG TCCTGCACCC AGACTCCGGA
                   ********** ********** ********** ********** **********
                   ***               *** ********** ********** ******
                   ***               *** *******

alignment position 1251...... 1261...... 1271...... 1281...... 1291......
P914197        884 GACCtccgag ctccgtcgcc tccttggcct cccactg--- ----------
P914198        883 GTCTCAATCT CC-----CCC AGTGCATCTA AGATACCCTC TACCTTTTAT
P914199        839 GTCCAAATCT CCttaatCCC AGTGCATCTA GGACTCTTTC TACCTTATAT
                   ********** **     *** ********** ********** **********
                                     *** ********** ********** **********

alignment position 1301...... 1311...... 1321...... 1331...... 1341......
P914197        922 ---------- ---------- --CACCCCGG A--------- --CCTCACCT
P914198        928 CTGAGAcgcC CCGGTGCTGT CACTCCagat cacttcccac gcCCTCCCGT
P914199        889 CCGAGAaa-C CCGGAGCTGT CACCCCCAGG A--------- --CCTCCCAT
                   ******   * ********** ********** *            ********
                   ******                                        ********
                                                                 ********

alignment position 1351...... 1361...... 1371...... 1381...... 1391......
P914197        939 Cccaggatcc cttactctcc cCTGCACCCC GGGATGCCCC GCTTCTTCCC
P914198        978 CTACCCTG-- ---------- -CTGCACCGC AGGATAGTCC ACTTCTTTCC
P914199        927 CTACCCTG-- ---------- -CTGCACCGC GGGATGGTCC ACTTCTTCCC
                   ********               ********* ********** **********
                   ********               ********* ********** **********
                   ********               ********* ********** **********
                                          ********* ********** *****   **
                                          ********* ********** *****   **
                                          ********* ********** *****

alignment position 1401...... 1411...... 1421...... 1431...... 1441......
P914197        989 AGGACTcttc cct------- ---------- ---------- ----------
P914198       1015 GGGACTACCC TGTCTATAAT CCTTTCTGTC TTCAGCAgaa ccccaactaa
P914199        964 AGGACTAACC TGTCTATAAT TCTTTCTGCC TTCAGCAa-- ----------
                   ********** ********** ********** *******
                   ********** ********** ********** *******
                   ********** ********** ********** *******
                   ******
                   ******

alignment position 1451...... 1461...... 1471...... 1481
P914197       1002 ---------- ---------- ---------- ----
P914198       1065 cctttcgtcg accccggtcg ttcttttaag cggt
P914199       1002 ---------- ---------- ---------- ----
```

Pairwise similarities:

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

	P914198 (1098 bp)	**P914199 (1001 bp)**
P914197 (1001 bp)	0.204 32 %	0.221 31 %
P914198 (1098 bp)		1.000 72 %

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

Extract alignment region	
Positions in alignment	from: ☐ to: ☐
Output file	dialign.seq

Extract aligned sequences

For comments, questions or bug reports, please contact support@genomatix.de

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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 Jun 7 17:53:39 2005**

Solution parameters:

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

Aligned Sequences:

No.	Sequence Name	Sequence Description	Length
1	P961889	sym=P17.3|loc=Loc54539|taxid=9606|spec=Homo sapiens|chr=X|ctg=NT_079573|str=(-)|start=9853400|end=9854746|len=1347| tss=501,847| comm=neuronal protein 17.3; (AK000501/847/gold;NM_019056/501/silver;)	1347 bp
2	P961890	sym=Np15|loc=Loc104130|taxid=10090|spec=Mus musculus|chr=X|ctg=NT_039700|str=(-)|start=13827557|end=13828828|len=1272| tss=501,772| comm=nuclear protein 15.6; (AK028121/815/gold;NM_019435/544/silver;)	1272 bp
3	P961891	sym=na|loc=Loc299310|taxid=10116|spec=Rattus norvegicus|chr=X|ctg=NW_048034|str=(+)|start=486187|end=487187| len=1001|tss=501| comm=similar to neuronal protein 15.6; (XM_216785/541/bronze;)	1001 bp

Alignment (DiAlign format):

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

V$TALE V$AIRE V$CDEF V$PAX3 V$ECAT V$PCAT V$COMP V$PBXC V$GLIF V$TBPF V$GKLF V$LEFF
V$IRFF V$SNAP V$SP1F V$E2FF V$ZBPF V$EGRF V$CREB

```
alignment
position        1 . . . . . . . . .   1 1 . . . . . . . .   2 1 . . . . . . . .   3 1 . . . . . . . .   4 1 . . . . . . . .
P961889      1  g t  c  c  c  c  g  c  c  c   c  g  g  g  c  c  c  c  t  t   a  c  c  t  c  c  g  c  c  c   c  c  a  c  g  a  c  c  a  g   c  g  t  c  g  a  C G C T
P961890      1  - - - - - - - - - -   - - - - - - - - - -   - - - - - - - - - -   - - - - - - - - - -   - - - - - - - - - -
P961891      1  g - - - - - - - - -   - - - - - - - - - -   - - - - - - - - - -   - - - - - - - - - -   - - - - - - C G C T
```

```
                                                                      ****
                                                                      ****
                                                                      ****
alignment
position           51........ 61........ 71........ 81........ 91........
P961889         51 CACCTTCTCG GCCCGGGCTG TCAAGGAAGG GCTCCCAGAC ATCACCTCTG
P961890          1 CACCTTCTCG GCCCGGGCTG TCAAGGGAGG GCTCCCAGGC ATCACCTCCG
P961891          6 CACCTTCTCG GCCCGGGCTG TCAAGGGAGG GCTCCCAGGC ATCACCTCCG
                   ********** ********** ********** ********** **********
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                   ********** ********** ********** ********** **********
                   ********** ********** ********** ******** * **********
                   ********** ********** ****** *** ********
                   ********** ********** ****** *** ********
alignment
position           101....... 111....... 121....... 131....... 141.......
P961889        101 CCCGCCGCCA CCTCCTCCAa ctctcccagc tcagcc-GGA GCCGGAGCGC
P961890         51 CCCGCCACCA CCTCCTTCAG AACTGTTAGT tcaaatGGGA GCCAATGCAT
P961891         56 CCCGCCACTA CCTCCTTCAG AACTGTTAGT tcgac-GGGA GCCAATGCAT
                   ********** ********** **********       **** **********
                   ********** ********** **********       **** **********
                   ********** ********** **********       **** **********
                   ********** ********** **********       **** **********
                   ********** *********                    *** **********
                   ********** *********                    *** **********
                   ********** ******                       *** **********
                   ********** ******
alignment
position           151....... 161....... 171....... 181....... 191.......
P961889        150 GCAACAACCA AGTCCGAGAC TGGAGGC--- ----AGATCG GGGGGAGGGG
P961890        101 GCAACTACCA AGTCCAAGAC TGGgaGCAAA AAGGAGGAAA GGGGGAGGGG
P961891        105 GCAACTACCA AGTCCAAGAC TGGAGGCAAA AGGGAGGACA GGGGGAAGGG
                   ********** ********** ********** ********** **********
                   ********** ********** ********** ********** **********
                   ********** ********** ***  **        ****** **********
                   ********** ********** ***  **
                   ********** ********** ***
                   ********** ********** ***
                   ********** ********** ***
alignment
position           201....... 211....... 221....... 231....... 241.......
P961889        193 AGAAGCGCCA AgCGCGCTGC CCTCCCAGGG AAACTCACTG CCGCCTACTC
P961890        151 AGACGCGACC gACGCGTTGC CCTCCCAAGG AAACTCGGTG CCACCTCCTC
P961891        155 AGACGCGCCC AACGCGTTGC CCTCCCAAGG AAACTCAGTG CCGCCTCCTC
                   ********** ********** ********** ********** **********
                   **********  ********* ********** ********** **********
                   **********  ********* ********** ********** **********
                               ********* ********** ********** **********
                                ******** ********** ********** **********
                                ******** ********** ********** ****** ***
                                ******** ********** ********** ****** ***
                                                                      ***
                                                                      ***
alignment
position           251....... 261....... 271....... 281....... 291.......
P961889        243 CCAGCCGGCC ACAGTCACCA GCTCAAAATG GCGACGAcga GAAGGGAGTC
P961890        201 CtAGCCGGCC ACAGTCACCA ACACAAAATG GCGACGA--- GAAGAGAGCC
P961891        205 CCAGCCGGCC ACAGTCACCA ACACAAAATG GCGACGA--- GAAGAGAGCC
```

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

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

P961889  293 GGCGCTCCGA CCACCATCCA CCTACTAAGG aAGCGCGCTC TGGCCGGCCC
P961890  248 GGCGATCCGA CCACCATCCA CCTACTAAGG GAGCGCGCTC TGGCCGGCCT
P961891  252 GGCGCTCCGA CCACCATCCA CCTACTAAGG GAGCGCGCTC TGGCCGGCCT
             ********** ********** ********** ********** **********
             ********** ********** ********** ********** **********
             ********** ********** ********** ********** **********
             ********** ********** ********** ********** **********
             ********** ********** **********  ********* **********
             ********** ********** **********  ********* **********
             ********** ********** **********  ********* **********
             ********** ********** **********
             ********** ********** **********
             ********** ********** **********

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

P961889  343 CGGCGATTGG TCACCGcCCG CTAGGGGACA GCCCTGGCCT CCTCTGATTG
P961890  298 TGACGATTGG TTGCCGGTCA CCATtGGCTG GCCCTGGCAT TCTCTGATTG
P961891  302 TGACGATTGG TTGCCGGCCA CTATGGGCTG GCCCTGGCAT TCTCTGATTG
             ********** ********** ********** ********** **********
             ********** ********** ********** ********** **********
             ********** ********** **** ***** ********** **********
             ********** ********** **** ***** ********** **********
             ********** ****** *** **** ***** ********** **********
             ********** ******          ***** ********** **********
             ********** ******                ********** **********

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

P961889  393 GCAAGCgctg GCCACCTCCC CACACCCCTT GCGAACGctc ccctagtgga
P961890  348 GCAAGCATAT GCTACCTCCC CATTCCCTGT GAGAACGGCC CAGGAGTCCa
P961891  352 GCAAGCATAT GCTACCTCCC CATTCCCCGT GAGAATGGCC CAGGAGTCCt
             ********** ********** ********** ********** *********
             ********** ********** ********** ********** *********
             ********** ********** ********** ********** *********
             ********** ********** ********** *******
             ********** *****
             ******     *****
             ******

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

P961889  443 g-AAAAGGAG TAGCTATTAG Ccaattcggc agggcCC-GC TTTTTAGAAG
P961890  398 GAAAAAAGAG TAGCTATTGG CTACCCCTAA GAGG-CCcGC TCTTTAGAAG
P961891  402 GAAAAAAGAG TAGCTATTGG CTATCCCTAT GAGG-CC-GC TTTTTAGAAG
             ********** ********** ********** **** ** ** **********
             ********** ********** ********** **** ** ** **********
             ********** ********** ********** **** ** ** **********
               ******** ********** *               ** ** **********
                                                   ** ** **********
                                                   ** ** **********
                                                      ** **********
                                                      ** **********

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

P961889  491 CTTGATTTCC TTTGAAGATG AAAGACTAGC GGAAGCTCTG CCTCTTTCCC
```

```
P961890      447 CTTGCTGTCC TTTGAAGTTG AAAGACAACT AGAAGCTCCA CCTCTTTCCC
P961891      450 CTTGCTGTCC TTTGAAGTTG AAAGACAAgT AGAAGCTCCA CCTCTTTCCC
                 ********** ********** ********** ********** **********
                 ********** ********** ********** ********** **********
                 ********** ********** ******** * ********** **********
                 ********** ********** ******** * ********** **********
                 ********** ********** ********    ********* **********
                 ********** ********** ******
                 ********** ********** ******
                 ********** ******* ** ******

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

P961889      541 CAGTGGGCGa gggaactcgg ggcgattggc tgggaactgt atccacccaa
P961890      497 TACAGGGCca TCTAG----- ---------- ---------- ----------
P961891      500 TACAGGGCGg TCTAG----- ---------- ---------- ----------
                 *********  *****
                 ********   *****
                 ********   *****
                 ********   *****
                 ********

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

P961889      591 ATGTCACCGA TTTCTTCCTA TGCAGGAAAT GAGCAGACCc aTCAATAAGA
P961890      512 ATGTCACCGC TTTCTTCTTA CGAAGAAAAT GAACAGACCT CTCAAAAACA
P961891      515 ATGTCACCGC TTTCTTCTTA TGAAGAAAAT GAACAGACCT CTTAAAAACA
                 ********** ********** ********** ********** **********
                 ********** ********** ********** ********** **********
                 ********** ********** ********** *********
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                 ********** ********** ********** *********
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                 ********** ********** ********** *****
                 ********** ********** ********** *****

alignment
position             651.......  661.......  671.......  681.......  691.......

P961889      641 AATTTCTCag cctggccgaa aatggttggc cccacgaagc cacgacaact
P961890      562 ACTCTCTCCC AGACTAACAG AAAtgATAAC GTTGATTCGG TAGCGACACG
P961891      565 AATTTCTTCC AGCCTAACAG AAAcaATAAA GCTAATTCGA TTGCGACGCG
                 ********** ********** ***  ***** ********** **********
                 ********** ********** ***  ***** ********** **********

alignment
position             701.......  711.......  721.......  731.......  741.......

P961889      691 -----GGAGG CAAAgagggt tgcTCAACGC CCCGCCTCAT TGGAAAACCA
P961890      612 GCGTGGGAGG CAAAATAGAG ---TCCGCAC CTCGCCGAAC TCGTAAACAA
P961891      615 GCGTGGAAGG tAAAATAGAG ---TCCACAC CTCGCCACAC TCGAAAACAA
                 ********** **********    ******* ********** **********
                 **********  *********    ******* ********** **********
                             *********    ******* ********** **********
                                          ******* ********** **********

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

P961889      736 AATCAGatct GGGACCTATA TAGCGTGGCG GAGGCGGGGC GAtgattgTC
P961890      659 ACTTAGgCCG GGGATCTATT TAGCAAGGTA AGGGCGGAGC GACAAAAaTC
P961891      662 ACTTAaaCCC GGGATCTATT TAGCGAGGTA AGGGCGGAGT GACAAAAtTC
                 ****** *** ********** ********** ********** ******* **
                 ****   *** ********** ********** ********** ******* **
                 ****   *** ********** ********** ********** ******* **
                 ****       ********** ********** ********** **      **
                                                                     **

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

P961889      786 GCGCTCGCAC CCACTGCAGC TGCGCACAgt cgcatttctt t------CCC
P961890      709 GCGCTGGGAT CAACCGCAGC TGCGCACATT GTATTTCCgt CTCCCTCCCC
```

```
P961891     712 GCGCTGGGAT CAACCGCAGT TGCGCACTTC GTATTTCCgg CTCCCCACCC
                ********** ********** ********** ********   **********
                ********** ********** ********** ********   **********
                ********** ********** ********** ********
                ********** ********** ********
                ********** ********** *******

alignment
position        851....... 861....... 871....... 881....... 891.......
P961889     830 CGCCCCtga- -----GACCC TGCAGCACCA TCTGTCATGG CGGCTGGGCT
P961890     759 CCCCCCGCCC CCCAGGACTC CGCAGTACAA GCTGTCATGG CGGCCCGACT
P961891     762 CGCCCCCACC CCCTGGACTC CTCAGTACAA GCGGTCATGG CGGCCCGGCT
                ********** ********** ********** ********** **********
                ********** ********** ********** ********** **********
                                ***** ********** ********** **********
                                ***** ********** ********** **********
                                               * ********** **********

alignment
position        901....... 911....... 921....... 931....... 941.......
P961889     874 GTTtgGTTTG AGCGCTCGCC GTCTTTTGGC GGCAGCGGCG ACGCGAGGGC
P961890     809 GTTAAGCTTG TATGGTCGCT GCCTGTCAGC AGCGGGGGCG ATGAGAGGGC
P961891     812 GTTAAGCTTG TATGCTCGCC GCCTGTCAGT AGCGGCGGCG ATACGAGAGG
                ********** ********** ********** ********** **********
                ********** *********  ********** ********** **********
                ********** *********  ********** ********** **********
                ***  ***** *********                   **** **********
                ***                                    **** *  *******
                                                               *******

alignment
position        951....... 961....... 971....... 981....... 991.......
P961889     924 TCCCGGCCGC CCGCGTCCGC TGGGAATCTa gcttcTCCAG GACTGTGGTC
P961890     859 TCCCGGCTGC TCGCGTTCGC TGGGAGTCC- -----TCCAG GGCTGTAATC
P961891     862 TCCCGGCTGC CCGTGTTCGC TGGGAATCT- -----TCCAG GGCTGTAATC
                ********** ********** *********       ***** **********
                ********** ********** *********       ***** **********
                ********** ********** *********       ***** **********
                ********** ********** *********       ***** **********
                **********  ********* *********       ***** **********
                **********  ********* *****           ***** **********
                            ********* *****

alignment
position        1001...... 1011...... 1021...... 1031...... 1041......
P961889     974 GCCCCGTCCG CTGTGGCGGG AAAGCGGCCC CCAGAACCGA CCACACCGTG
P961890     903 GCCCCATCCG GTGTGGAGAA AAAGCGGCAA CGAGAACCGA CCATGCAGTG
P961891     906 GCCCCGTCCG GTGTGGAGAG AAAGCGGCAA AGAGAACCGA CCATGgtaTG
                ********** ********** ********** ********** **********
                ********** ********** ********** ********** **********
                ********** ********** ********** ********** *****   **
                ***** **** ********** ********** ********** *****   **
                ***** **** ********** ********** ********** *****   **
                ***** **** ******     *****                         **
                      **** ******     *****                         **
                                                                    **

alignment
position        1051...... 1061...... 1071...... 1081...... 1091......
P961889    1024 GCAAGAGGAC CCAGAACCCG AGGACGAAAA CTTGTATGAG AAGGTGAGAG
P961890     953 GCAGGAGGAC CCAGAACCCG AGGACGAAAA CGTCTACGCG AAGGTGAGAG
P961891     956 GCAGGAGGAC CCAGAACCCG AGGACGAAAA CCTCTACGCG AAGGTG----
                ********** ********** ********** ********** **********
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```

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                           ********** ********** *
alignment
position        1101...... 1111...... 1121...... 1131...... 1141......
P961889    1074 gcgggggggg gggggggggt agtggggacg gaaccccgaa ggggtcagtc
P961890    1003 ggagggg--- ---------- ---------- ---------- ----------
P961891    1002 ---------- ---------- ---------- ---------- ----------

alignment
position        1151...... 1161...... 1171...... 1181...... 1191......
P961889    1124 cgggatcGGC AGATGGGGCG CTGTAGAGGA CGTTCTtagg cagta-----
P961890    1010 -------GGA AAACGGGACG CTGTAGGGGC CAATCTggac cagggaaacc
P961891    1002 ---------- ---------- ---------- ---------- ----------
                       *** ********** ********** ******
alignment
position        1201...... 1211...... 1221...... 1231...... 1241......
P961889    1169 ---------- ---------- -------GAG GACTGCGCGG CCGGCGAAAG
P961890    1053 agtgtcaaag cggacattct ccggcccGAG ATTTGAGCAG TGGACAAAAT
P961891    1002 ---------- ---------- ---------- ---------- ----------
                                             *** ********** **********
alignment
position        1251...... 1261...... 1271...... 1281...... 1291......
P961889    1192 CCTAGAAGAC TtgggAATTT TGCCTACCTT GTGTTCCTCC TTTGTctctc
P961890    1103 CTTCGAATAT TcagaAATTT TGCCTAGCTT GTTTTTCTCT TTCGTtgcct
P961891    1002 ---------- ---------- ---------- ---------- ----------
                ********** *    ***** ********** ********** *****
alignment
position        1301...... 1311...... 1321...... 1331...... 1341......
P961889    1242 ggtatcttcg ttccagggcc agaggcagga ttggttttat TTTGCAGACA
P961890    1153 ta-------- ---------- ---------- ---------- TTTGCAGTCA
P961891    1002 ---------- ---------- ---------- ---------- ----------
                                                            **********
alignment
position        1351...... 1361...... 1371...... 1381...... 1391......
P961889    1292 GAAATCACAC ctcAAGTGGA CAGCGCTCAA AACACGTTAG AAGCAGTATA
P961890    1165 GAAATCACAC tgaAAGAGGG CAGCACCCAA AGCATGTTAG AAACTTTATA
P961891    1002 ---------- ---------- ---------- ---------- ----------
                **********    ******* ********** ********** **********
alignment
position        1401...... 1411...... 1421...... 1431...... 1441......
P961889    1342 GTacaa---- ---------- ---------- ---------- ----------
P961890    1215 ATtagggtaa tactaaactc taaggtaaca cgtgcataat gccaggctgt
P961891    1002 ---------- ---------- ---------- ---------- ----------
                **
alignment
position        1451....
P961889    1348 --------
P961890    1265 gctagaca
P961891    1002 --------
```

Pairwise similarities:

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

	P961890 (1272 bp)	**P961891 (1001 bp)**

P961889 **(1347 bp)**	0.488 59 %	0.481 67 %
P961890 **(1272 bp)**		1.000 89 %

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

Extract alignment region	
Positions in alignment	from: ☐ to: ☐
Output file	dialign.seq

Extract aligned sequences

For comments, questions or bug reports, please contact support@genomatix.de

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License Agreement

GEMS Launcher 4.1.1

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GEMS Launcher Task: *DiAlign TF*: Multiple alignment plus TF sites
working on C1-NDUFC1 (3 seq.)

[Alignment] [Pairwise similarities]

DiAlign professional TF Release 3.1 December 2004 **Tue Jun 7 19:15:08 2005**

Solution parameters:

Sequence file:	C1-NDUFC1 (3 seq.)
Type of sequences:	nucleotide sequences
Threshold T:	0.00
'*' signs below alignment denote:	diagonal similarity (max. similarity is represented by 10 '*' signs)
Alignment output:	complete alignment is shown # nucleic acids per line: 50
TF output:	common TF matches located in aligned regions (common to 3 (100.0 %) sequences)
Family matches:	yes
MatInspector library:	Matrix Family Library Version 5.0 (February 2005)
Selected groups (core/matrix sim):	• ALL user_defined.lib (0.75/Optimized) • ALL vertebrates.lib (0.75/Optimized)

Aligned Sequences:

No.	Sequence Name	Sequence Description	Length
1	P855801	P855801 sym=NDUFC1|loc=Loc4717|taxid=9606|spec=Homo sapiens|chr=4|ctg=NT_016354|str=(-)|start=64711588|end=64712588|len=1001|tss=501|comm=NADH dehydrogenase (ubiquinone) 1, subcomplex unknown, 1, 6kDa; (NM_002494/501/bronze;)	1001 bp
2	mNDUFC1	mNDUFC1 m6_dna range=chr3:51040462-51041402 5'pad=0 3'pad=0 revComp=TRUE strand=? repeatMasking=none	941 bp
3	rNDUFC1	rNDUFC1 n3_dna range=chr2:140251319-140252373 5'pad=0 3'pad=0 revComp=TRUE strand=? repeatMasking=none	1055 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$MOKF V$NRSF V$RORA V$EREF U$EREF V$LEFF

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alignment position 1.........  11.........  21.........  31.........  41.........
P855801    1 aaa------- ---------- ---------- ---------- ----------
mNDUFC1    1 caccccgaTG AATAACAGAA CCTACCTCAT AGGACTGAGA GGAATCaatg
rNDUFC1    1 ctccccggTG AATAACAGAA CCTATCTCAC AGGACTGAGA GGAATCtatg
                     ** ********** ********** ********** ******
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alignment position 51.........  61.........  71.........  81.........  91.........
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P855801          4 ---------- ---------- ---------- ---------- ------ATAT
mNDUFC1         51 tgattTTGAG TATAAGTGGA TTTTAGGAAC TGTTAAGAGC CTTTGCAAAT
rNDUFC1         51 tggtcTTGAG TATAAGTGGA TTTTAGGAAC TGTTAAGAGG CTTTGCAAAT
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alignment position 101....... 111....... 121....... 131....... 141.......
P855801          8 AATATGTCAC CTTGGATGAG TAGCTgtctt cttttaagctt ----------
mNDUFC1        101 ACAAAGTTCC CTTCGTCAAC AAGTTTATCT TTGa------ ----------
rNDUFC1        101 ACAAAGTTCC CTTAGTCGAC AAGTTTGTCT TTGggcacac ctcttttctt
                   ********** ********** ********** ***
                   ********** ********** ********** ***
                   ********** ********** ********** ***

alignment position 151....... 161....... 171....... 181....... 191.......
P855801         48 ---------- ---------- ---------- ---------- ----------
mNDUFC1        135 ---------- ---------- ---------- ---------- ----------
rNDUFC1        151 tttttttttt tttttttttg gttctttttt tcggagctgg ggaccgaacc

alignment position 201....... 211....... 221....... 231....... 241.......
P855801         48 ---------- ---------- ---------- ---------- ----------
mNDUFC1        135 ---------- ---------- ---------- ---------- ----------
rNDUFC1        201 cagggccttg cgcttcctag gtaagcgctc taccactgag ctaaatcccc

alignment position 251....... 261....... 271....... 281....... 291.......
P855801         48 ---------- --CATCTGTA AATTGAGGCT TATAACCACG GCATgatatg
mNDUFC1        135 ---------G CACATCTCTT AGTAGATGCT AATAATCACA GCACatccta
rNDUFC1        251 agcccctggG CACACCTCTT AATTGTTGCT AATAATCACA ----------
                            * ********** ********** ********** ****
                            * ********** ********** **********
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alignment position 301....... 311....... 321....... 331....... 341.......
P855801         86 tgctcgtttt gaagatgaaa taagacaatg aatgtaaacc atatgataca
mNDUFC1        176 cagtcactgt aatgactcgt gtaaagcaca cg-------- ----------
rNDUFC1        291 ---------- ---------- ---------- ---------- ----------

alignment position 351....... 361....... 371....... 381....... 391.......
P855801        136 ttaatgcacc gtgcctggac cacagaattc aatccaaatg ctagttatta
mNDUFC1        208 ---------- ---------- ---------- ---------- ----------
rNDUFC1        291 ---------- ---------- ---------- ---------- ----------

alignment position 401....... 411....... 421....... 431....... 441.......
P855801        186 ttcagcacga cacttttCTT TCTTCTGGCT CATGTAGGAA AATTTTAATA
mNDUFC1        208 ---------- ---------A GTTTTTGGCT GACAAACGAA CTCTGTAGTA
rNDUFC1        291 ---------- -------CTA GTTTTTGACT GACAGACGAA CACTGGAGTA
                                  *** ********** ********** **********
                                    * ********** ********** **********
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alignment position 451....... 461....... 471....... 481....... 491.......
P855801        236 AACCTcttga tgaatagccg tagagatggg gtgaaaaacc cccagaggac
mNDUFC1        239 AACCTGACcA GCA------- ---------- ---------- ----------
rNDUFC1        324 AACCTGACaA GCA------- ---------- ---------- ----------
                   ******** * ***
                   ******** * ***
                   ******** * ***

alignment position 501....... 511....... 521....... 531....... 541.......
P855801        286 agagaatagg taaactcttt tttcttttaa ttattttctt cctaatTCCA
mNDUFC1        252 ---------- ---------- ---------- ---------- ------CCCT
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rNDUFC1         337 ---------- ---------- ---------- ---------- ------TCCT
                                                          ****
                                                          ****
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alignment position  551....... 561....... 571....... 581....... 591.......
P855801         336 CTGTATAGAC AGAAGGCTg- ---------- ---------- ----------
mNDUFC1         256 GGAGATGGAC AAACTGCTTT CCCAGCCCca a--------- ----------
rNDUFC1         341 GGGGATAGAC AAACTGCTTT CCCAGCCCaa gccccagtag agccccagcc
                    ********** ********** ********
                    ********** ********** ********
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alignment position  601....... 611....... 621....... 631....... 641.......
P855801         355 ---------- ---------- ---------- ---------- ------AGGC
mNDUFC1         287 ---------- CCCTCTTCGT ACCCTTTGTT TTATTCACAG CCCACTAAGT
rNDUFC1         391 ccagccccag CCCTCTTTGC ACCTTGTGTT TTATGCACAG ACTCCTGAGT
                               ********** ********** ********** **********
                               ********** ********** ********** **********

alignment position  651....... 661....... 671....... 681....... 691.......
P855801         359 CGGGGTGCTA GAGAACCTTG CCGTGCTGGA Attcacgttg acgcccccac
mNDUFC1         327 CCGGGTTCTT GGGAACCTTG TACTGAATGA AggtaggagT CTGGCCCACC
rNDUFC1         441 ---------- --GAACCTTG TCCTGtagct acgac----T CTGGCCCACC
                    ********** ********** ********** *        * **********
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alignment position  701....... 711....... 721....... 731....... 741.......
P855801         409 ggagctctgc tgcagagccc tCGAGTCCCg cacTTCCGGC CGCCAGGTGG
mNDUFC1         377 TG-------- ---------- -CGAGTCCCA ---GTTCTGC TGCCAGGGGG
rNDUFC1         475 TG-------- ---------- -CGAGTCCCA ---TTTCTGC TGCCAGGGGG
                    **                     *********    ******* **********
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                    **                     *********    ******* **********

alignment position  751....... 761....... 771....... 781....... 791.......
P855801         459 CGCTGgttct ---------- ---------- ---------- --------GT
mNDUFC1         405 CGCTGCGCTC TGCGCCACCA ACCGGAGATG CGCGCGCAGG gaGAAGGCGG
rNDUFC1         503 CGCTGCGCTC TGCGGTACCT GCCGGAGATG CGCGCGCAGG agGAAGGCGG
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alignment position  801....... 811....... 821....... 831....... 841.......
P855801         471 TGCCAACTCG GAGAGACtga gctgggcca- ---------- -------CGC
mNDUFC1         455 TGCCAGCTCG GCCAAACGAG CAAccCGAGA AGAGGCGGAG CCTGCGGAAC
rNDUFC1         553 TGCCCGCTCG GCAAAACGAG CAAagCGAGA AGAGGAGGAG CCTGAAGCGC
                    ********** ********** ***  ***** ********** **********
                    ********** ********** ***  ***** ********** **********
                    ********** ********** ***                          ***
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alignment position  851....... 861....... 871....... 881....... 891.......
P855801         503 AAGATGGCGC CGTCCGCCTT GCTGCGTCCC CTTTCcCGGC TGCTGGCCCC
mNDUFC1         505 AAGATGGCGC CGTCCGTAGT GCTGCGCTCG TTTTCGCGGC TGCTGGCCCC
rNDUFC1         603 AACATGGCGC CGCCCGTAGT ACTGCGCTCG TTTTCGCGGC TGCTGGCCCC
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alignment position  901....... 911....... 921....... 931....... 941.......
P855801         553 CGCCAGGCTC CCGAGCGGCC GTGAGTatcc tcctcgTGCA G-GCCGACTC
mNDUFC1         555 CGCCCGGCTG CCGAGCTGCT GTGAGTGTCT T-----TTCA GaGCCCATTC
rNDUFC1         653 CGCCAGGCTG CCGAGCTGCT GTGAGTGTCT T-----TTCA G-GCCCATTC
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                    ********** ********** ********** *     **** *
                    ********** ********** ********** *     **** *
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                    ***  ***** ********** *******
alignment position  951....... 961....... 971....... 981....... 991.......
P855801         602 GACCCTCAGA TTACCCCTCc taaggcggac ccagcc---- ---CACGGGT
mNDUFC1         600 GGCCCTCAGC CTAGCCCTCA TCCAACACGA GCCACCCTGG AATCTCCGGA
rNDUFC1         697 GGCCTTTAGC CTAt-CCTCA CCCAGCATGA GCCACACTGG AATCTCTGTA
                    ********** ********** ********** ********** **********
                    ********** ***  ***** ********** ********** **********
                                    ****                           *******
alignment position  1001...... 1011...... 1021...... 1031...... 1041......
P855801         645 GCAGGAGGCG GCAGCGGCCC GGGttCGTCC TGCAGTGACC TTCGCCGGCa
mNDUFC1         650 GGAGGAGGAG GTCGCGGTCC AGGC-CGACC TGCAGTGACC TTCACTGGCC
rNDUFC1         746 GTAGGAGGAG GTCGCGGTCC AGGC-CGTCC TGCAGTGACC TTCACCGtCC
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                        ****** ********** **** ***** ********** *****   *
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alignment position  1051...... 1061...... 1071...... 1081...... 1091......
P855801         695 gacgacccaa ggcccagccc acgcctgtcc cctacGCAGG GCTCTCTGCT
mNDUFC1         699 GCGA------ ---------- ---------- -----GCCGG GTTCTCCACT
rNDUFC1         795 GCGA------ ---------- ---------- -----GCCGG GTTCTCCACT
                    ****                                  ***** **********
                    ****                                  ***** **********
                    ****                                  ***** **********
                    ****                                  ***** **********
alignment position  1101...... 1111...... 1121...... 1131...... 1141......
P855801         745 CCCCATCACC CGCCtctagc acttatccaa gttcaacctg accACTCTTG
mNDUFC1         718 CATCATTAGC CGTCAG---- CTTTCCTCCA GGCTA----- ---AACCCTG
rNDUFC1         814 CCTCATCAGC CGTCAGtcag CTTTCCTCCA AACTA----- ---ACCCCTG
                    ********** ******     ********** *****         *******
                    ********** ******     ********** *****         *******
                    ********** ******     ********** *****         *******
                    ********** ******                                 ****
alignment position  1151...... 1161...... 1171...... 1181...... 1191......
P855801         795 GCCTTTGTAA ATGGACTTTG GGTCCTTGcc ttccccacct ctgtacgtta
mNDUFC1         756 ACCTCTGCGA ATGGATTTTG AGTCTTTTtG TCCCAGGCTT TTCAATGTCT
rNDUFC1         856 ACCTCTACGA ATGAATTTTG GGTCTTTT-G TCCCAGGCTC TTAATTGCCT
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                    ********** ********
alignment position  1201...... 1211...... 1221...... 1231...... 1241......
P855801         845 ggtcccgt-- AAACCGGGAG AggagacACC CTCCCCGGGG CGCCCCTTAC
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mNDUFC1             806 GGGAG----- ---------- -------ACC CTTCCGGGGC TGCCTCCCAA
rNDUFC1             905 CGGAGacaac AAACAGGGAG At-------C CTTCCGGGGC TGCCTCCCAA
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                                                       * ********** **********

alignment position      1251...... 1261...... 1271...... 1281...... 1291......
P855801             893 ATGACCACTC CCGAGTCgTC TGAGGGTCCG CAAGCCCTTA AACGAGGCTT
mNDUFC1             834 CCTCCCACTC CAGAGCC-TA TGAGGGCCGA CGAGGCTTTA ACCCAAGCTT
rNDUFC1             948 CCTCCCACTC TAGAGCC-Tt TGAGGGCCGA CGAGACTTTA ACCTAAGCTT
                        ********** ******* ** ********** ********** **********
                        ********** ******* *  ********** ********** **********
                        ********** ******* *  ********** ********** **********
                        ********** ******* *  ********** ********** **********
                        ********** *****   *  ********** ********** **********

alignment position      1301...... 1311...... 1321...... 1331...... 1341......
P855801             943 TGAAAGCctc ggacaggaca ggtgcgtcct gtctaactcg ccagtggccc
mNDUFC1             883 TGAAGGCGCC ctgagtaCCA AGGACGACCT TCTGTCTCTG CTGGTGTCCC
rNDUFC1             997 TGAAGACGCC atgagccCCA AGGACGACCT TCTGTCTCTG CTGGTGTCCC
                        **********        *** ********** ********** **********
                        **********        *** ********** ********** **********
                        **********        *** ********** ********** **********
                        **********        *** ********** ********** **********
                        *****             *** ********** ********** **********

alignment position      1351......
P855801             993 tgggcgagg
mNDUFC1             933 CGAACaaat
rNDUFC1            1047 CGAACgaat
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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.

	mNDUFC1 (941 bp)	**rNDUFC1 (1055 bp)**
P855801 (1001 bp)	0.151 34 %	0.140 32 %
mNDUFC1 (941 bp)		1.000 79 %

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

Extract alignment region	
Positions in alignment	from: to:
Output file	dialign.seq

Extract aligned sequences

For comments, questions or bug reports, please contact support@genomatix.de

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GEMS Launcher 4.1.1

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

[Alignment] [Pairwise_similarities]

DiAlign professional TF Release 3.1 December 2004 **Tue Jun 7 19:27:17 2005**

Solution parameters:

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

Aligned Sequences:

No.	Sequence Name	Sequence Description	Length
1	P914220	sym=NDUFC2|loc=Loc4718|taxid=9606|spec=Homo sapiens|chr=11|ctg=NT_033927|str=(-)|start=8013089|end=8014180|len=1092| tss=501,526,545,592| comm=NADH dehydrogenase (ubiquinone) 1, subcomplex unknown, 2, 14.5kDa; (AK098173/545/gold;AK023013/526/gold;AK022785/592/gold; NM_004549/501/silver;)	1092 bp
2	P914221	sym=Ndufc2|loc=Loc68197|taxid=10090|spec=Mus musculus|chr=7|ctg=NT_039433|str=(+)|start=15232116|end=15233139|len=1024| tss=501,516,520,524| comm=NADH dehydrogenase (ubiquinone) 1, subcomplex unknown, 2; (AK002373/536/gold;AK008889/536/gold;AK019002/517/gold; AK003380/540/gold;NM_024220/532/bronze;)	1024 bp
3	P914222	sym=na|loc=Loc293130|taxid=10116|spec=Rattus norvegicus|chr=1|ctg=NW_047561|str=(+)|start=13521471|end=13522471| len=1001|tss=501| comm=similar to RIKEN cDNA 1810004I06; (XM_214989/545/bronze;)	1001 bp

Alignment (DiAlign format):

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

V$TBPF V$ETSF V$EGRF V$INSM V$SP1F V$PBXC

```
alignment position 1.........  11........  21........  31........  41........
P914220          1 gtgaaacatt  ttagggtgct  gcctccgaat  ctgaatttca  acaatagact
P914221          1 agggT-----  ----------  ----------  ----------  ----------
P914222          1 t---T-----  ----------  ----------  ----------  ----------
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alignment position 51........ 61........ 71........ 81........ 91........
P914220         51 aAAACGATCC AGTCCTGGGC TTCTCTAAAT tcTTTTGTTG CTGGCCAGAC
P914221          6 -AAATGATTC GCTCCTGACC TCCgaatacc c----TGGTG CTGACCTTAC
P914222          3 -AAAGGATCT GCTCCTGGCC TTCTCTGAAT a-TTCTGCTA CTGACCTTCC
                    ********* ********** **********   ******** **********
                                                      ******** **********
                                                           ***** **********
                                                               **********
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alignment position 101....... 111....... 121....... 131....... 141.......
P914220        101 CTTAATTTTA GGCTTTGGAG G--------- --GAGTGTCT ATGCGAATGA
P914221         51 CTTCATTTTA GGCTTTGGGG GTGGGGga-- -----AGTAA CTGCAAACGA
P914222         51 CTTAATTTTA GGCATTGGGG GTGGGGcgtg aaGGGAGTAA CTGCAAATGA
                   ********** ********** ******       ******** **********
                   ********** ********** ******          ***** **********
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alignment position 151....... 161....... 171....... 181....... 191.......
P914220        140 ACGACTGAAA ACTCAGAAAa cgaaaaCTAG CTTTTATGGA ATTTCAATTA
P914221         94 ACTGCTGGAA CCCCAGAAAG ------CTTG CTTTTATAGG CTTTAGATAA
P914222        101 ACTGTCGGAA CCCCAGAAAG ------CTAG CTTTTATGCG TTTTCAACAA
                   ********** **********       **** ********** **********
                   ********** **********       **** *                  **
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alignment position 201....... 211....... 221....... 231....... 241.......
P914220        190 ATTacgttta tcaaAACTAC GCATCATGCC CATTTGTGGG TATTGGATGa
P914221        138 ATG------- ----AACTAG CCATTATGAC CACTTGTAGA TGTTGa-TTT
P914222        145 ATG------- ----AACTAC CTATCACGAC CACCTGTAGG TGTTGGGTTT
                   ***            ****** ********** ********** **********
                   ***            ****** ********** ********** *****  ***
                   **             ****** ********** *********         ***

alignment position 251....... 261....... 271....... 281....... 291.......
P914220        240 aaagata--- ----AATCTT TCCAGAA--- ---------- -GGGGCAGGG
P914221        176 TTGGATGCTA AGATAATGTT TTCTGAAGAG CCATaggcct gGGGGCAAGT
P914222        184 TTGGATGCTA AAATAATCTT TTCTGAACAG TCATgaggct -GGGGCAAGT
                   ********** ********** ********** ****        *********
                   ********** ********** ********** ****        *********
                   ********** ********** ********** ****

alignment position 301....... 311....... 321....... 331....... 341.......
P914220        269 GAGGGAGAGG CAATTCTGGT TGGGGAagtt gggagaaaag a---------
P914221        226 AAGTGAGAGA CAATTTCGAT TGTGGTAACT GGACTACATA CATACATACA
P914222        233 GAGTGAGAa- -AATTTCGTA TGCGACAACT GAACTAAATA AACAAATAAA
                   ********** ********** ********** ********** **********
                   ********    ********* ******

alignment position 351....... 361....... 371....... 381....... 391.......
P914220        310 ---------- ---------A AATCAGTATC TCCTAGTCTT CGCCCAGTTT
P914221        276 Tacatacata catacatacA TACCAATGTT TCCTAGCCTT TGCCCACTGT
P914222        281 Taaatag--- ---------- ---CAACGTT TCCTAGTCTT TGCCCACTGT
                   *                   * ********** ********** **********
                                            ******* ********** **********
                                            ******* ********** **********
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alignment position 401....... 411....... 421....... 431....... 441.......
P914220        341 GGCTCGTTTG GGGTACTCCT cgaccccgcg t-TACCAGGC CCgtgaatCC
P914221        326 GGGTTATTTA TTataacccc cccccacaca cacacacaca ca------CA
P914222        315 GGGTTATTTA TTTTACCCCT ggactggctt agTACCTGGC CCccagcacc
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                   ********** **********            ******** **      **
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alignment position 451....... 461....... 471....... 481....... 491.......
P914220        390 CACTCCCACC AGAGAATTAG CGCGGGCgga cgagcaaagt gaa--ACTTA
P914221        370 CACACACACT ACAATGTCAG CGCAAGCCTT CACGCGTTGT GGGCCACTTA
P914222        365 ctcat----T ACAACATCAG CCCAATCCAG CAGGCGTTGT CGGCCACTTA
                   ********** ********** ********** ********** **********
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                                                                    ****
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alignment position 501....... 511....... 521....... 531....... 541.......
P914220        438 GTAGCCCGGA ACTTCGCGTG CCGGGTTCCC GCAGcaaca- CGTACCGGGA
P914221        420 GAAGCCCGGA ACCTCGCGTG CAGAGGTTGC TAAGGCTGAG CGCACAGGGA
P914222        411 ATATCCCGGA ACCTTGCATG CAGAGGTTCC TAAGGCTGCG CGCgCAGGGA
                   ********** ********** ********** ********** **********
                   ********** ********** ********** ********** **********
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                       ****** ********** *                           ****
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alignment position 551....... 561....... 571....... 581....... 591.......
P914220        487 AGCGTTTGGG CGCTGCACCG CGCTGCGCCG TGCCCGTGAG TCCGGCGCGC
P914221        470 AGCTTTTGGG TGCTGCACCG CCGTACGCAA TGCCCTTCAG CCTAGAGCGC
P914222        461 AGCTTTTGGG TGCTGCACCG CCCTACGCtt TGCCCTTCAG CCCGGAGCTC
                   ********** ********** ********** ********** **********
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                   ********** ********** ********
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                   ********** ********** *

alignment position 601....... 611....... 621....... 631....... 641.......
P914220        537 AGAGGAGGAG Gagaaagctg accgctTAGG CCGGGGTAGT GGTCGTCGTG
P914221        520 GGAGGAGGAC GGTAGC---- ------TcGG TCACGGCGTT TGGAGTCGTT
P914222        511 GGAAGAGGAG GGTAGC---- ------TAGG TCGCGGGGTT TGTAGTCGTG
                   ********** ******            **** ********** **********
                   ********** ******            **** ********** **********
                   ********** *                 * ** ********** **********

alignment position 651....... 661....... 671....... 681....... 691.......
P914220        587 GTTTTCCTTG TAGTTCGTGg tctGAGACCA GGCCTCAAGT GGAAACGGCG
P914221        560 GTTTTTCCTA TAGTTGGAGT C--GAGGTCA AACCTCTCGT GGAACCTGCC
P914222        551 GTTTTTCTTA TAGTTGGAGT C--GAGGTCA GACCTCACGT GGAACCCGCA
                   ********** ********** *  ******* ********** **********
                   ********** ********** *  ******* ********** **********
                   *******  ** ********** *  ******* ********** *********
                           ** *****        ******* ********** *********

alignment position 701....... 711....... 721....... 731....... 741.......
P914220        637 TCACCATGAT ---CGCACGG CGGAACCCAG AACCCTTACG GTTTCTGCCG
P914221        608 TCAAGATGAT GAACGGCCGG CCGGGCCATG AGCCCTTAAA ATTCTTGCCG
P914222        599 TCAATATGAT GAACGGCCGG CCGGGCCATG AGCCCTTAAG ATTCTTGCCG
                   ********** ********** ********** ********** **********
                   ********** ********** ********** *********  **********
                   ********** ********** ********** *********  **********
                   ********** ********** ********** *********       *****
                   **********                                       *****
                                                                    *****

alignment position 751....... 761....... 771....... 781....... 791.......
P914220        684 GATGAGGCCC GGAGCCTGCC CCCGCCCAAG CTGACCGACC CGCGGCTCCT
P914221        658 GACGAGGCCC GGAGCCTGCC CCCGCCCAAG CTGAACGACC CGCGGCTTGT
P914222        649 GATGAGGCCC GGAGACTGCC CCCGCCCAAG CTGAACGACC CGCGGCTTGT
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                          *** ********** ********** ********** **********
                          *** ********** ********** **** ***** *******  *
                          *** ********** ********** **** ***** *******  *
                                           ******** **** ***** *******

alignment position 801....... 811....... 821....... 831....... 841.......
P914220        734 CTACATCGGC TTCTTGGGCT ACTGCTCCGG CCTGATTGAT AACCTAATCC
P914221        708 CTACATGGGC TTGTTGGGCT ACTGCACGGG CCTGATGGAC AACATGcTGC
P914222        699 CTACATCGGC TTCCTGGGCT ACTGCACGGG CCTGATGGAC AACATGATGC
                   ********** ********** ********** ********** **********
                   ********** ********** ********** ********** ****** ***
                   ********** ********** ********** ********** ****** ***
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                   ********** ********** ********** *********
                   ********** **  ****** *****   ** *********
                   ********** **  ****** *****
                   ********** **  ****** *****
                   ********** **

alignment position 851....... 861....... 871....... 881....... 891.......
P914220        784 GGCGGAGGCC GATCGCGACG GCTGGTGAGT GCTGCGCGGC CGggatcggc
P914221        758 GGATGCGACC GGTGATGAGA GCAGGTGAGG GCTGCGggcg atcccgct-C
P914222        749 GAATGAGACC TGTGATGAAA GCAGGTGAGG GCTGCGAGGC CGtcctaccC
                   ********** ********** ********** ********** **       *
                   ********** ********** ********** ******              *
                   ********** ********** ********** ******
                   **********            ********** ******

alignment position 901....... 911....... 921....... 931....... 941.......
P914220        834 tgggaggaga aggGGTCGTA GGGCTGCAGA CTGGCCCGgc cgtaggcccc
P914221        807 ---------- ---GGACGAG GAGCTGCAGG GTTGCCCGCT GAGGTCAt--
P914222        799 ---------- ---GGAGGAG GAGCTACAGG GTTGTCTACT AAGGTCAgcc
                                 ******* ********** ********** *******
                                 ******* ********** ********** *******

alignment position 951....... 961....... 971....... 981....... 991.......
P914220        884 cctgaggtgC TCTGCTTTTC CGTGCCTTTT TGCCTAGCTG GCCCCATCTC
P914221        842 ---------C TGTGCTCTAC GAGGCCTTCC TGCCTAGCTG GGGGCGCCTG
P914222        836 tcccggatcc g-TGCTTTTC Ccgg------ -GCCTAGCTG GGAGCGCCTG
                            * ********** ********** ********** **********
                                                     ********* **********
                                                     ********* **********
                                                     ********* *

alignment position 1001...... 1011...... 1021...... 1031...... 1041......
P914220        934 GCCTTTCCGG GGAGTCCGCG CCCCATTAGC TCTTTAGaat caagcagagc
P914221        883 GCTCTCCCAG GGCGTGCATC CCCTCTCGGG TTCTCAGCGC caagagtAGC
P914222        878 GCTTTCCCAG GTCGTGCACC CCGTCTAGAG TTTTCAGCGC g------AGC
                   ********** ********** ********** **********        ***
                   ********** ********                                ***
                   ********** ********

alignment position 1051...... 1061...... 1071...... 1081...... 1091......
P914220        984 cagagtgtca tttggcacTT GAAGAAACTG AGGTGCAGTG AAGCAGGAAC
P914221        933 CACA------ --------TT GAAGAAAACC AAGTGCAGTG CAATGGGGAC
P914222        922 CACA------ --------TT AAAGAAACCC AAGTGCGCCG CAACTGGGAA
                   ****               ** ********** ********** **********
                   ****               ** ********** ******   * **********

alignment position 1101...... 1111...... 1121...... 1131...... 1141......
P914220       1034 Tg-------- --------AG TCTGTGAAGG ACCCGAAAct a-CTCTCCTC
P914221        969 TTCTAAACCC CACGGTtaAG TCTGCGAAGG ACTCAAGAAG GGCTCCTCAC
P914222        958 TTCTAAACCT CCCAGTt-AG TCCGTAAAGG ACTCAAGAGG GGCTC-----
```

```
                        **** **** ** **** **    ** ********** **** **** ** **********
                                                ** ********** **
alignment position 1151......  1161.......  1171..
P914220       1067 AGTTCGtgtt  gtgctgtgtg  cgcaaa
P914221       1019 AGTTCG----  ----------  ------
P914222       1002 ----------  ----------  ------
                   **** **
```

Pairwise similarities:

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

	P914221 (1024 bp)	**P914222 (1001 bp)**
P914220 (1092 bp)	0.340 51 %	0.354 53 %
P914221 (1024 bp)		1.000 74 %

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

Extract alignment region	
Positions in alignment	from: ☐ to: ☐
Output file	dialign.seq

Extract aligned sequences

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

[Alignment] [Pairwise similarities]

DiAlign professional TF Release 3.1 December 2004 **Tue Jun 7 19:41:50 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)
Selected groups (core/matrix sim):	• ALL user_defined.lib (0.75/Optimized) • ALL vertebrates.lib (0.75/Optimized)

Aligned Sequences:

No.	Sequence Name	Sequence Description	Length
1	P922028	sym=NDUFS1|loc=Loc4719|taxid=9606|spec=Homo sapiens|chr=2|ctg=NT_005403|str=(-)|start=57233028|end=57234103|len=1076| tss=501,576| comm=NADH dehydrogenase (ubiquinone) Fe-S protein 1, 75kDa (NADH-coenzyme Q reductase);(AK098395/637/gold;NM_005006/562/bronze;)	1076 bp
2	P922029	sym=Ndufs1|loc=Loc227197|taxid=10090|spec=Mus musculus|chr=1|ctg=NT_039170|str=(-)|start=40865305|end=40866347| len=1043|tss=501,525,543|comm=NADH dehydrogenase (ubiquinone) Fe-S protein 1;(AK078590/619/gold;AK036926/601/gold;NM_145518/577/bronze;)	1043 bp
3	P922030	sym=nalloc=Loc301458|taxid=10116|spec=Rattus norvegicus|chr=9|ctg=NW_047816|str=(-)|start=5260820|end=5261820| len=1001|tss=501| comm=similar to RIKEN cDNA 9930026A05; (XM_217417/501/silver;)	1001 bp

Alignment (DiAlign format):

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

V$MOKF V$ETSF V$TBPF V$SRFF V$PERO V$HNF4 V$COUP V$EREF U$EREF V$GKLF V$RORA V$BRNF
V$HNF1 V$LHXF V$RBIT V$HOMF V$HOXF V$SP1F V$DEAF V$NFKB V$SORY V$YY1F V$HNF6 V$SF1F
V$EGRF

```
alignment         1.........  11.........  21.........  31.........  41.........
position
P922028        1  ----------  ----------  ----------  ----------  ----------
```

```
P922029        1 cgaagg---- ---------- ---------- ---------- ----------
P922030        1 cccctcaatg tagctcttgt ccgccaggta atcgttgagc acctggaggc

alignment
position         51........ 61........ 71........ 81........ 91........
P922028        1 ---------- ---------- ---------- ---------- -------GAG
P922029        7 ---------- ---------- ---------- ---------C TGGAACGGGG
P922030       51 cggcgggggt tttcaggtct ccgaaaccca tggcgtcgaC TGTAACCGGG
                                                           * **********

alignment
position         101....... 111....... 121....... 131....... 141.......
P922028        4 AGCTGGGGAG CAGCAGAAAG AGAGCGCGCA AATTGTGGGC GCCCCACGCT
P922029       18 AGCTGTGCAA AAGCGGAGGA CGAGAGCGCC GGGAGGCCGC GGCCAGCGCT
P922030      101 AGCGGAGGAA AAG------- ----AGCGCT AGAAGCCCGC GGCCAGCGCT
                 ********** ********** ********** ********** **********
                                           ****** ********** **********
                                           ****** ********** **********

alignment
position         151....... 161....... 171....... 181....... 191.......
P922028       54 GAAGagagGA AAAAGGACCC GAAGAGACCG GAAAAtTCCT TATATAGAGA
P922029       68 GAGGGA--AA AAAAGGACCC AGAGCGTCCG GAAAACTCCT TATATAGAGA
P922030      140 GAGGGA--GA AAAAGGGCCG GGACCGGCCG GAAAAGTCCT TATATAGAGA
                 ******  ** ********** ********** ********** **********
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                 ******  ** *******           *** ********** **********
                          * *******           *** ********** **********
                                              *** ***** **** **********
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                                                        **** **********
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                                                        **** **********

alignment
position         201....... 211....... 221....... 231....... 241.......
P922028      104 CGGAGGCGTT TCCCTCCACC GCGCCGgacc gaAGGTTAAA GGTCAAAGTA
P922029      116 CGGAGGCGTT TCCCTCCGCC GCCCCGGCTA G-AGGTTAAA GGTCAAGGTC
P922030      188 CGGAGGCGTT TCCCTCCACT GCACCGGCTA G-AGGTTAAA GGTCAAAGTA
                 ********** ********** ********** * ******** **********
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                 ********** ********** ********** * ******** **********
                 ********** ********** ******       ******** **********
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alignment
position         251....... 261....... 271....... 281....... 291.......
P922028      154 CTTTTGCATT CCCACTTCTC CACGTAcgaa ttgggggccc TGAATTAAAT
P922029      165 CGTTCCTAGT CTCGGTCCTC CGCGTACCAC TGCGACTTG- GTAACTAAAG
P922030      237 CGTTACTAGT CTCGTTCCTT CACGTAAAAC TGCGTCTTG- TGAATTAGAC
                 ********** ********** ********** *********  **********
                 ********** **** ***** *                     **********
                 ********** ****
                 ********** ****
                 *

alignment
position         301....... 311....... 321....... 331....... 341.......
P922028      204 GGCCCACAAA TTGTCCATGG ACCTTTCGTT GCGTTTGGAA GTAAATTAAT
P922029      214 GGCCCACAGG TCGTCCGCCG GCCTTCCCTT GTCTTTGGAA GAAAATTAAT
P922030      286 GACCCACAGG TCGTCCGCGG GCTTTTCCTT GTGTTTGGAA GGAAATTAAT
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              * ******** ********** ********** ********** **********
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                ******** ******      ********* ********** **********
                                     ********* ********** * ********
                                       ******* ********** * ********
                                       ******* ********** *

alignment     351....... 361....... 371....... 381....... 391.......
position
P922028   254 AAAATAGGCA TgtcTTAAGT TCGTAC-CTC CACGGCTCCC GAAGATGACG
P922029   264 AAAGGAGGCA TTT-TAAAAT GCCTtcgCTC CAAGGACTCC GAAACGAAGG
P922030   336 AAAAGATGCA TTT-TAAAAC GCCTAC-CTC CAAGGATTCT AAAACTAAAG
              ********** *** ****** ****** *** ********** **********
              ********** *** ****** ****   *** ********** **********
              ********** *
              ********** *
              ********** *
              ********** *

alignment     401....... 411....... 421....... 431....... 441.......
position
P922028   303 GGAACcagCC CTAGAAGCGC CGGAGATGAC CGAAGACGCC CGGCCTCGAG
P922029   313 GAAACGC-CC tcTGAGGAGC CGGAGTTGAA CGAAAGCGCT CGGACGCAAG
P922030   384 GAAACGC-CC CTTGAGGAGC CGGAGTTGAA CGAAAGCATT CGGCCTCAAG
              ******* ** ********** ********** ********** **********
              ******* **   ******** ********** ********** **********
                      **   ******** ********** *******          ****
                            ******* ********** *******          ****
                                                                ****
                                                                *

alignment     451....... 461....... 471....... 481....... 491.......
position
P922028   353 GCtggGGCCA CTTCCGGCGG AACTGCGGGT CCAAGTTGTC ct--------
P922029   362 GCCTCGGCTA CTTCCGGCGG AACTGCAGGT CCAAGTCGTC TTCTCCGCTT
P922030   433 GCCTCGGCTA CTTCCGGCGG AACTGCAGGT CCAAGTTGTC TTCTCCGCTT
              ********** ********** ********** ********** **********
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alignment     501....... 511....... 521....... 531....... 541.......
position
P922028   395 --TCCCGCCT CCgggctggg ccgacctcag ctccgccctc tggtcgGCTG
P922029   412 CCTCCCGGgc tc-------- ---------- ---------- ------GCTC
P922030   483 TCTCCCGGCT CCctctcgt- ---------- ---------- ------GCTG
              ********** **                                   ****
              ********                                        ****

alignment     551....... 561....... 571....... 581....... 591.......
position
P922028   443 ACGGAAATTG CCGAcaaac- ---------- ----TT---G TCGAATgcaa
P922029   428 TCGGAAATTG CCGAACAGGT CCGAAGACGG GgaaaaacaG TCGAATCTGT
P922030   506 ACGGAAATTG CCGAACAGGT CCAAAGAGGG GagaTT---G TCGAATCTGG
              ********** ********** ********** *   **   * **********
              ********** ********** ********** *
               ********* ****
               ********* ****

alignment     601....... 611....... 621....... 631....... 641.......
position
P922028   475 ggaTTCTAGT CCCTCCGGGC TTTCCGTTCT CCAGGcccGG CTGACAGAGT
P922029   478 GT-TTCTAGT CCCTCCTGGC TTTCCGTCCT CCAGGTCGGG CTGACAGAGG
P922030   553 CT-TTGTTGT CCCTCCTGGC TTTCCGTCCG CCAGGTCAGG CTGACGGAGT
```

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                  ** ******* ********** ********** ********** **********
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                     ******* ********** ********** ********** **********
                     ******* ********** ********** *****      **********
                          ** ********** ********** *****   ** **********
                          ** ********** ********** *****   ** ********
                          ** ********** ********** *****   ** ********
                                                           ** ********

alignment
position          651....... 661....... 671....... 681....... 691.......
P922028       525 TAGCCGAGGC CGCCATATTG AATAAGCGac ccggcctcct agGGGGTCGT
P922029       527 TTGCCGTGGC CGCCATATTG ACTTAGCGGC caGGGTTTTG A-GGGGTCAG
P922030       602 TAGCCGTGGC CGCCATATTG ACTTAGCGGC t-GGGTTTTG A-GGGGTCAG
                  ********** ********** **********   ******** * ********
                  ********** ********** **********   ******** * ********
                  ********** ********** **********   ******** * ********
                  ********** ********** ********
                  ********** ********** ********
                    ******** ********** ********
                    ******** ********** ********
                    ******** ********** ********

alignment
position          701....... 711....... 721....... 731....... 741.......
P922028       575 CGTGGTCCAG ACAGTTTAGC AGAACAGCCT ccgcGGCTCC GGGGAGAAGG
P922029       576 GGAGACCCGG ACAGGTCCGC GGAACtACTC GGTGGGCTCC GGAGGAAAGG
P922030       650 GGGGATCCGG ACAAATCAGC GGGACAACTT GGTGAGCTCT AGAGGAAAGG
                  ********** ********** ********** ********** **********
                  ********** ********** **    **** ********** **********
                  ********** ********** **    **** ********** **********
                                                                    ****

alignment
position          751....... 761....... 771....... 781....... 791.......
P922028       625 TGAGGTCTTG TATGGATGGG AAGGGTGAGG TGCGTCGGCC AGAGGCTTAT
P922029       626 TGAGGACGCG TTGAAGTGGG CAAGTTGAAG CGCTTCGAGT GGTGTTTTCT
P922030       700 TGAGGACGCG TTTAAGAGAG AAAGTTGAAG TGCTTCGAGT GGTGTTTTCT
                  ********** ********** ********** ********** **********
                  ********** ******      ********* ********** **********
                  ********** ******      ********* ********** **********
                  ********** *           ********* ********** **********

alignment
position          801....... 811....... 821....... 831....... 841.......
P922028       675 TTATTGACGG GACTGTTTCC TTTGGCCCAc gcgacgtagT CTTCTGTTGT
P922029       676 TTTTTGGCAG Gtctgcatcc caTAGGTCAG ACAAGCCGTT CTCCTCTTGC
P922030       750 TTCTTAGCAG GACTGTGTTC TTTAGGTCAA ACAAGTCATT CTCCTCTTGT
                  ********** ********** ********** ********** **********
                  ********** *            ******** ********** **********
                  ********** *                                      ****
                  ********** *                                      ***
                                                                    ***

alignment
position          851....... 861....... 871....... 881....... 891.......
P922028       725 CCTTGACTGG GCGCCGCCTC CCGCCCCGCC GCCTCGGAAG CCCCTGAGAG
P922029       726 CCTTGACTGG GTACCAGCTC CTGCCCCGCC ACCTCTGGAA CCCGGGAGAG
P922030       800 CCTTGACTGG GCACCACCTC CTGCCCCGCC ACCTCcaGAA CCCCGGAGAA
                  ********** ********** ********** ********** **********
                  ********** ********** ********** ********** **********
                  ********** ********** ********** *****  *** **********
                  ********** ********** ********** *****  *** **********
                  ********** ********** ********** *****
                  ********** *      *** ********** *****
                                    *** ********** *****

alignment
position          901....... 911....... 921....... 931....... 941.......
P922028       775 CCGGCAGATG ggGGGCTTTT AGCCACGGTC TCTGGTCTGA TGAAGCAGAA
```

```
P922029      776 CCGGCAGGTG A-GGGTTATG AGCCTTGGTT TCTGGTCTGA TGGAGCCTAA
P922030      850 CCGGCAGGTG A-AGGTTAcT AGCCATAGTT TCTGGTCTGA TGGAGCATAA
                 ********** * ******** ********** ********** **********
                 ********** * ****** * ********** ********** **********
                 *******      ****** * ********** ********** **********
                 *******               ********** ********** *******

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

P922028      825 aagaagATGA GGATCAGGGG GTCCTCGGGA acgctgtcac gaatgtaGGC
P922029      825 GCc------- -GATCAGGAG ACCTTTGGGA GTCCG----- -------GGC
P922030      899 GC----AAGA TGATCAGGAA ACCTTTGGGA GTTCC----- -------GGC
                 **    **** ********** ********** *****             ***
                 **          ********* ********** *****             ***
                             ********* ********** *****             ***
                                                                    ***

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

P922028      875 TTGCAGGTGA CCTTCCCTCT GCAGGGAAAa ttCAGGACAT TTCCCTCTCA
P922029      855 TTGCGAGCTA CTCTCTCTTT GCAGGGGAAG A-CAGGAGAT GGCCCTGTCA
P922030      933 TTGCTAGCTA CTTTCTCTCT GCAGGGGAAG A-CAGGAGAT GGCCCTGTCt
                 ********** ********** ********** * ******** **********
                 ********** ********** ********** * ******** *********
                 ********** ** ******* ********** * ******** *********
                 ********** ** ******* *********
                               ******* *********

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

P922028      925 gaGGAGGAGG CCGTTTTATT CCCCGGGaga ggaccagtgt ccgatgactt
P922029      904 tc--AGGAGA CCGGTTCATC TCCCAGGgtc acgagagact taaacctcag
P922030      982 --GGAGGAGA CCGGGTCATT TC-------- ---------- ----------
                   ******** ********** *******

alignment
position         1101...... 1111...... 1121...... 1131...... 1141......

P922028      975 aggccttaag actaagcctt tccccccaga ttttacacg ccctgatacag
P922029      952 gcatcg---- ---------- ---------- ---------- ----------
P922030     1002 ---------- ---------- ---------- ---------- ----------

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

P922028     1025 tgcatgattG TTTGGTCGCT GTTGTGttag caatggctCA CGCTTCTGTT
P922029      958 ---------G TTTAGTTGCT GTCTTGaacc tgtc----CA CGCTACTGTT
P922030     1002 ---------- ---------- ---------- ---------- ----------
                          * ********** ******             ** **********

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

P922028     1075 TG-------- ---------- ---------- ---------- ---------
P922029      995 TGtttttgtc tagcccggtg atcatgttgg gtagtatttt attcattcc
P922030     1002 ---------- ---------- ---------- ---------- ---------
                 **
```

Pairwise similarities:

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

	P922029 (1043 bp)	**P922030 (1001 bp)**
P922028 (1076 bp)	0.396 54 %	0.442 55 %

P922029 (1043 bp)		1.000 73 %

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

Extract alignment region	
Positions in alignment	from: ☐ to: ☐
Output file	dialign.seq

Extract aligned sequences

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GEMS Launcher Task: *DiAlign TF*: Multiple alignment plus TF sites
working on C1-NDUFS2 (3 seq.)

[Alignment] [Pairwise_similarities]

DiAlign professional TF Release 3.1 December 2004 **Tue Jun 7 20:32:24 2005**

Solution parameters:

Sequence file:	C1-NDUFS2 (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	Lengt
1	hNDUFS2	hNDUFS2 g17_dna range=chr1:157983624-157985875 5'pad=0 3'pad=0 revComp=FALSE strand=? repeatMasking=none	225 b
2	P914253	P914253 sym=Ndufs2|loc=Loc226646|taxid=10090|spec=Mus musculus|chr=1|ctg=NT_039185|str=(-)|start=15158394|end=15159394|len=1001|tss=501|comm=NADH dehydrogenase (ubiquinone) Fe-S protein 2; (NM_153064/501/bronze;)	100 b
3	P914254	P914254 sym=na|loc=Loc289218|taxid=10116|spec=Rattus norvegicus|chr=13|ctg=NW_047399|str=(-)|start=4601374|end=4602374|len=1001|tss=501|comm=similar to NADH dehydrogenase (ubiquinone) Fe-S protein 2; (XM_213940/524/bronze;)	100 b

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$ETSF V$DMTF V$YY1F V$MYOD

```
alignment position  1.........  11........  21........  31........  41........
hNDUFS2          1  ccagagaact  ctactgcccc  tttccactcc  cctatttgag  atgaggacaa
P914253          1  acttgagtc-  ----------  ----------  ----------  ----------
P914254          1  nnnnnnnnnn  nnnnnnnnnn  nnnnnnnnnn  nnnnnnnnnn  nnnnnnnnnn

alignment position  51........  61........  71........  81........  91........
hNDUFS2         51  agggggtgac  taagcaatga  aagacaaagg  gctttagagt  ggctgcagca
```

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P914253        10 - - - - - - - - - -  - - - - - - - - - -  - - - - - - - - - -  - - - - - - - - - -  - - - - - - - - - -
P914254        51 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 1 0 1 . . . . . . .  1 1 1 . . . . . . .  1 2 1 . . . . . . .  1 3 1 . . . . . . .  1 4 1 . . . . . . .
hNDUFS2       101 g t g t g t g t g g  g g g t g t t g g c  a g c a g g g a g a  a g g c a c a a a a  g c t g c a g t g t
P914253        10 - - - - - - - - - -  - - - - - - - - - -  - - - - - - - - - -  - - - - - - - - - -  - - - - - - - - - -
P914254       101 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 1 5 1 . . . . . . .  1 6 1 . . . . . . .  1 7 1 . . . . . . .  1 8 1 . . . . . . .  1 9 1 . . . . . . .
hNDUFS2       151 c c t a g g c a g c  c c c t c a g g a g  c c c c c c a c c c  c a g t c c c a g c  t c a a g c t g c c
P914253        10 - - - - - - - - - -  - - - - - - - - - -  - - - - - - - - - -  - - - - - - - - - -  - - - - - - - - - -
P914254       151 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 2 0 1 . . . . . . .  2 1 1 . . . . . . .  2 2 1 . . . . . . .  2 3 1 . . . . . . .  2 4 1 . . . . . . .
hNDUFS2       201 t c c a g g g c c a  a g c a g c c c a a  a g t c t a t c c t  g a c t t c t c c c  a g g c t g g a t c
P914253        10 - - - - - - - - - -  - - - - - - - - - -  - - - - - - - - - -  - - - - - - - - - -  - - - - - - - - - -
P914254       201 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 2 5 1 . . . . . . .  2 6 1 . . . . . . .  2 7 1 . . . . . . .  2 8 1 . . . . . . .  2 9 1 . . . . . . .
hNDUFS2       251 a a g g c a a a t a  a a t g c a g t c c  t t c c c a t c c c  c c a c c a c c a t  g g c c a c a t t t
P914253        10 - - - - - - - - - -  - - - - - - - - - -  - - - - - - - - - -  - - - - - - - - - -  - - - - - - - - - -
P914254       251 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 a  t - - - - - - - - -

alignment position 3 0 1 . . . . . . .  3 1 1 . . . . . . .  3 2 1 . . . . . . .  3 3 1 . . . . . . .  3 4 1 . . . . . . .
hNDUFS2       301 g c t g t g t t t c  a a c a a t a g a a  a g a a g g c c c a  g g g a a a g a g c  a a g g a a t g a g
P914253        10 - - - - - - - - - -  - - - - - - - - - -  - - - - - - - - - -  - - - - - - - - - -  - - - - - - - - - -
P914254       292 - - - - - - - - - -  - - - - - - - - - -  - - - - - - - - - -  - - - - - - - - - -  - - - - - - - - - -

alignment position 3 5 1 . . . . . . .  3 6 1 . . . . . . .  3 7 1 . . . . . . .  3 8 1 . . . . . . .  3 9 1 . . . . . . .
hNDUFS2       351 g a c a a c a g a g  g g a c c a a a c c  t c t g c c c t g g  c t c t g t g g c a  g c t g c c t t g t
P914253        10 - - - - - - - - - -  - - - - - - - - - -  - - - - - - - - - -  - - - - - - - - - -  - - - - - - - - - -
P914254       292 - - - - - - - - - -  - - - - - - - - - -  - - - - - - - - - -  - - - - - - - - - -  - - - - - - - - - -

alignment position 4 0 1 . . . . . . .  4 1 1 . . . . . . .  4 2 1 . . . . . . .  4 3 1 . . . . . . .  4 4 1 . . . . . . .
hNDUFS2       401 c t a g c c c a g g  t c c t g g t c a g  t t c c c a c a g c  t a a g g a t c t g  g c c c c a c c c t
P914253        10 - - - - - - - - - -  - - - - - - - - - -  - - - - - - - - - -  - - - - - - - - - -  - - - - - - - - - -
P914254       292 - - - - - - - - - -  - - - - - - - - - -  - - - - - - - - - -  - - - - - - - - - -  - - - - - - - - - -

alignment position 4 5 1 . . . . . . .  4 6 1 . . . . . . .  4 7 1 . . . . . . .  4 8 1 . . . . . . .  4 9 1 . . . . . . .
hNDUFS2       451 t t g g t a c a g t  t c c c a t t a g g  t c a a t t c c c a  g g c c a g a a g t  c t g g c t t t c c
P914253        10 - - - - - - - - - -  - - - - - - - - - -  - - - - - - - - - -  - - - - - - - - - -  - - - - - - - - - -
P914254       292 - - - - - - - - - -  - - - - - - - - - -  - - - - - - - - - -  - - - - - - - - - -  - - - - - - - - - -

alignment position 5 0 1 . . . . . . .  5 1 1 . . . . . . .  5 2 1 . . . . . . .  5 3 1 . . . . . . .  5 4 1 . . . . . . .
hNDUFS2       501 c c t c t t t c t c  t g c a g t g a a g  a a t t c c a c c a  t c t c t g c t t c  c t g g t c t g t c
P914253        10 - - - - - - - - - -  - - - - - - - - - -  - - - - - - - - - -  - - - - - - - - - -  - - - - - - - - - -
P914254       292 - - - - - - - - - -  - - - - - - - - - -  - - - - - - - - - -  - - - - - - - - - -  - - - - - - - - - -

alignment position 5 5 1 . . . . . . .  5 6 1 . . . . . . .  5 7 1 . . . . . . .  5 8 1 . . . . . . .  5 9 1 . . . . . . .
hNDUFS2       551 t g c c t c a c c c  t g c t g c g c t g  c t g g t g g g c t  g t g t c c c t g g  g a t c c t g t c t
P914253        10 - - - - - - - - - -  - - - - - - - - - -  - - - - - - - - - -  - - - - - - - - - -  - - - - - - - - - -
P914254       292 - - - - - - - - - -  - - - - - - - - - -  - - - - - - - - - -  - - - - - - - - - -  - - - - - - - - - -

alignment position 6 0 1 . . . . . . .  6 1 1 . . . . . . .  6 2 1 . . . . . . .  6 3 1 . . . . . . .  6 4 1 . . . . . . .
hNDUFS2       601 a g g g g a t a t c  t g g g g a a g g c  c t c t t t c c a g  g c t c a g a g t t  g g a g a g t t g t
P914253        10 - - - - - - - - - -  - - - - - - - - - -  - - - - - - - - - -  - - - - - - - - - -  - - - - - - - - - -
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P914254        292 - - - - - - - - - -  - - - - - - - - - -  - - - - - - - - - -  - - - - - - - - - -  - - - - - - - - - -

alignment  position 6 5 1 . . . . . . .  6 6 1 . . . . . . .  6 7 1 . . . . . . .  6 8 1 . . . . . . .  6 9 1 . . . . . . .
hNDUFS2        651 a c a a a c t c t a  c g g g t g g g t g  g c c c a g c t g g  a g t t g g g c t t  a g a g g c a g a g
P914253         10 - - - - - - - - - -  - - - - - - - - - -  - - - - - - - - - -  - - - - - - - - - -  - - - - - - - - - -
P914254        292 - - - - - - - - - -  - - - - - - - - - -  - - - - - - - - - -  - - - - - - - - - -  - - - - - - - - - -

alignment  position 7 0 1 . . . . . . .  7 1 1 . . . . . . .  7 2 1 . . . . . . .  7 3 1 . . . . . . .  7 4 1 . . . . . . .
hNDUFS2        701 g g a g a a a a c a  g g a a c t a g c c  t c t a a g g c t g  g a a g a a t c t t  t g t c c a t a c a
P914253         10 - - - - - - - - - -  - - - - - - - - - -  - - - - - - - - - -  - - - - - - - - - -  - - - - - - - - - -
P914254        292 - - - - - - - - - -  - - - - - - - - - -  - - - - - - - - - -  - - - - - - - - - -  - - - - - - - - - -

alignment  position 7 5 1 . . . . . . .  7 6 1 . . . . . . .  7 7 1 . . . . . . .  7 8 1 . . . . . . .  7 9 1 . . . . . . .
hNDUFS2        751 g a a t t g t g a t  c a g a c t c c t g  g t g c t a c t a c  a t t t c c g t g c  t g t t g g c c a t
P914253         10 - - - - - - - - - -  - - - - - - - - - -  - - - - - - - - - -  - - - - - - - - - -  - - - - - - - - - -
P914254        292 - - - - - - - - - -  - - - - - - - - - -  - - - - - - - - - -  - - - - - - - - - -  - - - - - - - - - -

alignment  position 8 0 1 . . . . . . .  8 1 1 . . . . . . .  8 2 1 . . . . . . .  8 3 1 . . . . . . .  8 4 1 . . . . . . .
hNDUFS2        801 t a c c c a g g a g  g g c t a t a g c a  g g g t c a g a a a  g a c g t t a g g g  a a a a g a g g c t
P914253         10 - - - - - - - - - -  - - - - - - - - - -  - - - - - - - - - -  - - - - - - - - - -  - - - - - - - - - -
P914254        292 - - - - - - - - - -  - - - - - - - - - -  - - - - - - - - - -  - - - - - - - - - -  - - - - - - - - - -

alignment  position 8 5 1 . . . . . . .  8 6 1 . . . . . . .  8 7 1 . . . . . . .  8 8 1 . . . . . . .  8 9 1 . . . . . . .
hNDUFS2        851 g a c g c a a g a c  g g a a g t g g g g  t g t g a g g c a t  c t c t a a g g g c  g c t t c c t g g g
P914253         10 - - - - - - - - - -  - - - - - - - - - -  - - - - - - - - - -  - - - - - - - - - -  - - - - - - - - - -
P914254        292 - - - - - - - - - -  - - - - - - - - - -  - - - - - - - - - -  - - - - - - - - - -  - - - - - - - - - -

alignment  position 9 0 1 . . . . . . .  9 1 1 . . . . . . .  9 2 1 . . . . . . .  9 3 1 . . . . . . .  9 4 1 . . . . . . .
hNDUFS2        901 t c t g t g a t t c  t g t a g g t t c g  g g a a g c c t g g  a g g a t g t c a g  g g t c a c c c a c
P914253         10 - - - - - - - - - -  - - - - - - - - - -  - - - - - - - - - -  - - - - - - - - - -  - - - - - - - - - -
P914254        292 - - - - - - - - - -  - - - - - - - - - -  - - - - - - - - - -  - - - - - - - - - -  - - - - - - - - - -

alignment  position 9 5 1 . . . . . . .  9 6 1 . . . . . . .  9 7 1 . . . . . . .  9 8 1 . . . . . . .  9 9 1 . . . . . . .
hNDUFS2        951 a g a g g a c c t c  c a c t c c c c c a  t c t g g g a t g a  g g t g g c t c c t  a c a c a c c c c g
P914253         10 - - - - - - - - - -  - - - - - - - - - -  - - - - - - - - - -  - - - - - - - - - -  - - - - - - - - - -
P914254        292 - - - - - - - - - -  - - - - - - - - - -  - - - - - - - - - -  - - - - - - - - - -  - - - - - - - - - -

alignment  position 1 0 0 1 . . . . . .  1 0 1 1 . . . . . .  1 0 2 1 . . . . . .  1 0 3 1 . . . . . .  1 0 4 1 . . . . . .
hNDUFS2       1001 a c a c t c c c c t  c c g c a c c a c c  a a t g c c g g c g  g c c t t g g c a t  c c t a t t c t t t
P914253         10 - - - - - - - - - -  - - - - - - - - - -  - - - - - - - - - -  - - - - - - - - - -  - - - - - - - - - -
P914254        292 - - - - - - - - - -  - - - - - - - - - -  - - - - - - - - - -  - - - - - - - - - -  - - - - - - - - - -

alignment  position 1 0 5 1 . . . . . .  1 0 6 1 . . . . . .  1 0 7 1 . . . . . .  1 0 8 1 . . . . . .  1 0 9 1 . . . . . .
hNDUFS2       1051 t t t g t t t t g g  t t t g g c g g g a  g c t c t c a g a c  c c g c c c a g c c  c c a c t t a g g c
P914253         10 - - - - - - - - - -  - - - - - - - - - -  - - - - - - - - - -  - - - - - - - - - -  - - - - - - - - - -
P914254        292 - - - - - - - - - -  - - - - - - - - - -  - - - - - - - - - -  - - - - - - - - - -  - - - - - - - - - -

alignment  position 1 1 0 1 . . . . . .  1 1 1 1 . . . . . .  1 1 2 1 . . . . . .  1 1 3 1 . . . . . .  1 1 4 1 . . . . . .
hNDUFS2       1101 t C C T T T C T C C  A A T C T C A A T T  T A T G A C A T C T  G G A A A T T A G C  t g g c t t t c c c
P914253         10 - C C T T C A C A C  A A G C C C G T T T  C C G G A C C T C T  G G A A A T G A A C  a - - - - - - - - -
P914254        292 - - - - - - - - - -  - - - - - - - - - -  - - - - - - - - - -  - - - - - - - - - -  - - - - - - - - - -
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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 . . . . . .
hNDUFS2       1151 a a c t c c t g t C  T T T T G G A T T C  A G T G A T G G G A  A A G T A A T T G G  C A A A G C C T G g
P914253         50 - - - - - - - - - C  T T T T G G A T T T  C G T A G T A A A G  A G A T A G T C A T  C A A A A C T T G g
P914254        292 - - - - - - - - - -  - - - - - - - - - -  - - - - - - - - - -  - - - - - - - - - -  - - - - - - - - - -
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alignment position 1201...... 1211...... 1221...... 1231...... 1241......
hNDUFS2       1201 ggctacccta taagggcagg gctcagatac aaTCCGAGAG CAGGACTAAA
P914253         91 gggcttctg- ---------- ---------- --TCGGAAAG CAGGACTACC
P914254        292 ---------- ---------- ---------- ---------- ----------
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alignment position 1251...... 1261...... 1271...... 1281...... 1291......
hNDUFS2       1251 GCATGAGGGC GGCCAAGGCG Gaagggagta gggaaggaag cgccgcgcgt
P914253        118 GCAGGAGACT GACCAAGATG Gtaagatagt caaggaacgc ccatacagag
P914254        292 ---------- ---------- ---------- ---------- ----------
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alignment position 1301...... 1311...... 1321...... 1331...... 1341......
hNDUFS2       1301 ttccaagata cgcaggcggg ctcggc---- ---------- ----------
P914253        168 agtgcgtagg ggacctagag ggagcgcagt ttctaaggaa agttcgagtg
P914254        292 ---------- ---------- ---------- ---------- ----------

alignment position 1351...... 1361...... 1371...... 1381...... 1391......
hNDUFS2       1327 ---------- ---------- ---------- ---------- ----------
P914253        218 cagagcgtgg acctagcggg aagtgctgga ttctgcgcga agttgcctca
P914254        292 ---------- ---------- ---------- ---------- ----------

alignment position 1401...... 1411...... 1421...... 1431...... 1441......
hNDUFS2       1327 -GAGAGAGCA CGAAGTATCT GCCCCACGCA GGAACGGcaa ttttcccttg
P914253        268 gGAGAGAGCA GTAAATCTCT CACGCCCAGA GAAGCCGtgg gaggg-----
P914254        292 ---------- ---------- ---------- ---------- ----------
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alignment position 1451...... 1461...... 1471...... 1481...... 1491......
hNDUFS2       1376 ctcgctccta gaaaagccag ccaggagctg tgggaggaaA CGCCCTCAGT
P914253        313 ---------- ---------- ---------- ---------A CGCCCTTACT
P914254        292 ---------- ---------- ---------- ---------- -GCCCTAACT
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alignment position 1501...... 1511...... 1521...... 1531...... 1541......
hNDUFS2       1426 AAAGATGACC GCGGTCACTG TTATCTAAAC GCAAGTGAAG CCGAGTCACA
P914253        324 AAAGATGACG GCAGTCGTCG TTATTGAAAC GCAAGTGAAG CTGAGAAGCG
P914254        301 AAAGATGACA GCAGTCGTTG TTATTTAAGC GtgAGTGAAG CTGAGAAGCA
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alignment position 1551...... 1561...... 1571...... 1581...... 1591......
hNDUFS2       1476 GGACCCGGAT GTTGTcagtt cgacggtaaa cgaCCCTGCC AGCTTCCAAG
P914253        374 GAATCCGGAT GTTGTTCCGT TCGCAATTGA CCTCCCTGCC AGCTTCCAAG
P914254        351 GGATCCGGAT GTTGTTCCGT TCGCAATTGA CCTTCCTGCC AGCTTCCAAG
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alignment position 1601...... 1611...... 1621...... 1631...... 1641......
hNDUFS2       1526 AGGGCGGCTT CACTGTGCGA AT-AGgtgag aagccaagAA GGAGGCGCGC
P914253        424 ATGGGGACTC CGTTGTGgcg ataAGAAGGG AAGCCCACCA GGGGGCGCGC
P914254        401 ATGGTGACTC CATTGTGCCA AT-AGAGGGG AAGTCCATAA GGAGGCGCGC
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alignment position 1651...... 1661...... 1671...... 1681...... 1691......
hNDUFS2       1575 TGGAGTTACT TCCGCCCGGT TCTCCTTCCc gCAGTCTGCA GCCGGAGTAA
P914253        474 GGGAGCGACT TCCGCCCGGC TCTCCTTCCT ACAGTCTGCA GCCCGGTAAA
P914254        450 GTGAGTCACT TCCGCCCGGT TCTCCTTCCT AAGGTCTGCA GCCCAGTAAA
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alignment position 1701...... 1711...... 1721...... 1731...... 1741......
hNDUFS2       1625 GATGGCGGCG CTGAGGGCTt TGTGCGGCTT CCGGGGCGTC GCGGCCCAGG
P914253        524 GATGGCGGCC CTGAGGGCGC TGCGCTGCCT CCGTGGGGTC GGAGCCCCGG
P914254        500 GATGGCGGCC CTCAGGGCTG TGTGCAGCCT CCGCGGTGTC GGGGCCCAGG
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alignment position 1751...... 1761...... 1771...... 1781...... 1791......
hNDUFS2       1675 TGCTGCGGCC tGGGGCTGGA GTCCGATTGC CGATTCAGCC CAGCAGGTGA
P914253        574 TGCTGCGGCC CGGGTCTGGG ATCCGCTTGC CAAGTCAGCC CAGCAGGTGA
P914254        550 TGCTGCGGGC CGGGTCTGGG ATTCGTCTGC CGAGTCAGCC CAGCAGGTGA
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alignment position 1801...... 1811...... 1821...... 1831...... 1841......
hNDUFS2       1725 Gatcgagggc agctctcgac acacTTTCTC CAAGGCTAGG GTTTCTCAGG
P914253        624 GGAGGAGGCG GtcCCTACAT GCGGTCTCTG CAGAACTGCA ATGTCTCcac
P914254        600 GGAGGAGGCG GctCCTACAT GCGTTCTCTT CAAAACTGGA GTTTCTCGAG
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alignment position 1851...... 1861...... 1871...... 1881...... 1891......
hNDUFS2       1775 Ttggggacgc tttact---- --------CC CCCAGAAAAT AATAACCCAA
P914253        674 TCTGAGGACA TTTCAAGGGC TCTGTGACCC CTGAGGAGAG AATGACCCAG
P914254        650 TCTGAGGACA TTTCAAGGGC TCTGTGACCC CTGAGGAAAG AATGACCCAG
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                   *                             ** ******* ** **********
                                                 ** *******
alignment position 1901...... 1911...... 1921...... 1931...... 1941......
hNDUFS2       1813 GCCTGTGACC Ccattgtcca tc-CCTGAT- --TTCTTGGG CTACGGGATG
P914253        724 GCCTGTAACC CTCCTCACGC AGACCAGAtt tcTTCCTAGG TTCCTAGGTG
P914254        700 GCCTATAACC CTCCTTACGC TGACCAGAT- --TTCTTAGG TTCCTAGATG
                   ********** ********** *********    ******** **********
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                   ********** *             *****
                   ********** *
alignment position 1951...... 1961...... 1971...... 1981...... 1991......
hNDUFS2       1859 CAGtggcGCC CACTCTGGCG AGGGAGGGGA GAgggtctag agttcgttcg
P914253        774 CAGCCA-GCC TCCTGTGGCA AAGGATGGGA AATAAGGGAG ATGAATTTtt
P914254        747 CAGTCA-GCT TCCTGTGGCG GAGGATGGGA AGTAAGGGAG ATGATTTTat
                   ****** *** ********** ********** ********** ********
                   ****** *** *********   ********* ********** ********
                   ****** *** *********   ********* ********** ********
                   ***
alignment position 2001...... 2011...... 2021...... 2031...... 2041......
hNDUFS2       1909 tg-------- ---CCGAGGT GAAATCAGCG GAGTGGGAGA CTCTGCTTTT
P914253        823 at---TTTTT TGTCAGAAGC GAAATATGTG GGATGAAATA TCCTACCCTT
P914254        796 ttttaTTTTT TGTCAGAAGC GAAATATGTA GCGTGAAAGA CCCTACCCTT
                        ***** ********** ********** ********** **********
                        ***** ********** *********     ******* **********
                        ***** ********** *********
alignment position 2051...... 2061...... 2071...... 2081...... 2091......
hNDUFS2       1948 TAGcttcagT AAT----TTG AATGCACCTC TCCTGTCata cctgagtaga
P914253        870 CAGA-----T GAatggcTAG AGAGTACCTC CCATATCCGA AGGAGACCCC
P914254        846 CAAA-----T GAT----TAG AGCGTACCTC CCATATCCGA AGGAGACCCC
                   ****     * ***    *** ********** ********** **********
                   ****     * **     *** ********** ********** **********
                                     *** ********** ********** **********
                                     *** ********** ********** **********
alignment position 2101...... 2111...... 2121...... 2131...... 2141......
hNDUFS2       1994 gctcagccaa agagccaga- ---------- ---------- ----------
P914253        915 -CTCTTCTCT GAGCCCTCTT TCCCCAGTTC Cct------C TTTTTTGCTC
P914254        887 tCTCTTTTCT GAGCCCTCCT TCCCCAGTTC CtctcttccC TCTTTCGCTC
                    ********* ********** ********** *        * **********
                    ********* ********** ********** *
                    ********* ********** ********** *
alignment position 2151...... 2161...... 2171...... 2181...... 2191......
hNDUFS2       2013 ----ATGCT- -------CGC TGTCTCTCTg tcgttgacct tgaacaaaca
P914253        958 GCCTATGCT- -------CTT TCCCTCTCTC CTCCCGCCTT CCATACTCCC
P914254        937 GCATATGCga ggttgcaCTT TCCCTCTTTC CTCCCGCCTT CCCTACTCCC
                   *********         *** ********** ********** **********
                                     *** ********** ********** **********
                                     *** ********** ********** **********
                                     *** ********** ********** **********
alignment position 2201...... 2211...... 2221...... 2231...... 2241......
```

```
hNDUFS2   2051 c t t t t c t c a c  g t t c a t a t t c  a c c t g g t t g a  t a a t a t c a a t  a t g a t g a a a a
P914253   1000 t g - - - - - - - -  - - - - - - - - - -  - - - - - - - - - -  - - - - - - - - - -  - - - - - - - - - -
P914254    987 c c c g c c c c c a  t c t c t - - - - -  - - - - - - - - - -  - - - - - - - - - -  - - - - - - - - - -

alignment position 2 2 5 1 . . . . . .  2 2 6 1 . . . . . .  2 2 7 1 . . . . . .  2 2 8 1 . . . . . .  2 2 9 1 . . . . . .
hNDUFS2   2101 t a t g a a g a a g  c t a g g a t c c c  a a c c t t g c a t  g c c c a g g g g t  g a t g g g t g g a
P914253   1002 - - - - - - - - - -  - - - - - - - - - -  - - - - - - - - - -  - - - - - - - - - -  - - - - - - - - - -
P914254   1002 - - - - - - - - - -  - - - - - - - - - -  - - - - - - - - - -  - - - - - - - - - -  - - - - - - - - - -

alignment position 2 3 0 1 . . . . . .  2 3 1 1 . . . . . .  2 3 2 1 . . . . . .  2 3 3 1 . . . . . .  2 3 4 1 . . . . . .
hNDUFS2   2151 g t t a t t c c a g  g a a t a a t t t g  t t a g t a g g a a  t g g a a c c t c t  a g a g t t c c a g
P914253   1002 - - - - - - - - - -  - - - - - - - - - -  - - - - - - - - - -  - - - - - - - - - -  - - - - - - - - - -
P914254   1002 - - - - - - - - - -  - - - - - - - - - -  - - - - - - - - - -  - - - - - - - - - -  - - - - - - - - - -

alignment position 2 3 5 1 . . . . . .  2 3 6 1 . . . . . .  2 3 7 1 . . . . . .  2 3 8 1 . . . . . .  2 3 9 1 . . . . . .
hNDUFS2   2201 c t t g t t t t g c  c g a a g c t a c a  t t a a c t t c a g  a t c a g t g a c t  t g g c a t t a a a
P914253   1002 - - - - - - - - - -  - - - - - - - - - -  - - - - - - - - - -  - - - - - - - - - -  - - - - - - - - - -
P914254   1002 - - - - - - - - - -  - - - - - - - - - -  - - - - - - - - - -  - - - - - - - - - -  - - - - - - - - - -

alignment position 2 4 0 1
hNDUFS2   2251 a a
P914253   1002 - -
P914254   1002 - -
```

Pairwise similarities:

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

	P914253 (1001 bp)	**P914254 (1001 bp)**
hNDUFS2 (2252 bp)	0.307 39 %	0.324 32 %
P914253 (1001 bp)		<u>1.000</u> <u>57 %</u>

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

Extract alignment region	
Positions in alignment	from: ☐ to: ☐
Output file	dialign.seq

Extract aligned sequences

For comments, questions or bug reports, please contact support@genomatix.de

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

[Alignment] [Pairwise_similarities]

DiAlign professional TF Release 3.1 December 2004 **Tue Jun 7 20:56:18 2005**

Solution parameters:

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

Aligned Sequences:

No.	Sequence Name	Sequence Description	Length
1	P878333	sym=NDUFS3|loc=Loc4722|taxid=9606|spec=Homo sapiens|chr=11|ctg=NT_009237|str=(+)|start=46387373|end=46388373|len=1001| tss=501| comm=NADH dehydrogenase (ubiquinone) Fe-S protein 3, 30kDa (NADH-coenzyme Q reductase); (NM_004551/560/silver;)	1001 bp
2	P878334	sym=na|loc=Loc433454|taxid=10090|spec=Mus musculus|chr=2|ctg=NT_039207|str=(-)|start=31738929|end=31740003|len=1075| tss=501,530,575| comm=similar to NADH-ubiquinone oxidoreductase 30 kDa subunit, mitochondrial precursor (Complex I-30KD) (CI-30KD); (AK088337/501/gold;AK002501/530/gold;XM_485037/575/bronze;)	1075 bp
3	P878335	sym=na|loc=Loc295923|taxid=10116|spec=Rattus norvegicus|chr=3|ctg=NW_047657|str=(-)|start=16664085|end=16665085| len=1001|tss=501| comm=similar to NADH-ubiquinone oxidoreductase 30 kDa subunit, mitochondrial precursor (Complex I-30KD) (CI-30KD); (XM_215776/550/bronze;)	1001 bp

Alignment (DiAlign format):

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

V$XBBF V$VMYB V$AREB V$SP1F V$RREB V$ZBPF V$EGRF V$GABF V$ETSF V$ZF35 V$EREF V$MOKF

```
alignment
position           1 . . . . . . . . .   1 1 . . . . . . . .   2 1 . . . . . . . .   3 1 . . . . . . . .   4 1 . . . . . . . .
P878333      1 - - - - - - - - - -   - - - - - - - - - -   - - - - - - - - - -   - - - - - - - - - -   - - - - - - - - - -
P878334      1 c c a a t  a c t g a   g g c t  t g g g c c   t g g a c t t c c a   c t t t t a c t c t   t t t c t a a g c T
P878335      1 - - - - - - - - - -   - - - - - - - - - -   - - - - - - - - - -   - - - - - - - - - -   - - - - - - - - - T
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                                                                  *
                                                                  *
alignment
position     51........ 61........ 71........ 81........ 91........
P878333    1 ---------- ---------C TCGCTCGAAA GACTCCCTAT GGCTGCGTcc
P878334   51 GCTGTTTCTT ACTTACCT-C TCGCTCCAGT GAGTTCTTAA AGAAGCCctt
P878335    2 GCTGTTTCTT ACTTACCTaC TCGCTCCAAT GAGTTCTTAA AGAAGCCTga
             ********** ******** * ********** ********** ********
             ********** ******** * ********** ********** *******
                                 * ********** ********** *******

alignment
position     101....... 111....... 121....... 131....... 141.......
P878333   32 cagaacttGA GTCCATCCGC CCCCAGGCCG GGGCACTGGG AGGCCCATCA
P878334  100 GA------GA GCCCAGCCGT CCCCGGCCGG GGGCACAAGG AAGTCCATAA
P878335   52 GA------GA GCCCAGCCGT CCCCGGCCGG GGGCACAAGG AAGTCCATAA
             **      ** ********** ********** ********** **********
             **      ** ********** ********** ********** **********
             **      ** ********** ********** ********** **********
             **      ** ********** ********** ********** **********
             **      ** ********** ********** ********** **********
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                                   ********** *****   ** **********
                                                      ** ******

alignment
position     151....... 161....... 171....... 181....... 191.......
P878333   82 CCCTGTGCAA TGTCCCCGCT CCACCTTGAG TCGTCTTGGA AACGGTCGCC
P878334  144 CCCTGTGCAA TCTGACCGTG CCACCTGGAG TCGCCTAGGA AACGGTCTCC
P878335   96 CCCTGTGCAA TCTGACCGCG CCACCTAGAG TCGCCTAGGA AACGGTCTCC
             ********** ********** ********** ********** **********
             ********** ********** ********** ********** **********
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                                   ****** *** ********** **********
                                                   ***** **********

alignment
position     201....... 211....... 221....... 231....... 241.......
P878333  132 AGGGAAACCG TTCTTCccgc tcaggcccg- --CCCGCCCT CGTCAAAA--
P878334  194 AAGGAAACCG TCCATCGTCT CCCCCcccca CCCCGCCCCC CATTAAAAaa
P878335  146 AAGGAAACCG TCCATCGACT CCCCCac--- CCCCGCCCCC CATTAAAA--
             ********** ********** *****      ********** ********
             ********** ********** *****      ********** ********
             ********** ********** *****
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alignment
position     251....... 261....... 271....... 281....... 291.......
P878333  177 GCTTGGCTCA GaGAGCGGGG GAGGGGTGTG TAGCGTAGAA CCCAAAACGC
P878334  244 GCTTAGCTCA A-GAGCCGGc --GCGGTGTA GAACTTAGAA CCCAGAACGC
P878335  191 GCTTAGCTCA G-GAGCCAGA GAGCGGTGTA GAACTTAGAA CCCAGAACGC
             ********** * ******** ********** ********** **********
             ********** * *******    ******** ********** **********
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                                     ******** ********** **********
                                                   ***** **********
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```

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alignment
position        301....... 311....... 321....... 331....... 341.......
P878333     227 CCGCCCCCTC CCCTCCTCTC ACCCGCCTGG TTCTTcagcg tCCTCGCCTT
P878334     291 CCACCCTTTC CCTTTCTCTC ACCGGTGCGG TTCGTTG--- -CGTCTTCTT
P878335     240 CCACCCTTTC CCTTTCTCTC ACCCGTCCGA TTCTTTG--- -CGTCTTCTT
                ********** ********** ********** *******     *********
                ********** ********** ********** *******     *********
                ********** ********** ********** *****             ***
                ********** ********** ********** *****             ***
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alignment
position        351....... 361....... 371....... 381....... 391.......
P878333     277 CTCTCTAGGC TCTGCCACAA GGAGCTAGGA CCACGCTC-A CCTCACGATT
P878334     337 CTCTTCGGCC TCCGCTGTAC CGAGATAGGG CTACGTAC-A CCTCACGGTT
P878335     286 CTCTTCGGCC TCCGCCGTAC CAAAATAGGG CTACGTAgaA CCTCACGGTT
                ********** ********** ********** ******** * **********
                ********** ********** ********** ******** * **********
                ********** ********** ********** *******  * **********
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alignment
position        401....... 411....... 421....... 431....... 441.......
P878333     326 TCCCTACCTG CctgtctcgC TTTCTCACCT GCGTTCCCTC CTTTCATCCC
P878334     386 TCCCCACCTG CGGGT----C TTTCTTACCT GCGATACCTC CTTTCATGCC
P878335     336 TCCCCACCTG CGGGT----C TTTCTTACCT GCGTTACCTC CTTTCATGCC
                ********** *****    * ********** ********** **********
                ********** *****    * ********** ********** **********
                ********** *****    * ********** ********** **********
                ********** *****    * ********** ********** **********
                ********** *****    * ********** *** ****** **********
                ********** *        * ********** ***
                ********** *        * ********** ***
                                    * ********** ***

alignment
position        451....... 461....... 471....... 481....... 491.......
P878333     376 GGAGC----- -CCGGAACCT CCGCTTCCGG CTCCACGTCC GCCCGGAAGA
P878334     432 AGGGCTCAGA TCCGGAACCT CTGCTTCCCG CCCCGCGTCC GCCCGGAAGA
P878335     382 AatgtTCAGA TCCGGAACCT CTGCTTCCCG CCCCGTGTCC GCCCGGAAGA
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                *    ***** ********** ********** ********** **********
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                            ********* ********** ***** **** **********

alignment
position        501....... 511....... 521....... 531....... 541.......
P878333     420 AgatctgCTG CACACTTCCG TTTCCGGTCC GTGCCCTTGG GGCTCCGTgt
P878334     482 AGAGTCACTG CACATTTCCA CTTCCGGTCC GTGCCCTTGG GGCTCCGTGG
P878335     432 AGATTCATTG CACATTTCCA CTTCCGGTCC GTGCCCTTGA GGCTCCGTGG
                ********** ********** ********** ********** **********
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                ********** ********** ********** ********** **********
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                     ** ********** ******

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

P878333  470 cctgcTGTCT TTCCGTCCGC TGCCTAGTCT GCAt-CTGAG TAACATGGCG
P878334  532 CCTG-CGTGT GTTCTCCGGC TACTTAGTCG GCACACTAAG GAACATGGCG
P878335  482 CCTG-TGTGT GTTTTCCGGC TACTTAGTCG GCACCCTAAG GAACATGGCG
             **** ***** ********** ********** ********** **********
             **** ***** *** ****** ********** ********** **********
             **** ***** *** ****** ********** ********** **********
                            ****** ********** ********** **********
                                                    ***** **********

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

P878333  519 GCGGCGGCgg tAGCCAGGCT GTGGTGGCGC GGGATCTTGG GGGCCtcggc
P878334  581 GCGGCTGC-- -AGCCAGGGT CTGGTGTCGT GGGCTCTTGG GGGCCGCTTC
P878335  531 TCTGCTGC-- -AGCCAGGGT CTGGTGCCGT GGGCTCTTGG GGGCtGCTTC
             ********    ********* ********** ********** **********
                *****    ********* ********** ********** **********
                *****    ********* ********** ********** **** *****
                *****    ********* ********** ********** ****
                **       ********* ********** ********** ****
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alignment
position     651....... 661....... 671....... 681....... 691.......

P878333  569 gctgaCCAGG GGTGAGCACG Gg-CAGCCA- --GCTGAGAC CGGGGTCAGG
P878334  628 CGTAGGCAGG GGTGAGCAAG GAACAGCAGc agGTTGAGAC CACGGGCAGC
P878335  578 CGTAGCCAGG GGTGAGCAAA GAACAGCAG- --GCCGAGAC CACGGGCAGC
             ********** ********** *********    ******** **********
             ********** ********** *********       ***** **********
             ********** ********** *********
                   **** ********      ******

alignment
position     701....... 711....... 721....... 731....... 741.......

P878333  615 CGCAGCGGcg tgcccagtgC AGAGAGCTCC TCAGGGCTCA tCCCGCGCGT
P878334  678 a--------- ---------C GGAGACCTCC CCGAGTCTCA -CCCGCGCCT
P878335  625 GGCAGAGGca caccttgcaC ATAGACCTCC TCGGGTCTCA -CCCGCGCCT
             ********            * ********** **********  *********
                                     ******** **********  *********
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alignment
position     751....... 761....... 771....... 781....... 791.......

P878333  665 CTGTGCCTTT TATCTCCCTG TGCAGGGaCT GGGCGACCCT CCGTTCTGTT
P878334  709 TTGTGCCTTT TCTCTCCCTG TGCAGGGGCT GGGCGACCCT CCGTGCTGTG
P878335  674 TTGTGCCTTT TATCTTCCTG TGCAGGGGCT GGGCGACCCT CAGTGCTGTT
             ********** ********** ********** ********** **********
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             ********** *     **** *******

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

P878333  715 GCTGCCG--- GTGAGGCGGG AGAGCGCCGG GGCCGACACG CGCCGTGAGT
P878334  759 GCAGCAC--- GTAAGAAGGG AGAGCGCGGC GGCTGACAAG CGCCGTGAGT
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P878335    724 GCAGCAgcgt GTGAGAAGGG AGAGCGCGGC GGCTGACAAG CGCCGTGAGT
               *******    ********** ********** ********** **********
               *******    ********** ********** ********** **********
               ******        ******* ********** ********** **********
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               **            **  *** ********** ********** **********
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                                                    ****** **********
                                                    ****** **********

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

P878333    762 ATGTGCGGGC AGCGCTCTTC TCTGAACTAT CGGCGGGGCC CCTT------
P878334    806 ATGTGCGGAT GGCGCTTTTT CCCCCAACGT TAGCTGGGGC CTTTcgTTGT
P878335    774 ATGTGCGGAT AGCGCTCTTC TCTTCAACGT TAGCAGGGGT CTTccaTTGT
               ********** ********** ********** ********** ****  ****
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               ********** ********** ***                        ****
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alignment
position       901....... 911....... 921....... 931....... 941.......

P878333    806 -------AGA TGCCTGTCCT TGCCCTAGGA TGCCCTTCCC Tacgtcct CC
P878334    856 TTCTGTCAGA TGTTTGTCCT TGCCTTGGAA TGTCCTTCCC T-------CC
P878335    824 TTCTGCCAGA TGTTTGTCCT TGCCCTGGAA TGTCCTTCCC T-------TC
               ********** ********** ********** ********** *       **
               ********** ********** ********** ********** *       **
               ********** ********** ********** ********** *       **
                      *** ********** **** ***** ********** *       **
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alignment
position       951....... 961....... 971....... 981....... 991.......

P878333    849 TGGCAAATCT tggagatctg ac-----TTG CAGTGGTCTT CACCCTGCAT
P878334    899 TGGCAAATCT CTGCTTGtCC TTGGAGATTG CTATGGTCTC CACTTTGCTG
P878335    867 TGGCAAATCT CTGCTTGcCC TTGGAGATTG CTATGGTCTC CACCTTGCTG
               ********** ******* ** ********** ********** **********
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               ********** ******* ** ********** ********** **********
                                             ******* **********

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

P878333    894 GCAGAATCGA GCCCTCCCTG TGCCCTtagg cctgttatgg c------CCT
P878334    949 TTAGAATCGA GCACTTCCTG TGCCCTAGAT ATTTGTTCCC TTCTGATCTT
P878335    917 TTAGAAACGA GTACTTCCTG TGCCCTAGAT ATTTGTTCCC TTCTGATCTT
               ********** ********** ********** ********** **********
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                      *** ********** ***

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

P878333    938 GATTGTTCCT TGTCCATTTC AATCATCCCC ---------T TTTTGTCTGA
P878334    999 GATCGCCTTT TGCTCGTTAT CAggatttga tttttttttT TGTCCTCCGA
P878335    967 GATCGCCCTT TGCTCGTTTT CACAATCTTC ---------T ATTT------
```

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                     ********** ********** **********                    * **********
                     ********** ********** **

alignment
position             1101...... 1111...... 1121...
P878333          979 TTAAACTGTC agctctttga aag----
P878334         1049 TGAAATTGTC tttgagcgca ggtaaca
P878335         1002 ---------- ---------- -------
                     **********
```

Pairwise similarities:

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

	P878334 (1075 bp)	P878335 (1001 bp)
P878333 (1001 bp)	0.356 60 %	0.366 64 %
P878334 (1075 bp)		1.000 88 %

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

Extract alignment region	
Positions in alignment	from: ☐ to: ☐
Output file	dialign.seq

Extract aligned sequences

For comments, questions or bug reports, please contact support@genomatix.de

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GEMS Launcher 4.1.1

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GEMS Launcher Task: *DiAlign TF*: Multiple alignment plus TF sites
working on C1-NDUFS4 (3 seq.)

[Alignment] [Pairwise similarities]

DiAlign professional TF Release 3.1 December 2004 **Tue Jun 7 22:10:52 2005**

Solution parameters:

Sequence file:	C1-NDUFS4 (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	P855897	P855897 sym=NDUFS4|loc=Loc4724|taxid=9606|spec=Homo sapiens|chr=5|ctg=NT_006713|str=(+)|start=3450344|end=3451344|len=1001|tss=501|comm=NADH dehydrogenase (ubiquinone) Fe-S protein 4, 18kDa (NADH-coenzyme Q reductase); (NM_002495/516/bronze;)
2	P855898	P855898 sym=Ndufs4|loc=Loc17993|taxid=10090|spec=Mus musculus|chr=13|ctg=NT_039590|str=(-)|start=22613656|end=22614693|len=1038|tss=501,533,538|comm=NADH dehydrogenase (ubiquinone) Fe-S protein 4; (AK011124/501/gold;AK020552/533/gold;NM_010887/538/bronze;)
3	rNDUFS4	rNDUFS4 n3_dna range=chr2:46407330-46408355 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$NFAT V$AP4R V$BRNF V$NKXH V$MYOD V$FKHD V$ETSF V$YY1F V$NEUR V$TALE V$WHZF V$RORA
V$SP1F

```
alignment
position      1.........  11........  21........  31........  41........

P855897     1 tttcgtt---  ----------  ----------  -------TGG  AAAATACGAA
P855898     1 c---TTTTTT  TTTTTTTGCG  AGGCTAGCTT  TTTAGTGTGG  AAAATATGAT
rNDUFS4     1 ttttTTTTTT  ATCTTTGGCG  AGGCCAGATT  TTTAGTGTGG  AAAATATGAT
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alignment
position            51........ 61........ 71........ 81........ 91........
P855897         21  CATTACTACT ACAGAATATC AAACTGAata cagcCCTGTC CTGAGGGCTT
P855898         48  TATTATAACT ACAGACCATC AAACTGAGTG CAG-CCTGTT CTGAAGGCTT
rNDUFS4         51  TATTATAACT ACAGACCATC AAACTGAGTG CAG-CCTGTT ATGAAGGCTT
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alignment
position            101....... 111....... 121....... 131....... 141.......
P855897         71  GCAAAGTGAA TCTGGCAAtA CTTTGGAAAA GTACTACTGC AGGTTCTCAA
P855898         97  GCAAACGGAA TCTGGCAACA CTTTGGGAAA GTACTACTTT AGTTTCTCAA
rNDUFS4        100  GCAAACGGAA TCTGGCAACA CTTTGGGAAA GTACTACTTT AGTTTCTCAA
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alignment
position            151....... 161....... 171....... 181....... 191.......
P855897        121  GGACCCAAaG AGCTCTCCAG CTTTTCCAGT GGGTTCAGCC CCAAATATcC
P855898        147  AGACTCAAGa AGCCCTCCGG CTCTTCCAGT GGGCCCAGCC TCAGATATTC
rNDUFS4        150  AGACTCAAGG AGCCCTCCGG CTCTTCCAGT GGGCTCAGTC TCAGATATTC
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alignment
position            201....... 211....... 221....... 231....... 241.......
P855897        171  TAATTTCTTC AATAAATTAC GAGTTGCAGG TGTTTAAA-T atgcaag---
P855898        197  cGAGTTCTTT GAAAAATTAT GAGTTACAGG TGTTTAcatT TTTCGAAGCG
rNDUFS4        200  TGAGTTCTTT GAAAAATTAT GAGTTACAGG TGTTTATA-T TTTTGAAGTG
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alignment
position            251....... 261....... 271....... 281....... 291.......
P855897        217  -TATATTTTG GTCTTTTCGT TATCATTGTA AAACACCAgt cctaacaagc
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P855898      247 TTTTCTTTTG GGCTTCTCAG CCTCAATGTA AATGACCAAC CTTACTAAC-
rNDUFS4      249 TTTTCTTTGG GGCTTCTCAG CCTCAGTGTA AATGACCAAC CTTACTAAC-
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alignment
position         301....... 311....... 321....... 331....... 341.......
P855897      266 agtAAAGATT ACACTTTATG GTGGTAATAT TTACAGTTAA TGcacttctg
P855898      296 ---AAGGATT ACTTTCTATA GAGGCATCAT TTGCATTCAC TGagtcc-TT
rNDUFS4      298 ---AAGTATT ACTTctc--- ---------- ---CATTCAC TaaattttTT
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alignment
position         351....... 361....... 371....... 381....... 391.......
P855897      316 catttcttcc cgcaCATTTT TCTTCTTACT TATTTAAACT AAGCGTTTcc
P855898      342 TCATC----- ----CATTTC CCTCTTTAGT TCTTTCAGCT AGAACTTTAA
rNDUFS4      329 TCATC----- ----CATTTT CCTCCTTATT TCCTTTAACT AGAtCTTTTA
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alignment
position         401....... 411....... 421....... 431....... 441.......
P855897      366 cCTCTTTTTT TAAGCCCCAG TATTAAAAAG AAAATAAAat cccaaagaat
P855898      383 TTTCTTTTCT AGGTCCTCAA TCGCAAAAGG AAAACAAACA GAACATGcct
rNDUFS4      370 TCTCTTTTCT AGACTCTCAA TATCAAAAAG AAAACAAACA CAACATGatt
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alignment
position         451....... 461....... 471....... 481....... 491.......
P855897      416 ttcgcaacat tgcgattGCA CTGGCTTGAG AACGAAGGAA GTTAGTCCCT
P855898      433 ctgtttcacT GCGGCC-GCA TTGCTTTGAG AACGGAGGAA GTGAGTCCCT
rNDUFS4      420 tgtgtttt-T GCGGCC-GCA CTGCTTTGAG AACGAAGGAA GTGAGTCCCT
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alignment
position         501....... 511....... 521....... 531....... 541.......
P855897      466 TGCGGTGATC CGTCCTTTCA TCCTGGCGTT TGCCTGCAGC AAGATGGCGG
P855898      482 AGCGGGGATC CGTACTCGCA TCCTGGCGTT TGCCTACAGG AAGATGGCGG
rNDUFS4      468 AGCGGGGATC CGTACTCCCA TCCTGGCGTT TGCCCACAGG AAGATGGCGG
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alignment
position         551....... 561....... 571....... 581....... 591.......
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P855897     516 CGGTGTCAAT GTCAGTGGTA CTGAGGCAGA CGTTGTGGCG GAGAAGGGCA
P855898     532 CGGTCTCAAT GTCAGTGTCG CTGAGACAGG CGATGTTGGG GCGAAGGGCA
rNDUFS4     518 CGGTCTCAAT GTCAGTGTCG CTGAGACAGG CGTTGTTGAG GCAAAGGGCA
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alignment           
position        601....... 611....... 621....... 631....... 641.......

P855897     566 GTGGCTGTAG CTGCCCTTTC CGTTTCCAGG GTTCCGACCA GGTAATAGAA
P855898     582 ATGGCTACAG CTGCCGTTTC CGTCTGTAGA GTTCCATCCA GGTAACATAA
rNDUFS4     568 GTAGCTACAG CTGCGGTTTC CGTCTGCAGA GTTCCATCCA GGTAACATAA
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alignment
position        651....... 661....... 671....... 681....... 691.......

P855897     616 TTTTCACACT TTTC------ ----TTCAAG CTTCTTGGGT CCCTCCATTT
P855898     632 CTGTCAGCCT TGTCGAGCTA TTCATTCAGG GTTCCCAGGT CGCTCCACTT
rNDUFS4     618 TTGTCAGCCT aGTCGAGCTA TTCATTCAGG ATTCCCAGGT CGCTCCACTT
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alignment
position        701....... 711....... 721....... 731....... 741.......

P855897     656 TTGCGGAGTC TctGCTGGCT GAGTTCCGGA GGAGGCCTcg GGGAAGGCGT
P855898     682 TGGGGGAGGC TGGGCCGGCT GGGCCCCGGA GGCGGCCTT- GGGAACGCGT
rNDUFS4     668 TGGCGGGGGC CGGGCCTGCT GGGCCCTGGA GGCGGTCTT- GGGAACGCGT
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alignment
position        751....... 761....... 771....... 781....... 791.......

P855897     706 CCTCTGTTGA CCCTT----- ---------- ---------- ----------
P855898     731 CCTCCCTTGA CCCTTCCTCG GGATGCGGGG ACcGACGCTG GTTTCCGGCG
rNDUFS4     717 CCTCCTCTGA CCCTTCCTCG GGATGCGGGG ACgGACTCTG GTCTCCCGCA
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alignment
position        801....... 811....... 821....... 831....... 841.......

P855897     721 ---------- ---------- -TTCTCGGGA Gaagtcgggc ggactaggga
P855898     781 AGGCGCCTGC GGGGCCTGGG GTT------- ---------- ----------
rNDUFS4     767 AGGCGCCTAT GGAGCCTCGG GTTCTCGGGA Gccc------ ----------
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alignment
position        851....... 861....... 871....... 881....... 891.......
P855897     750 ctgtctgcta tcaatgggcg ttggccaggc gagtgagggc gtgagtgcga
P855898     804 ---------- ---------- ---------- ---------- ----------
rNDUFS4     801 ---------- ---------- ---------- ---------- ----------

alignment
position        901....... 911....... 921....... 931....... 941.......
P855897     800 ggccggggag gaggacctgt ggttttctgg aagctttcgt atTCGGCTTG
P855898     804 ---------- ---------- ---------- ---------- -------CTG
rNDUFS4     801 ---------- ---------- ---------- ---------- --TGGGTCTG
                                                              ********

alignment
position        951....... 961....... 971....... 981....... 991.......
P855897     850 TCGCTGAGGG A----GAGGG TCCGTGgagg ttttgcctcc GGAGCTGCAA
P855898     807 CAGCTGCGGa cgggcGAGGG TCTGTGCGGA ---------- GGAGCTGTGA
rNDUFS4     809 CAGCTGCGGG T----GAGGG TCTATGCGGA ---------- GGAGCTGTGA
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alignment
position        1001...... 1011...... 1021...... 1031...... 1041......
P855897     896 GCTGAACCTT AGCCCtcaGA GAAGGGGAGG AGTCTcactg atttctgttt
P855898     847 ACTGGATCGT GGCTCCT-GA GAAGGGGAGG AGTCTGGGCG ACCTCTCTCC
rNDUFS4     845 ACCGGACTGT GGCTCCT-GA GAAGGGGAGG AGTCTGGGCG ACTTCTCTCC
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alignment
position        1051...... 1061...... 1071...... 1081...... 1091......
P855897     946 ccactttC-T GCATCCCTTC CATTTGTCAC CTGTTTGCCC accactccag
P855898     896 CAATGTcC-T ACATCCCTTC CGCTTGTCAC CTGCTTGCCC CATTCCAGCC
rNDUFS4     894 CAATGTcctT GCATCCCTTC CGTTTGTCAC CTGTTTGCCC CATTCCAGCC
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alignment
position        1101...... 1111...... 1121...... 1131...... 1141......
P855897     995 tccttac--- ---------- ---------- ---------- ----------
P855898     945 TGAAAGGGTA AATCCCTGCT ATCCTTTCCC TGGCTTTAGT TaataTCGGC
rNDUFS4     944 TGAAAGGGTA AATCCCTGCT TTCCTTTCCC TGGCATTAGT TactgTCGAC
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alignment
position        1151...... 1161...... 1171...... 1181...... 1191
P855897    1002 ---------- ---------- ---------- ---------- ----
P855898     995 TGGGCTTCCA AACAGAAAGG TTGTTGTATT CATcattgtg cata
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```
rNDUFS4     994 TGAGCTTCTG AACAGAAAGG ATGTTGTATT CAT------- ----
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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.

	P855898 (1038 bp)	rNDUFS4 (1026 bp)
P855897 (1001 bp)	0.320 54 %	0.335 54 %
P855898 (1038 bp)		1.000 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: ☐ to: ☐
Output file	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 C1-NDUFS5 (3 seq.)

[Alignment] [Pairwise similarities]

DiAlign professional TF Release 3.1 December 2004 **Tue Jun 7 22:52:13 2005**

Solution parameters:

Sequence file:	C1-NDUFS5 (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	P914276	P914276 sym=NDUFS5|loc=Loc4725|taxid=9606|spec=Homo sapiens|chr=1|ctg=NT_004511|str=(+)|start=9463424|end=9464424|len=1001|tss=501|comm=NADH dehydrogenase (ubiquinone) Fe-S protein 5, 15kDa (NADH-coenzyme Q reductase); (NM_004552/501/bronze;)	1001 bp
2	mNDUFS5	mNDUFS5 m6_dna range=chr4:122744619-122745729 5'pad=0 3'pad=0 revComp=TRUE strand=? repeatMasking=none	1111 bp
3	P914277	P914277 sym=n|loc=Loc362588|taxid=10116|spec=Rattus norvegicus|chr=5|ctg=NW_047719|str=(-)|start=4185309|end=4186309|len=1001|tss=501|comm=similar to NADH dehydrogenase (ubiquinone) Fe-S protein 5; (XM_342907/501/bronze;)	1001 bp

Alignment (DiAlign format):

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

V$FKHD V$HOXF V$EGRF V$ETSF

```
alignment position 1 . . . . . . . . .   1 1 . . . . . . . .   2 1 . . . . . . . .   3 1 . . . . . . . .   4 1 . . . . . . . .
P914276          1 t g g c t a g g c c   t t c c c t g t g t   c t c t g t a a t t   g a t g g g t t t g   g g t t t t t t t t
mNDUFS5          1 T T A A A C C G A -   - - - - - - - - - -   - - - - - - - - - -   - - - - - - - - - -   - - - - - - - - - -
P914277          1 T T A A A C C G G -   - - - - - - - - - -   - - - - - - - - - -   - - - - - - - - - -   - - - - - - - - - -
                   * * * * * * * * *
                   * * * * * * * * *
                   * * * * * * * * *

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

```
P914276      51 cctttctctc tctctacctc ctctctctct tcttcatcct ctctctctca
mNDUFS5      10 ---------- ---------- ---------- ---------- ----------
P914277      10 ---------- ---------- ---------- ---------- ----------

alignment position 101....... 111....... 121....... 131....... 141.......
P914276     101 ctctccccct gagataaggt cttgctctgt tgccagggct ggaatgcaat
mNDUFS5      10 ---------- ---------- ---------- ---------- ----------
P914277      10 ---------- ---------- ---------- ---------- ----------

alignment position 151....... 161....... 171....... 181....... 191.......
P914276     151 ggaatggtgt gatcatggct cactacagcc tcaatctcct gggctcaaGG
mNDUFS5      10 ---------- ---------- ---------- ---------- --------GG
P914277      10 ---------- ---------- ---------- ---------- --------GG
                                                                    **
                                                                    **
                                                                    **

alignment position 201....... 211....... 221....... 231....... 241.......
P914276     201 GATCCTCCCA CCTCAACctc ctgagtagct ggaaccacag gcatgcacca
mNDUFS5      12 ACCTCTCCCA GATCAACAaA TGCTCTTAAC CTCTGAGCTG TCTCTCCA--
P914277      12 GCCTCTCCCA GAGCAACAcA TGCTCTTAAC CTCTGAGCTG TCTCTTCA--
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alignment position 251....... 261....... 271....... 281....... 291.......
P914276     251 cctcGCCCGG CTAATTTTTT ATTTtttgta gaga------ -----GGGGA
mNDUFS5      60 ----GCCCGG CTATTATGTT TATTACCAAA AAGGGAAACT GCCACcgtga
P914277      60 ----GCCa-G CCATTATGTT TATTATCAGA AAAGAAAACA GTCACGGAGA
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alignment position 301....... 311....... 321....... 331....... 341.......
P914276     290 GTTTCGCCA- -TGTTGCCCA GGCTGTtttc gaactcctgg gctgaa----
mNDUFS5     106 aactgggaaa cAGTCACACA AGTTTTGGGG TCACGGCACA CGAGCTTTAA
P914277     105 GATTGGGAG- -AGTCACCCA AGTTTTGGGG TCACGGCCCA CGAGCTTTAA
                *********   ********* ********** ********** **********
                            ********* ********** ********** **********
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alignment position 351....... 361....... 371....... 381....... 391.......
P914276     334 ---------- ---------- ---------- ---------- ------GTGA
mNDUFS5     156 tcaccacatt tcCTTGGGGT GAGGGAAGCA CTACTCTTTC TCGAGTGTGA
P914277     153 ccactacgtt ttCTTAGGGC GAGGGAAGCA ATACTCTTTC TCAAGTGTGA
                             ******** ********** ********** **********
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alignment position 401....... 411....... 421....... 431....... 441.......
P914276     338 TCTTCCTCcc ---------- ---------- ---------- ----------
mNDUFS5     206 CCTTGCTCAA GTAGCACAAC AATCAACGGT CACGACAGTG CTgaaaggga
P914277     203 CCTTGCTCAA GTAGCACAAC AATCAACTGT CATGACAGTG CTg-------
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alignment position 451....... 461....... 471....... 481....... 491.......
P914276     348 ---------- ---------- ---------- -----TCAGC CTTCCA----
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mNDUFS5        256 gaactcacta cCGGGCGCAG TAGTATG-GG GAAAGTCGGT TTATCagctg
P914277        246 ---------- -CTGGCACAG TAGCACGaGG AAAAGTCAGT TTATCC----
                               ********* ******* ** ********** ******

alignment position 501....... 511....... 521....... 531....... 541.......
P914276        359 ---------- -------AGG TGCTGGGATT GCAGACGTCA G-CCACcgta
mNDUFS5        305 tcagcgtctg gaggctgGGC TGCTTGCTGC GCAGGCGCAg acCCGCTGT-
P914277        281 ---------- -------GGC CGCTGGCTGC GCAGGCGCAA A-CCGCTCT-
                                     *** ********** ********** * ********
                                     *** ********** *********

alignment position 551....... 561....... 571....... 581....... 591.......
P914276        391 ccaggccaac ggGCTCGGTT TCTATGGTTt tgtggggaga cggctgaggg
mNDUFS5        354 ---------- --GCTTGGTT TCTACAGTTc ctc------- --GGCCGGT-
P914277        312 ---------- --GCTTGGTT TCCCTGGTTg ccgcagggac aaGGCCGGC-
                                ******** *********               ********
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alignment position 601....... 611....... 621....... 631....... 641.......
P914276        441 aaGGTCGGCT TCCGGCGTCG CGCTGC--AA ACGTCTCGCT GAGGTCATCC
mNDUFS5        382 --GGTTGATT TACGGCGTCG CTCTGG--AG ATGTCGtGCT GCGGGCGTCC
P914277        349 --GGTCGATT TACGGCGTCG CGCTctgtAG ATGTCGCACC GCGGGCGTCC
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alignment position 651....... 661....... 671....... 681....... 691.......
P914276        489 TTTACGGCAG GCGTCCGCGT Cgctagcta- --GTCGTTCT GAAGCGGCGG
mNDUFS5        428 TTTACGGCAG GCGTCTGCGT CCTCCcgcAG CCGGCGGTCG GGAATTGCa-
P914277        397 TTTACGGCAG GCGTCTGCGT CCTCCttaAG CCGGCGGTCG TGAGCTGCGC
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alignment position 701....... 711....... 721....... 731....... 741.......
P914276        536 CCAGAGAAGA GTCAAGGGCA CgaGCATCGG GTAGGTAGGG GCTGCTTATG
mNDUFS5        477 CCAGGGACCT GACAAGGGCA CT-GCAGAGG TGCGGTAGGC GC-TGCTGTG
P914277        447 CCAGGGACCT GAGAAGGGCA TT-GCTGAGG TGCGGTAGGC GCTTGCTGTG
                   ********** ********** ** ******* ********** **********
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alignment position 751....... 761....... 771....... 781....... 791.......
P914276        586 TCCGCGCGGC agcttagctt aaggaccttc cttccgaggt CTCTTTAACA
mNDUFS5        525 TCCGCACAGC CAAGAAGTTT CGTTCAGGAT TaG------- CTCCTTGACA
P914277        496 TCCGGTCAGC CAAGAAGGTT CGCTAGGGAT T-G------- CTCCTAGACA
                   ********** ********** ********** * *        **********
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                   ********** ********** ********** *          **********

alignment position 801....... 811....... 821....... 831....... 841.......
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P914276        636 GATTTCCTCT T---Ggcttg ctgtgtgtcc ccttctccca gacctgaacT
mNDUFS5        568 CATTTCCTCT CtctGTGGGT GGCCCAGG-- ---------- ---------T
P914277        538 AATTTCCTCT C---GTGGGT GACCCAGG-- ---------- ---------T
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                                  ****** ********                     *
                                  *

alignment position 851....... 861....... 871....... 881....... 891.......
P914276        683 CAGGGCGTGT TCCCTGCCCT CCCaggccgc t--------- ----TCACCT
mNDUFS5        597 CTGGGCGTGT CCTCCTGCCT TCCCTTCACC CCGTAACTAG GTCgTCACCC
P914277        564 CCGGGCGTGT CCTCCTGCCT TCCCTTCATC CCACAACTCG GTCc------
                   ********** ********** ********** ********** *** ******
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                   ********** ********** *****

alignment position 901....... 911....... 921....... 931....... 941.......
P914276        720 CCACagctaa tggcaccgaa gcctggagat tgccgctctc tccactttcc
mNDUFS5        647 CCACCCCCGG CCCTCCGGAG CAAATCCACC G--------- ----------
P914277        608 ---CCTCCAG CCCTCCAGAG TGATTCCGCC C--------- ----------
                   ********** ********** ********** *
                      ******* ********** ********** *

alignment position 951....... 961....... 971....... 981....... 991.......
P914276        770 acatttgttt aggttTTTGC CGGACTAATG TTTTGGCTTT CTgtttctta
mNDUFS5        678 ---------- -----TCTGC CGGACTCCTG CCTTGGCCTC CTTCCTACCC
P914277        636 ---------- -----TCTGC CGGACTCCTG CCTTGGCCTC CTTCCTACCC
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                                              ***** ********** **

alignment position 1001...... 1011...... 1021...... 1031...... 1041......
P914276        820 acctaaagtc tacgatcctt atcccagctt tccaggctct gcgtgatttc
mNDUFS5        713 TGACATCCCG CTCCTttttg TTTTTGTTTT GAGACAGGGT TTCTCTGTGT
P914277        671 TGACATCCCG CTCCT----- TTTTTGTTTT GAGACATGGT TTTTCTGTGT
                   ********** *****      ********** ********** **********
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alignment position 1051...... 1061...... 1071...... 1081...... 1091......
P914276        870 ggccc----- ---------- ---------- ---------- ----------
mNDUFS5        763 AG-----GCT GGAATTCACT CTGTAGACCA AGCTGGCCTT GAACTCAcag
P914277        716 AGccctgGCT GAAATTCATT GTATAGACCA AGCTGGCCTT GAACTCAacg
                   **     *** ********** ********** ********** *******
                   **     *** ********** ********** ********** *******
                   **     *** ********** ********** ********** *******
                   **     *** ********** ********** ********** *******

alignment position 1101...... 1111...... 1121...... 1131...... 1141......
P914276        875 ---------- ---------- ---------- ---------- ----------
mNDUFS5        808 -AGAAGCATC TGCCTCTGTC TTCCAAGTGT TGAGATTAAA GGCGTGCACC
P914277        766 tAGAAGCACC TGCCTCTGTC TCCCAAGGGT TGAGATTAAA GGCGTGCGCT
                    ********* ********** ********** ********** **********
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                    ********* ********** ********** ********** *
alignment position 1151...... 1161...... 1171...... 1181...... 1191......
P914276        875 ---------- ------CGCC GGCCTCCTGA GCTCATTTCA TTCTTttcac
mNDUFS5        857 ACATCCTGAT TTTGGTCCCC Agagccctct a-------CT TTCTTCCTG-
P914277        816 CCATACTGAT TTTGATCCCC AATCTCCTGA GACCTCTGCT TTCTTCCTG-
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alignment position 1201...... 1211...... 1221...... 1231...... 1241......
P914276        909 cgtcatgcac gctgcgctcc aTTGTCCCCC AAACATAGCC AGCACTTCCG
mNDUFS5        899 ---------- ---------- -TTGTGCACT TGGCTCAGCA GCCGCTCCAG
P914277        865 ---------- ---------- -TTGTGCACC TGACTGAGCA GCCGCTCCAG
                                           ********* ********** **********
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                                           ********* ********** **********
                                           ********* ********** **********

alignment position 1251...... 1261...... 1271...... 1281...... 1291......
P914276        959 GCTGT----- ---------- -----AACTC Cgggctgttg cccaactgga
mNDUFS5        928 agcctctgtc cgtcctcatt gtcatAACTT CTGTTGTCta tgtttGTGTG
P914277        894 ATTGG----- ---------- -----AACTT CTGTTGTCat tgcccGTGTG
                   *****                      ***** ********        *****
                                                                    *****

alignment position 1301...... 1311...... 1321...... 1331...... 1341......
P914276        989 acactctgcc cac------- ---------- ---------- ----------
mNDUFS5        978 TGTGTGTGTG TGTGTGTGTG TGTGTGTGTG TGtgtgtgtg agagagagag
P914277        924 CGCGTGTGTG CGTTTGCGTG CGTGTGTGCG TGctcgcgcg cgcaattgtg
                   ********** ********** ********** **
                   ********** ********** ********** **

alignment position 1351...... 1361...... 1371...... 1381...... 1391......
P914276       1002 ---------- ---------- ---------- ---------- ----------
mNDUFS5       1028 agagagagag agagagagag agagagagag agagcgagag agagagcgat
P914277        974 tgggt----- ---------- ---------- ---------- ----------

alignment position 1401...... 1411...... 1421...... 1431...
P914276       1002 ---------- ---------- ---------- -------
mNDUFS5       1078 gtagatcctc cTCTGGGACT TTTtctATTC TCCC---
P914277        979 ---------- -TCTGGGACT TTT---ATTC TCCCgag
                               ********* ***   **** ****
```

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.

	mNDUFS5 (1111 bp)	**P914277 (1001 bp)**
P914276 (1001 bp)	0.068 21 %	0.069 26 %
mNDUFS5 (1111 bp)		1.000 76 %

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

Extract alignment region	
Positions in alignment	from: ☐ to: ☐
Output file	dialign.seq

Extract aligned sequences

For comments, questions or bug reports, please contact support@genomatix.de

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GEMS Launcher Task: *DiAlign TF*: Multiple alignment plus TF sites
working on C1-NDUFS6 (3 seq.)

[Alignment] [Pairwise similarities]

DiAlign professional TF Release 3.1 December 2004 **Tue Jun 7 23:36:06 2005**

Solution parameters:

Sequence file:	C1-NDUFS6 (3 seq.)
Type of sequences:	nucleotide sequences
Threshold T:	0.00
'*' signs below alignment denote:	diagonal similarity (max. similarity is represented by 10 '*' signs)
Alignment output:	complete alignment is shown # nucleic acids per line: 50
TF output:	common TF matches located in aligned regions (common to 3 (100.0 %) sequences)
Family matches:	yes
MatInspector library:	Matrix Family Library Version 5.0 (February 2005)
Selected groups (core/matrix sim):	• ALL user_defined.lib (0.75/Optimized) • ALL vertebrates.lib (0.75/Optimized)

Aligned Sequences:

No.	Sequence Name	Sequence Description	Length
1	P878337	P878337 sym=NDUFS6|loc=Loc4726|taxid=9606|spec=Homo sapiens|chr=5|ctg=NT_006576|str=(+)|start=1791009|end=1792014|len=1006|tss=501,506|comm=NADH dehydrogenase (ubiquinone) Fe-S protein 6, 13kDa (NADH-coenzyme Q reductase);(AK022503/506/gold;NM_004553/501/silver;)	1006 bp
2	mNDUFS6	mNDUFS6 sym=mNDUFS6|chr=13|start=69383481|end=69384469|tss=519	989 bp
3	rNDUFS6	rNDUFS6 sym=rNDUFS6|chr=17|start=44230|end=45095|tss=420	866 bp

---

Alignment (DiAlign format):

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

V$NRF1 U$NRF1 V$YY1F V$RORA V$CMYB V$VMYB

```
alignment position 1.........  11.........  21.........  31.........  41.........
P878337          1 ----------  ----------  ----------  ----------  ----------
mNDUFS6          1 ttccggacag  cttttccaAT  GCTGGGTAAC  TTCCTTGCAG  TCTAACTGGA
rNDUFS6          1 ttttcc----  -------ATA  CTGGGAAAAC  TCCCTTGCAG  TCTAACTGGA
                                      ***  **********  **********  **********
                                      ***  **********  **********  **********
                                      ***  **********  **********  **********

alignment position 51.........  61.........  71.........  81.........  91.........
P878337          1 ----------  ----------  ----------  ----------  ----------
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```
mNDUFS6         51 AACTgaACTA CTGCAGCGTT GCAAAAATGC TCAGAAATCT aaCTTTCCTA
rNDUFS6         39 AACTttACTA CCGCTGCATT GCAAAAATGC TCTTAAGTCT tcCTTTCCCA
                   ****  **** ********** ********** **********   ********
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alignment position 101....... 111....... 121....... 131....... 141.......
P878337          1 ---------- ---------- ---------T GCACTTCCAG TCTCGTCTGC
mNDUFS6        101 CACCAACATA CAGGACCAGG AGAGTTGACT GCacaaactG TTTCTTCTGC
rNDUFS6         89 CCCCAACATA CATAGCTAGG AAAGTTGACT GCATGTACTG GTTCTTCTAT
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                   ********** ********** ********** **          *********
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alignment position 151....... 161....... 171....... 181....... 191.......
P878337         22 TAAGCAGTTG ACTCCTTCAC CCAAtaattt tgatatttaa atgtctcatg
mNDUFS6        151 TGAACAACTT ACTTCTTTAC TCAAAACAAA acagaaaaca aaaaacaaac
rNDUFS6        139 TGAACAAGGT ATTTCTTTAC TGAAAACAAA taaaatct-- ----------
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alignment position 201....... 211....... 221....... 231....... 241.......
P878337         72 a--------- ---------- --TTATCGGT TACCATAAGA ATATAAACAA
mNDUFS6        201 caacccacGG AAAATCTGCA TTTTCTCCAT TGGCATAAAA GCACACACAG
rNDUFS6        177 --------GG GAAATCTGCA TTTTCTCCAT TGCTATAAAA GTGCACAC--
                           ** ********** ********** ********** **********
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alignment position 251....... 261....... 271....... 281....... 291.......
P878337        101 TGTATTTTCA GTTTACATCC t-----CCCC TGCCTgtccg ctaaataaga
mNDUFS6        251 CGCATCTTCA GTTTCCGTCC ccccacCCCC TGCCTTTGTC ACACTAGTAA
rNDUFS6        217 TGCATCTTCA GTTTTCATCC ---------- ---CTTTGTC ACGTTAGTAA
                   ********** **********       **** ********** **********
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alignment position 301....... 311....... 321....... 331....... 341.......
P878337        146 accactgggt actcctaatc gctgaaggtt tcgcacacca ttgcctgcct
mNDUFS6        301 CCTTTGAACA CT-------- ---------- ---------- ----------
rNDUFS6        254 ACTTTGAACA CG-------- ---------- ---------- ----------
                   ********** **
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                   ********** **

alignment position 351....... 361....... 371....... 381....... 391.......
P878337        196 catcagggcc ctagctctag cctgcggctg caactgcatg aggctgcacc
mNDUFS6        313 ---------- ---------- ---------- ---------- ----------
rNDUFS6        266 ---------- ---------- ---------- ---------- ----------

alignment position 401....... 411....... 421....... 431....... 441.......
P878337        246 tgccggcgca acggggccgc ttaactttta ggccattgat gaaaagtcaa
mNDUFS6        313 ---------- ---------- ---------- ---------- ----------
rNDUFS6        266 ---------- ---------- ---------- ---------- ----------

alignment position 451....... 461....... 471....... 481....... 491.......
P878337        296 acaaGCGCAC AGTactcggt gtaatcaggg gcatttttag cgagatacct
mNDUFS6        313 ----GCGCAC AGTTAAGCC- ---------- ---------- ----------
rNDUFS6        266 ----GCGCAC AGTTAAGCT- ---------- ---------- ----------
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alignment position 501....... 511....... 521....... 531....... 541.......
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P878337        346 gggatgaaaa cgggtgacca cctgaatcag agaGCAGCTC CGgcg-----
mNDUFS6        328 ---------- ---------- ---------- ---GCAGCTC CGCATCCTAT
rNDUFS6        281 ---------- ---------- ---------- ---GGAGCTC AGTATCCCCG
                                                      ******* **********

alignment position 551....... 561....... 571....... 581....... 591.......
P878337        391 -------CAC CCTCTGCCCC Gac-----CC GCGCTCCCCG CCCCCAGGGC
mNDUFS6        345 CCAGTTCCAC CACCAGCCCC G--------C CAGCCGCTCA GGCATAGGAC
rNDUFS6        298 TCAGGTCTAG CACCTACCCg gccagccgCC CAGCCGCTCA GCCACAGTAC
                   ********** ********** *       ** ********** **********
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alignment position 601....... 611....... 621....... 631....... 641.......
P878337        429 GAAATAAATA CCgggtgttt ggCGCCGCCA GAAGCCGTGC GCATGCGTTA
mNDUFS6        387 GAAAAAAGTT CCACAAGtAC T-CCCCGCCG ACTGCTGTGC GCCTGCGCCG
rNDUFS6        348 GAAAAAAGTT CCACAAGcAC T-CCCGGCCG AATGCTGTGC GCCTGCGCCG
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                   ********** *******      ******** ********** **********

alignment position 651....... 661....... 671....... 681....... 691.......
P878337        479 GCGCTaagCG GGACGTTGCG CCGGGTCAAA GGCCAGCGgc GCAAAATGGC
mNDUFS6        436 GCACTt---G GTACGACGCG TGGGGTCAAG GGTCACCG-- GCAAGATGGC
rNDUFS6        397 GCGCT---CT GTACGACGCG TGGGGTTAAG GGTCGTCG-- GCAAGATGGC
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alignment position 701....... 711....... 721....... 731....... 741.......
P878337        529 GGCGGCGATG ACCTTCTGCC GGCTGCTGAa ccggtgtggc gaggcggcgc
mNDUFS6        481 GGCGGTGCTG ACCTTCCGCC GGCTGTTGAC TCTC------ ----------
rNDUFS6        442 GGCGGCGCTG ACCTTCCGCC GGCTGTTGgC TCTC------ ----------
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alignment position 751....... 761....... 771....... 781....... 791.......
P878337        579 ggagcctgCC CCTGGGCGCC AGGTGTTTCG GGGTGCGGGT CTCGCCGAcC
mNDUFS6        515 --------CC CAGGGCTGCA CGGGGTTTCG GGGTTCAAGT GTCGCCGAGC
rNDUFS6        476 --------CC TAGGGCTGCC CGGGGCTTCG GGGTGCGAGT GTCGCGGAGC
                           ** ********** ********** ********** **********
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alignment position 801....... 811....... 821....... 831....... 841.......
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P878337        629 GGGGAGAAGG TCACGCACAC TGGCCAGGTA ACGGCCGCtg gg--------
mNDUFS6        557 GGGGAAAAGA TCACGCATAC CGGCCAGGTA ACGGCCGCGC CCGCCATGCC
rNDUFS6        518 GGGGAGAAGA TCACGCATAC CGGCCAGGTA ACGGCCGtGC CCGCCATGCC
                   ********** ********** ********** ********** **********
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alignment position 851....... 861....... 871....... 881....... 891.......
P878337        671 ---------- ---------- ---------- ---------- ----------
mNDUFS6        607 TGGAACCCAA GACTGACGGT AGCAGGGAgc gcaGCAAGGT GTGCTTCTGC
rNDUFS6        568 TGGAACCCGA GACTGACGGT AGCAGGGAgc gtgGCAAGGT GTGCTTCTGC
                   ********** ********** ********      ******* **********
                   ********** ********** ********      ******* **********
                   ********** ********** ********      ******* **********
                   ********** ********** ********      ******* **********
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alignment position 901....... 911....... 921....... 931....... 941.......
P878337        671 ---------- --------TA CAGGATGCAC CTTC---CTC CAGCCGCA--
mNDUFS6        657 CAGGCTAGCG CGCGGCaCTA CTGGGCTCAC CTTG---TGC AACCCGCT--
rNDUFS6        618 CAGGCTAGCG CGCGGCcCTA CTGGACTCAC CTTGgggTGC AGCCCGCTgc
                   ********** ****** *** ********** ****   *** ********
                   ********** ******
                   ********** ******
                   ********** ******

alignment position 951....... 961....... 971....... 981....... 991.......
P878337        698 ---CCTCGGG cg----ACTG GTGGCagtgg gctcgccggg catccgcggc
mNDUFS6        702 ---GCTCCGG TTTCTAGCTG GTGGCTTTcg gtT------- ----------
rNDUFS6        668 ccaGCTCTGA TTTCTAACTG GTGGCTTTgc c-T------- ----------
                      ******* ********** ********     *
                      ******* ********** ********     *
                                                      *

alignment position 1001...... 1011...... 1021...... 1031...... 1041......
P878337        741 cctggttctg cgccggcagc gcaggtcgtg gtaaggttgt gctgtcgctc
mNDUFS6        732 ---------- ---------- ---------- ---------- ----------
rNDUFS6        700 ---------- ---------- ---------- ---------- ----------

alignment position 1051...... 1061...... 1071...... 1081...... 1091......
P878337        791 acgcgccggg gaggacgccc gcgagtcggg acggtggtgg cagcctgtag
mNDUFS6        732 ---------- ---------- ---------- ---------- ----------
rNDUFS6        700 ---------- ---------- ---------- ---------- ----------

alignment position 1101...... 1111...... 1121...... 1131...... 1141......
P878337        841 cggtgggtct cgtccttcca gggcctgcgg gctctggaac gggaagtctc
mNDUFS6        732 ---------- ---------- ---------- ---------- ----------
rNDUFS6        700 ---------- ---------- ---------- ---------- ----------

alignment position 1151...... 1161...... 1171...... 1181...... 1191......
P878337        891 cccagcgggc agcacttgct gtggactggc tgcccatagG CGATTTGTGG
mNDUFS6        732 ---------- ---------- ---------- ---------G GGACTTGGAT
rNDUFS6        700 ---------- ---------- ---------- ---------G GGACTTGGAT
                                                            * **********
                                                            * **********
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alignment position 1201...... 1211...... 1221...... 1231...... 1241......
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P878337        941 CAGCCGATTA TTTGGGTCAG AACGTTtaga atttgtgtaa tattcaATAA
mNDUFS6        743 CTCCTCATTC TTTAGGCCAT ATCTTT---- ---------- ------ATAT
rNDUFS6        711 CTGCTCATTC TTTAGGTCAT AACTTT---- ---------- ------ATAA
                   ********** ********** ******                       ****
                   ********** ****** *** ******                       ****
                   ********** ****** *** ******

alignment position 1251...... 1261...... 1271...... 1281...... 1291......
P878337        991 TAAATTttag taacct---- ---------- ---------- ----------
mNDUFS6        773 TAAGTTCAAT GTTTTAACAA atgattgtTG TGTTTTGGAC CCGGGACaga
rNDUFS6        741 TAAGTTCCAA GTTTTAAGAA tggttg--TG TTTTTAGACC CCGGGACtgg
                   ********** **********         ** ********** *******
                   ********** **********

alignment position 1301...... 1311...... 1321...... 1331...... 1341......
P878337       1007 ---------- ---------- ---------- ---------- ----------
mNDUFS6        823 gGACTGAGGT GCATATTTTA CATATCAAAG GAGACCcGGC ATGCAGGTTC
rNDUFS6        789 aGACTGAGGT GCATATTTTA CATATCAAAG CAGACCtGGC ATCCAGGTTC
                    ********* ********** ********** ****** *** **********
                    ********* ********** ********** ****** *** **********
                    ********* ********** ********** ****** *** **********
                    ********* ********** ********** ****** *** **********

alignment position 1351...... 1361...... 1371...... 1381...... 1391......
P878337       1007 ---------- ---------- ---------- ---------- ----------
mNDUFS6        873 TCCCAGCATT CCTCAGTCCC TACCTGGcgt tgcagcccag gatcctccct
rNDUFS6        839 TCCCAGCATC CCTCAGTCCC TACCTGGc-- ---------- ----------
                   ********** ********** *******
                   ********** ********** *******
                   ********** ********** *******
                   ********** ********** *******

alignment position 1401...... 1411...... 1421...... 1431...... 1441......
P878337       1007 ---------- ---------- ---------- ---------- ----------
mNDUFS6        923 atataatcca ggcattttgg tttctcccac cctgtctctt tctcctctcc
rNDUFS6        867 ---------- ---------- ---------- ---------- ----------

alignment position 1451...... 1461...
P878337       1007 ---------- -------
mNDUFS6        973 ttgaacacac tcccttt
rNDUFS6        867 ---------- -------
```

Pairwise similarities:

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

	mNDUFS6 (989 bp)	rNDUFS6 (866 bp)
P878337 (1006 bp)	0.150 31 %	0.155 30 %
mNDUFS6 (989 bp)		1.000 81 %

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

Extract alignment region	
Positions in alignment	from: to:

Output file	dialign.seq

Extract aligned sequences

For comments, questions or bug reports, please contact support@genomatix.de

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

[Alignment] [Pairwise similarities]

DiAlign professional TF Release 3.1 December 2004 **Tue Jun 7 23:49:38 2005**

Solution parameters:

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

Aligned Sequences:

No.	Sequence Name	Sequence Description	Length
1	P968931	sym=NDUFS7|loc=Loc374291|taxid=9606|spec=Homo sapiens| chr=19|ctg=NT_011255|str=(+)|start=1323383|end=1324406| len=1024|tss=501,507,521,524| comm=NADH dehydrogenase (ubiquinone) Fe-S protein 7, 20kDa (NADH-coenzyme Q reductase); (AK092169/501/gold;AK091623/521/gold;AK128713/507/gold; NM_024407/524/bronze;)	1024 bp
2	P968933	sym=Ndufs7|loc=Loc75406|taxid=10090|spec=Mus musculus| chr=10|ctg=NT_039496|str=(+)|start=6105465|end=6106465| len=1001|tss=501| comm=NADH dehydrogenase (ubiquinone) Fe-S protein 7; (NM_029272/517/bronze;)	1001 bp
3	P968934	sym=na|loc=Loc362837|taxid=10116|spec=Rattus norvegicus| chr=7|ctg=NW_047773|str=(-)|start=10970711|end=10971711| len=1001|tss=501| comm=similar to NADH dehydrogenase (ubiquinone) Fe-S protein 7; (XM_343165/511/bronze;)	1001 bp

Alignment (DiAlign format):

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

V$GATA V$VMYB V$RORA V$NRF1 U$NRF1 V$TEAF V$DEAF V$LTUP V$FKHD V$IRFF V$ETSF V$BARB
V$PCAT V$HAML V$MINI V$EKLF V$GLIF V$YY1F

```
alignment position 1.........  11.........  21.........  31.........  41.........
P968931          1 ---------- ---------- ---------- ---------- --AGGGACCT
P968933          1 gtt aaaaaca ct-------- TGCCGAAACC CGGGATCGAA CCAGGGACCT
P968934          1 gtc gatggga taaaaacctc TGCCGAAACC CGGGATCGAA CCAGGGACCT
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                                                                 ********

alignment position 51........ 61........ 71........ 81........ 91........
P968931          9 TTAGATCTTC AGTCTAACGC TCTCCCAACT GAGCTATTTC GGCTGggcgg
P968933         43 TTAGATCTTC AGTCTAACGC TCTCCCAACT GAGCTATTTC GGCgacgcgc
P968934         51 TTAGATCTTC AGTCTAACGC TCTCCCAACT GAGCTATTTC GGCTGcgtga
                   ********** ********** ********** ********** *****
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alignment position 101....... 111....... 121....... 131....... 141.......
P968931         59 cagagtcgct ctcgccg-GG ACTCCGTCCC GCGCTGCGCC TTCCCTGCGC
P968933         93 tgtttgtcgg taacaccctc cCTCCGCCCC GTGCCATTGC TTTAGCGCGC
P968934        101 aggacgtcag cactgctcGG TCTCCGCCCC GTGCCATTGC TCCTGTGCGC
                                      ** ********** ********** **********
                                          ********* ********** **********
                                          ********* ********** **********

alignment position 151....... 161....... 171....... 181....... 191.......
P968931        108 AGGCGCAGTc gtttcgcgtc agcaggcccc acatcctttg taaggtctcc
P968933        143 AAGCGCACTT Cacaatttgt ctGTCAAACC TTGTAGGGTT ATACTATAAG
P968934        151 AAGCGCACTT Cacacttcat gaGTTAAACC TCGTAGGTTT ATACTATAGA
                   ********** *            ******** ********** **********
                   ********** *
                   ********** *

alignment position 201....... 211....... 221....... 231....... 241.......
P968931        158 cagggcgccg gagcgcagTG TCGTCTCTGT GGCGCAATCG GTTAGCGCGT
P968933        193 CAGCTgactA A-------TG TCGTCTCTGT GGCGCAATCG GTTAGCGCGT
P968934        201 AAGCTtcacA A-------TG TCGTCTCTGT GGCGCAATCG GTTAGCGCGT
                   *****    * *       ** ********** ********** **********
                            * *       ** ********** ********** **********
                            * *       ** ********** ********** **********
                            * *       ** ********** ********** **********
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                                      ** ********** ********** **********
                                      ** ********** ********** **********

alignment position 251....... 261....... 271....... 281....... 291.......
P968931        208 TCGGCTGTTA ACCGAAAGGT TGGTGGTTCG AGCCCACCCA GGGACGcgtg
P968933        236 TCGGCTGTTA ACCGAAAGGT TGGTGGTTCG AGCCCACCCA GGGACGacca
P968934        244 TCGGCTGTTA ACCGAAAGGT TGGTGGTTCG AGCCCACCCA GGGACGacta
                   ********** ********** ********** ********** *******
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                   ********** ********** ********** ********** ******
alignment position 301....... 311....... 321....... 331....... 341.......
P968931        258 --GTGA-CTT TTGCCCTCCT GGAATAACAA GAAAATGAGT GTcgcctctg
P968933        286 caGCGA-CTT TTTCATTCCC TAATACTGAA TAAAGTGGAA GTTCTTTA--
P968934        294 tgattcgCCT TTTTGTCCCC TAATt-TGAG TAAAATAGAA GTTTTTTC--
                     **** *** ********** ********** ********** ********

alignment position 351....... 361....... 371....... 381....... 391.......
P968931        305 tTTTTGTCGg tccgccgcag acccgcggcc cccacgt--G CGCACTCcga
P968933        333 -TTTTGTCGc TGTTTCCTGT TTGTCACAGG ACGACCGTGG CGCACTCTGC
P968934        341 -TTTTGTC-- TGTTTCCTGT TTGTCACAGG AGGACGGTTG TGTACACTGC
                    ********  ********** ********** ********** **********
                              ********** ********** ********** **********

alignment position 401....... 411....... 421....... 431....... 441.......
P968931        353 tgacctttcc gcctcgggtg atctgggggt gcacggcgca ACACGACCAC
P968933        382 gCGG------ ---------- ---------- ---------- ACGCGACCAC
P968934        388 tCGG------ ---------- ---------- ---------- GCGCGATCAC
                    ***                                       **********
                    ***                                       **********

alignment position 451....... 461....... 471....... 481....... 491.......
P968931        403 ggaggccgAA AGCGCAGCGG AACCTCCCGG CTCCAGGTTC CGGTTTCCgc
P968933        396 AGGTAT--AA AGCGGGTCAG AACCACTCGG CTTGTGGTGC GGGTTTCCGC
P968934        402 AGGAAA--AA AGCGGGTCGG AACCGCTCAG TTTGTGGTTC CGGTTTCCGC
                   ******  ** ********** ********** ********** **********
                   ******  ** ********** ********** ********** **********
                           ** ********** ********    ********* **********
                                                     ********* ********
                                                     ********* ********

alignment position 501....... 511....... 521....... 531....... 541.......
P968931        453 atgcgctccg agccgcTTTG GGCGGCGGCC CCGggaacCC GGAGCGCTAA
P968933        444 TGGTGTCTA- ------TTTG GGCGTTGGac tAGAA---CC GGAACTCTTT
P968934        450 TGGTGTCTA- ------TTTG GGCGTTGGAC CAGAA---CC GGAACTCTTT
                   *********        **** ********** *****   ** **********
                   *********        **** ********    ****   ** **********
                   *********        **** ********    ****   ** **********
                                                            ** **********
                                                            ** **********

alignment position 551....... 561....... 571....... 581....... 591.......
P968931        503 GGAGAACGGA CCTCAGAGGT TGTCTGAAGG CCGAGGCCAA GATGGCGGTG
P968933        484 GGAGGACGGA CCGCAGAGGT TGTCTGAAGG CCGAGGCCAA GATGGCGGCG
P968934        490 GGAAGACGGA CCGCAGAGGT TGTCTGAAGG CCGAGGCCAA GATGGCGGCG
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alignment position 601....... 611....... 621....... 631....... 641.......
P968931        553 CTGTCAGGTG AGcgcggcac cggcggcggg tgtggggccg cgcgggtctg
P968933        534 CTGGCGGGTG AGTGaagccc tTGCGGTC-- ---------- ----------
P968934        540 CTGGCGGGTG AGTGaagatc -TGAGATC-- ---------- ----------
                   ********** ****        *******
                   ********** ****        *******
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                   ********** **
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                   ********** **

alignment position 651....... 661....... 671....... 681....... 691.......
```

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P968931        603 gggccgtggg agcctcgGGT GTCGTGGTGG CGTCGGGGGt cggtgccggc
P968933        562 ---------- -------GGG AGAGTGGCGT AGTCCTGGG- ----------
P968934        567 ---------- -------GGG GTAGTGGCGC AGTCCTGGG- ----------
                              *** ********** *********
                              *** ********** *********

alignment position 701....... 711....... 721....... 731....... 741.......
P968931        653 gtcgtggccg cggtcctctc cgggcttCTC CGAGCCGGCc gct------C
P968933        584 ---------- ---------- -------CTC CGAGCTGGCg ctgCGGGGAC
P968934        589 ---------- ---------- -------CCT CGAGCTGGgc tt-CGGGGAC
                                                *** *********     *******
                                                *** ********      *******
                                                                  *******

alignment position 751....... 761....... 771....... 781....... 791.......
P968931        697 CTCGGGCTCC CCGCCCGGct tgcgatgaac ggtcgccgtt attgcgt---
P968933        607 CTTGGAGCCC AAGCCTAGTG TTGAGAGGCG TTGggaccgt --AGAGACCT
P968934        611 CTTGGAGCCC AAGCCCGGTA TTGACAGGCG TTGggatcgc agAGAGACCT
                   ********** ********** ********** ***          ********
                   ********** ********** ********** ***          ********
                   ********** ********** ********** ***          ********

alignment position 801....... 811....... 821....... 831....... 841.......
P968931        744 ---------- ---------- ---------- ---------- ----------
P968933        655 ATAGGTCAGA TCCCAGCCCT CGGTAATGTC GGtgTCTAGC ATTAGGCCGA
P968934        661 ATAGGTCAGA ACCCAGCCCG CGATAGTGTC GGgaTCTAGG ATTGGGCCGA
                   ********** ********** ********** **  ****** **********
                   ********** ********** ********** **  ****** **********
                   ********** ********** ********** **

alignment position 851....... 861....... 871....... 881....... 891.......
P968931        744 ---------- ---------- ---------- ---------- ----------
P968933        705 AGCATGTTTG AATTCACgtt ACACAGTTCT GCATGGTCTA CATAGCAAGT
P968934        711 AGTGTGTTTG AATCCACttc ACACAGTTAT GTCTGGTCTA CCTAGCAAGT
                   ********** *******    ********** ********** **********
                   ********** *******    ********** ********** **********

alignment position 901....... 911....... 921....... 931....... 941.......
P968931        744 ---------- ---------- -CCAGAGTAC AGTCGGGGAA ACCGAGGCCC
P968933        755 TGCAGGCCTC ctgctatcgt cCCTGATTAT AGTCGGGAAC GCTGAGGCCT
P968934        761 TCCAGGCCTC ccattactgc agCAGATTGT AGTTGTGGAC GCTGAGGCCT
                   **********             ********* ********** **********
                   **********                     * ********** **********

alignment position 951....... 961....... 971....... 981....... 991.......
P968931        773 Ggtaggtcat gacgcaagcc tccagcctca ggaaggcgCT CGGGGTGGAG
P968933        805 GTGTATCTTC CAAC------ ---------- --------CT CAGgaagCTG
P968934        811 GTATATCTCT CAAT------ ---------- --------CT CAGGAGACTG
                   ********** ****                          ** **********
                   ********** ****                          ** ***    ***

alignment position 1001...... 1011...... 1021...... 1031...... 1041......
P968931        823 GCTGGAGGGG CCCCATTCAC GTCCCCGAga ccagggcacg gcccgcgagg
P968933        831 ACTGCAGAAA CCCGGCTGAT GTCCCCGAAG CACAGAgtgg gaca------
P968934        837 ATTGCAGGAG CCCAGCTAAT GACCCTGAAG CTCAGAcag- ----------
                   ********** ********** ********** ******
                   ********** ********** ********** ******

alignment position 1051...... 1061...... 1071...... 1081...... 1091......
P968931        873 ctgctcttga gatgccctgg agagagcggg gcctgcctga caggctggga
P968933        875 ---------- ---------- ---------- ---------- ----------
P968934        876 ---------- ---------- ---------- ---------- ----------

alignment position 1101...... 1111...... 1121...... 1131...... 1141......
P968931        923 aactgaggcc cattgagggt cttcgaggtc acagggccgg gccTGGGAAG
P968933        875 ---------- ---------- ---------- ---------- ---------G
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P968934        876 ---------- ---------- ---------- ---------- ---TGGGACG
                                                                  *******
                                                                        *

alignment position 1151...... 1161...... 1171...... 1181...... 1191......
P968931        973 GAACAGGACC CAGGACATCC ACGCCACCCT GCTGGACCCT Ccacctccct
P968933        876 GGGAGAGGCC CAGGACACTT AGGCCACCCA CCCGGTGGCT CTTTCCATCT
P968934        883 GGAAGAGGCC CAGGACACTC AGGGCACTCA CCCtGTGGCT CTTTCACCTT
                   ********** ********** ********** ********** **********
                   ********** ********** ********** *** ****** **********
                         **** ********** *********

alignment position 1201...... 1211...... 1221...... 1231...... 1241......
P968931       1023 cc-------- ---------- ---------- ---------- ----------
P968933        926 CATCCCCAAC CTGGACAGCT AGcaagggcc tcTAGAGCAG ATGTCTTAGT
P968934        933 CATCACCGCC CTGGACAGCT AGggcaat-- --TAGAGCAG ATGCCTCAAT
                   ********** ********** **           ******** **********
                   ********** ********** **           ******** **********

alignment position 1251...... 1261...... 1271..
P968931       1025 ---------- ---------- ------
P968933        976 TTCCCTGCCA AAGCTTTGGT GTcttt
P968934        979 TTCCCTGCCG AAGTTATGGT GTc---
                   ********** ********** **
                   ********** ********** **
```

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.

	P968933 (1001 bp)	**P968934 (1001 bp)**
P968931 (1024 bp)	0.348 38 %	0.345 36 %
P968933 (1001 bp)		1.000 76 %

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

Extract alignment region	
Positions in alignment	from: ☐ to: ☐
Output file	dialign.seq

Extract aligned sequences

For comments, questions or bug reports, please contact support@genomatix.de

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

[Alignment] [Pairwise similarities]

DiAlign professional TF Release 3.1 December 2004 **Wed Jun 8 00:24:29 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)
Selected groups (core/matrix sim):	• ALL user_defined.lib (0.75/Optimized) • ALL vertebrates.lib (0.75/Optimized)

Aligned Sequences:

No.	Sequence Name	Sequence Description	Length
1	P855978	sym=NDUFS8|loc=Loc4728|taxid=9606|spec=Homo sapiens|chr=11|ctg=NT_033903|str=(+)|start=13103404|end=13104475|len=1072| tss=501,572| comm=NADH dehydrogenase (ubiquinone) Fe-S protein 8, 23kDa (NADH-coenzyme Q reductase); (AK002110/572/gold;NM_002496/501/silver;)	1072 bp
2	P855979	sym=Ndufs8|loc=Loc225887|taxid=10090|spec=Mus musculus|chr=19|ctg=NT_082868|str=(-)|start=700730|end=701730| len=1001|tss=501| comm=NADH dehydrogenase (ubiquinone) Fe-S protein 8; (NM_144870/536/bronze;)	1001 bp
3	P855980	sym=na|loc=Loc293652|taxid=10116|spec=Rattus norvegicus|chr=1|ctg=NW_047563|str=(-)|start=14967775|end=14968775| len=1001|tss=501| comm=similar to NADH dehydrogenase:ubiquinone Fe-S protein 8; (XM_215197/501/bronze;)	1001 bp

Alignment (DiAlign format):

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

V$ETSF V$SP1F V$NRSF V$YY1F V$MYT1 V$ECAT V$PCAT V$SF1F V$NRF1 U$NRF1 V$HOXF V$HOMF V$NKXH

```
alignment position 1.........  11.........  21.........  31.........  41.........
P855978          1 aaattcgctg  gtaggaaaca  taggctggtt  gagtacggga  gt--------
P855979          1 catgtccttc  ctggccttcc  agattctaca  ccgccagctt  agacACTACT
P855980          1 ----------  ----------  ----------  ----------  ----ACTATT
```

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                                                                 ******

alignment position 51........ 61........ 71........ 81........ 91........
P855978         43 ---------- ---------- --------CA TACAGATCAG GTGGATcagg
P855979         51 TCCTGAAGGA AGCATTTC-T GATCACTCCA TACAAGGCAT GCAGAT----
P855980          7 CCCTAAGGGA AGCCTTCCcT GATCACTCCA TACAAGACAT GCGGAT----
                   ********** ******** * ********** ********** ******
                                       * ********** ********** ******
                                       * ********** ********** ******
                                       * ********** ********** ******
                                       * ********** ********** ******

alignment position 101....... 111....... 121....... 131....... 141.......
P855978         65 cggccgcaca ccgcagctct acggcccggg aacgttacta aatactccca
P855979         96 ---------- ---------- ---------- ---------- ----------
P855980         53 ---------- ---------- ---------- ---------- ----------

alignment position 151....... 161....... 171....... 181....... 191.......
P855978        115 TGCCTCAGCT TCCCGCCTTA ACGTGGTAAC ACGTTACtgt agtttctCCA
P855979         96 TGCCTCATGG TTCtCTAGTC CTAGGGGCAG ACTTGACAAA AgTCCTGCTA
P855980         53 TGCCTCATGG TTCCCTAGTC CCAGGGGCAG ACTTGACAAA AaTCCTGCTA
                   ********** ********** ********** ********** * ********
                   ********** *** ****** ********** ********** * ********
                   ********** *** ****** ********** ********** * ********
                   ********** ***                                ********
                   ********** ***                                ********

alignment position 201....... 211....... 221....... 231....... 241.......
P855978        165 CGCAGAGCTG CTGTGAGGAT TAAAAGAGGC CGCGTgagtt gagcatc---
P855979        146 CCCGCGGCCG TTACAAGGAC CAGtg----- ------GTTA AAGCGCTTGT
P855980        103 CCCGCGGCCG TTACAAGGAC CAGAAGAAGC CAAGTaGTTA AAGAGCTTAT
                   ********** ********** ********** ***** **** **********
                   ********** ********** ***              **** **********
                   ********** ********** ***              **** **********
                   ********** ********** ***              **** **********
                   ********** ********** ***

alignment position 251....... 261....... 271....... 281....... 291.......
P855978        212 ------TCGT CGCCATTACC GTCATCACAC GCCCCCCACC CAACCCggcg
P855979        185 ACGCTGTCGC CATCTTTGCA GTATTCAAAT GAGCCCTACC CCTCCCGCCT
P855980        153 GAGCTGTCGC CATCTTTGCA GTATTTAAAT GAGCCCCACC ATTCCCTCCC
                   ********** ********** ********** ********** **********
                   ********** ********** ***** **** ********** ******
                   ********** ********** *****
                   ********** ********** *****

alignment position 301....... 311....... 321....... 331....... 341.......
P855978        256 ggcccaccct ctgcacccac ggcgaaagca ctctttCTAA ACCACGCCCC
P855979        235 CCCcggactg tag--CAGCG TC-------- ------CCAA ACCGAGGTCA
P855980        203 CTCccggaaa tgtacCAGCG TC-------- ------CCAA ACCGAGCTCA
                   ***             ***** **               **** **********
                                   ***** **               **** **********
                                   ***** **               **** **********
                                   ***** **               **** **********
                                   ***** **               **** **********
                                                          **** **********
                                                            ** **********
                                                            ** **********

alignment position 351....... 361....... 371....... 381....... 391.......
P855978        306 GGATGTCCCG CCTCCAGCGG CTCGGAggtc ttcactTATT GGCCTCCCCA
P855979        269 GGAAGTCCCG CCTTCAGGAT CTCGGAAGTC AGGCG-CATT AACCTCTCTG
P855980        239 GGAAGTCCCG CCTTCAGCAT CTCGGAAGTC AGGCG-TATT AACCTCTCCG
                   ********** ********** ********** ***** **** **********
                   ********** ********** ********** ***** **** **********
                   ********** ********** ********** ***** **** **********
                   ********** ******* ** ********** ***** **** **********
                   ********** ******* ** ********** ***** **** **********
```

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                       ********** ******* ** ******                 ****    **********
                       ********** ******* ** ******                  ***    **********
                       ********** *******

alignment position     401....... 411....... 421....... 431....... 441.......
P855978           356  AACCAACATG GCGGCCCCCT ACAAA-CTTC AAGCGCCGGT CTCTCCTAGC
P855979           318  ATACAACATG GCAGCTCCCT ACAAAACTTC AAGCATCTGC TCCCATCAGC
P855980           288  ATACAATATG GCAGCTCCCT ACAAAACTTC AAGCATCTGC TCCCATCAGC
                       ********** ********** ********** ********** **********
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                       ****** *** ********** ********** ********** **********
                       ****** *** ********** *****                      ****
                              *** ********** *****
                              *** ********** *****

alignment position     451....... 461....... 471....... 481....... 491.......
P855978           405  CAATCAAAAG AAAgatattt ctgaatcccg cctCTTTCAG CAGCCTTGCT
P855979           368  CAATTAGAGA AAAATATAGT CCTGGGCCCG ---CCTCCTa caggaccctA
P855980           338  CAATTAGAGA AAAATATAGT CCTGGGCCCG ---CCTCCTG CAGCACCGCA
                       ********** ********** **********    ******* **********
                       ********** ********** **********    ******* **********
                       ********** ********** **********    ******           *
                       ********** ********** **********    ******           *
                       ********** ********** **********    ******           *
                       ********** ********** **********    ******
                       ********** ***                      ******

alignment position     501....... 511....... 521....... 531....... 541.......
P855978           455  GGCCAATCAG ACCACACCAT GAAGCATCAA TAcaG-AAAA GGGGGAACCC
P855979           415  GGCCAATCAG ACCAAAGAAG GAAAGGGCAC TATGGaAAAA GGCGTGAGAA
P855980           385  GGCCAATCAG ACCAAAGAAG GAAAGGGAAC TCTGG-AAAA GGCGTGAGAA
                       ********** ********** ********** ***** **** **********
                       ********** ********** ********** ***** **** **********
                       ********** ********** ********** ***** **** **********
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alignment position     551....... 561....... 571....... 581....... 591.......
P855978           504  GCTGGCCCAA TGGCAGCGTC CTacAGTGTA GCCTCCGCCT CCCGATTGAC
P855979           465  GCTCGCCCAA TGGCAGCATC CTG-AGCTTA GGCTCCGCCT TCCGGTTGAA
P855980           434  GCTCGTCCAA TGGCAGCATC CcG-AACTTA GGCTCCGCCT TCCGGTTGAC
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alignment position     601....... 611....... 621....... 631....... 641.......
P855978           554  TGGCCTgCTT GGCAAGGCAA GTAGCGGCGG CGCTTCAAGG TGGGTGTtca
P855979           514  CCGCAT-CTG GGCCAGGGAA GGAGCCGCAG CACTTCAAGG TGGGTGgCCA
P855980           483  CCGCAc-CTG GGCCAGGGAC GGAGCCGCTG CACTTCAAGG TGGGTGTCCA
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alignment position     651....... 661....... 671....... 681....... 691.......
P855978           604  cgttttggcc gtgaaagtc- GGGCTTGGGC AGCGTGGCGT CGGGGGCGAG
P855979           563  GGGCAAGGCG GCGAAGACAG GGtc-TGGGT GACGCAACGA CAGGGTTGAA
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P855980        532 AGGCAAGGCA GCGAAGACAG GGGTTTGGGT GACGCAACGA CAGGGTCGga
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alignment position 701....... 711....... 721....... 731....... 741.......
P855978        653 TGTGGTGTCC CCGTTGGCGC CGCCAGCTCT gcgcctgggc ttcccctcgg
P855979        612 CGGGGTGTCA CCGCTGACCT TATGAAGTCT GGGATCTAGC GctTCGG---
P855980        582 c-GGGTGTCA CCACTGACCT CGTGAAGTCT TGTATCTAGC GggTCGG---
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alignment position 751....... 761....... 771....... 781....... 791.......
P855978        703 ctcaCTCAGG ATCCGCGGCC TCCGTGTCCT TCA-GGTGCA GCGGggagcc
P855979        659 ----CTCGGG ACCCGCGGCT TGTGCGTCCT TCC-CGAGCT GCGGACCggA
P855980        628 ----CTCCGG ACCTGCGGCT TCTGTGCCCT TtcgCGAACT GCGGGCCa-A
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alignment position 801....... 811....... 821....... 831....... 841.......
P855978        752 ggctctca-- ----GGGCGC ATGCGCCGCC cgctctgcgc caccggccta
P855979        704 AAGCCTGCAC CCTCAGGCGC ATGCGCTGCC TCGCCGGcTG CCTTCTGCGT
P855980        673 ACGCCCGCAC CCTCGGGCGC ATGCGCTGCC TCGCCGGaTG CCTTCTGCGT
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alignment position 851....... 861....... 871....... 881....... 891.......
P855978        796 gt-TAGGGTC GGAGATCACT GGGAAGGTg- --GGGAAGGT GCTGGGTTGG
P855979        754 TCATAGGGTC AGAGGTCAAG GGGAAGGTCT GAGAGAAAGT GGTAGGTTGG
P855980        723 TCATAGGGTC AGAGGTCAAG GGGAAGGTCT GAGAGAAAGT GGTAGGTTGG
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alignment position 901....... 911....... 921....... 931....... 941.......
P855978        842 -GTCCctgga actgcagtca gtgatccaaa ggagtgggcc tgttaggggg
P855979        804 -ATCCAGGAT TGCTTGGGGT CAAGAATTGG CCGACCC-CT ACAGGTCAAA
P855980        773 gATCCAGAAT TGCCTTGGGT CAAGAATTAG CCGACCCgCT ACAGGTCAAA
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alignment position 951....... 961....... 971....... 981....... 991.......
P855978        891 ttcacaggtc gtgggATGAG CTCTTATGAG CGCCGGCTAA GTGCCGGGCT
P855979        852 GGTCAC---- -----AAGAG GGCGCTAGAG CGTTGGTGAT CTGCCAGACT
P855980        823 GGTCAC---- -----AAGAG GGCGCTAGAG CGTTGGTGAT GTGCCAGACT
                   ******          ***** ********** ********** **********
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alignment position 1001...... 1011...... 1021...... 1031...... 1041......
P855978        941 CTGGGgtgcc cttggcatgt acgggctc-- CCCTAATTCC CAAGACCaac
P855979        893 CTTGGTCAAA ATCCCCTTGt TTGCATACAT CCCTAATTTT CGGGACC---
P855980        864 CTTGTTCAAC ATCCCCTTGg TTGCATACAT CCCTAATTTT CGGGACC---
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alignment position 1051...... 1061...... 1071...... 1081...... 1091......
P855978        989 cgcCCCCAAC CCACTTCATA GGTGAGAAgA CGGAGGTCAG GTCACATCAT
P855979        940 ---CCTCTTC CTACATtgta atCCAGAA-A CTGAGGCCAG GGGACATCAT
P855980        911 ---CCTCTTC CTACATCGCA GGCCAGAA-A CTGAGACCAA GGGACATCAT
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alignment position 1101...... 1111...... 1121...... 1131...... 1141.
P855978       1039 CTGCCCAAGG TCACGCGGCA GGCTGGGGga cagt------ -----
P855979        986 TTGCCCAAGG TCACtc---- ---------- ---------- -----
P855980        957 TTGCCCAAGG TCACTCCGCA GGCTGGGGag agttccagga ggtcc
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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.

	P855979 (1001 bp)	**P855980 (1001 bp)**
P855978 (1072 bp)	0.147 42 %	0.153 45 %
P855979 (1001 bp)		<u>1.000</u> <u>84 %</u>

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

Extract alignment region	
Positions in alignment	from: to:
Output file	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 **Wed Jun 8 00:54:44 2005**

Solution parameters:

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

Aligned Sequences:

No.	Sequence Name	Sequence Description	Length
1	P937020	sym=NDUFV1|loc=Loc4723|taxid=9606|spec=Homo sapiens|chr=11| ctg=NT_033903|str=(+)|start=12679702|end=12680702|len=1001| tss=501| comm=NADH dehydrogenase (ubiquinone) flavoprotein 1, 51kDa; (NM_007103/537/bronze;)	1001 bp
2	P937022	sym=Ndufv1|loc=Loc17995|taxid=10090|spec=Mus musculus| chr=19|ctg=NT_082868|str=(-)|start=800669|end=801695| len=1027|tss=501,522,527| comm=NADH dehydrogenase (ubiquinone) flavoprotein 1; (AK075692/527/gold;AK005021/522/gold;NM_133666/501/bronze;)	1027 bp
3	P937024	sym=na|loc=Loc293655|taxid=10116|spec=Rattus norvegicus| chr=1|ctg=NW_047563|str=(-)|start=15125430|end=15126430| len=1001|tss=501| comm=similar to NADH dehydrogenase (ubiquinone) flavoprotein 1; (XM_215176/531/bronze;)	1001 bp

Alignment (DiAlign format):

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

V$HOMF V$NKXH V$TEAF V$CREB V$ETSF V$E2FF V$HOXH V$TALE V$HMTB

```
alignment position 1.........  11.........  21.........  31.........  41.........
P937020          1 ga--------  ----------  ----------  ----------  ----------
P937022          1 aaggtttaca  gacacacagc  cctgagaagt  cctatgcaaa  ggttctgggg
P937024          1 ----------  ----------  ----------  ----------  ----------
```

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alignment position 51........ 61........ 71........ 81........ 91........
P937020          3 ---------- ---------- ---------- ---------- ----------
P937022         51 cAGCTTTGTG GGAGGTGAGg gacctcaccg gttctt---- ----------
P937024          1 -AGCTTTGTG GAAGGTGTGt gtggggatgg agtgggggag gcagcaatgg
                    ********* *********

alignment position 101....... 111....... 121....... 131....... 141.......
P937020          3 ---------- ---------- --------GC ACACGGACGC CCGGGGtggg
P937022         87 -----TTGTT AATGAGTACT TCTCCAAGGC ACACGGATGC TCAGGGggag
P937024         50 ttctgTTGTT AATAAATACT TCCCCAGGGC ACACGGATGC TCAagagg--
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alignment position 151....... 161....... 171....... 181....... 191.......
P937020         25 gaagcccacA GTCTGGCAGG GCTCGCACTG GGCAGAATAA TTGCAACgta
P937022        132 cgctT----A GTTCAGCAGG GCTCGGCTAG TTCAGCGTAA TTACACCAGA
P937024         98 ----T----A GTTCAGCAGG GCTTGGCTAG GTCAGCGTAA TTACACCAGA
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alignment position 201....... 211....... 221....... 231....... 241.......
P937020         75 gTCATGAGGA TCGGGCTATG ACCTGCCTGA CTTTtcactc ctcccatgat
P937022        178 -TCAGGACGA TTCCGCTGTA GTCCAACTAA TTTTCTCACC AGCTTCCATT
P937024        140 -TCAGGACGA TCCCGCTGTA GCCCAACTAA TTCTCTCCCC AGCATCTATT
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alignment position 251....... 261....... 271....... 281....... 291.......
P937020        125 acaccgatgc ataccGCAGG TGCACACTAA ACGCCGAATC TATAGAAAGT
P937022        227 CGTgcatata ta---GCTGG TGTCAACTAG ACGCAAAGTC TGTAGGAAGT
P937024        189 TGTac----- ------CTGG TGCCCACTAA ACACAGAGCC TGTAGGAAGT
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alignment position 301....... 311....... 321....... 331....... 341.......
P937020        175 GGAACACacc aGGACCCAGC AGAAGGCGAC ATGCGAGGTT TGTTTACTtg
P937022        274 GGAAtacttg -GGATCCAGC AGAGGGCGAC ACGTGAGCCT GGTTTACTAG
P937024        228 GAAAAACtta -----CCAGC AGAGGGCGAC ATGTGAGCCT TGTTTTCTAG
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alignment position 351....... 361....... 371....... 381....... 391.......
P937020        225 tggcatcaaa ggctgggagc cggcgagcta aggagggagc gaaagagcga
P937022        323 GAAAA----- ---------- ---------- ---------- ----------
P937024        273 AGAAAggaaa ctg------- ---------- ---------- ----------
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alignment position 401....... 411....... 421....... 431....... 441.......
P937020        275 gcggtgGGGA CAGCCACCGC TAAATGCCAG CCCGGtggag ggaggaaggc
P937022        328 ------GGAA GAGTCTCCGA GAAAGGAGAG TCTGGgcaAG C---------
P937024        286 ---------- --GTCTCCAA GAAAGGAGAG TCTGGctcAG C---------
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alignment position 451....... 461....... 471....... 481....... 491.......
P937020        325 ggacccaggc ccggtGGGAC CACATCTCCC AGAAGCCCcg gcgccaaggc
P937022        363 ---------- -----TGGAC TACATCTCCC AGAAGGCCtA GCACGAGAGT
P937024        315 ---------- -----GGGAC TACATCTCCC AGAAGaaccA GTACCAGAAT
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alignment position 501....... 511....... 521....... 531....... 541.......
P937020        375 ac-------- ------TGGC CTCTCAGTCC TCCCCCGAGG AGGCGGGGCC
P937022        398 AAATTTCCGG TCTCTGTGCC CGCGCACCtt t------AGT GGGCGAGGCC
P937024        350 AAATTTCCGG TCTCTGTGCC CTCGCACCCC TTAGTGAGGG GGGTGGGGgg
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alignment position 551....... 561....... 571....... 581....... 591.......
P937020        411 GCTGGCG--- -------AAG TTGAAGGGgC GCAGCGATAC CGGTGCGCGG
P937022        442 GAGGACA--- -------GAG CTCAAAGG-A ACGGAGGTCC CTGGACACGC
P937024        400 aaggagcgcg gagcgtgGAG CGCGAAGG-C GCGGAGGCAT CTGGACACGC
                   *******           *** ******** * ********** **********
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alignment position 601....... 611....... 621....... 631....... 641.......
P937020        451 CGCTGGCGTC -GGGCGCGTG ACGTCTTTCC TGCGCGCCAC Cta------G
P937022        481 CACTGGCTGC -GGATGTGTG ACGCACTTCC TGTGCGCTCC CCAcCCCGTG
P937024        449 CTCTGGCTgc gGGACGTGTG ACGCACTTCC TGTGCGCCCC CCA-CCCGTG
                   **********  ********* ********** ********** *** ******
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alignment position 651....... 661....... 671....... 681....... 691.......
P937020        494 CGTCTCTATC GCGCCAGTTC CTCAGcctca gtgctaTGAA GGTGACAGCG
P937022        530 TGTTTCTGTC GCGCCGGTCC CGCGGTTCGG AGTTG-TGAA GGTGACAGCC
P937024        498 TGTTTCTGTC GCGCCGGTCC CTCGGTTCGG AGTTG-TGAA GGTGACAGCC
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alignment position 701....... 711....... 721....... 731....... 741.......
P937020        544 TGAGGTGACC CATCTGGCcc gCCGCGATGC TGGCAACACG GCGGCTGCTC
P937022        579 GGAGGTGACC CGTCTGGCTC -CCGCGATGC TAGCGGCACG GCATTTTCTC
P937024        547 GGAGGTGACt ggtccGGCTT -CCGCGATGC TAGCAGCACG GCATTTTCTC
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alignment position 751....... 761....... 771....... 781....... 791.......
P937020        594 GGCTGGTCGC TTCCCGCGCG GGTATCTGTG CGTTTCAGCG GCGACACGGT
P937022        628 GGCGGGTTGG TTCCCGTGCG GGTATCTGTG CGTTTCAGCA GCGGCACGGT
P937024        596 GGCGGGTCGG TTCCCGTGCG GGTATCTGTG CGTCTCAGCA GCGGCACGGT
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alignment position  801....... 811....... 821....... 831....... 841.......
P937020         644 GAGGCCCAGC CTGGCTGGGG CCACGGGTGT TTGGGGCCGG GTGtcgcggc
P937022         678 Ga-GCCCGCC CTGATTCAGG CCCACGCCTA TGGCGGAGGA GTGgcgaGCG
P937024         646 GAGGCCCACC CTGATTCTGG CCTGGGGTGT ATGc------ -------GTG
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alignment position  851....... 861....... 871....... 881....... 891.......
P937020         694 cgcgcccgtg cacgagcagt ccctgGGGTC TGTAGTGGCC TCTGGAGAGC
P937022         727 GCGAGC---- ---------- -----GGGAT TGTGGTCCCC TCTGCAGAGT
P937024         683 GCGAGC---- ---------- -----GGGGT TTGGTTCCCC cggtagaag-
                    ******                     ***** ********** **********
                                               ***** **********

alignment position  901....... 911....... 921....... 931....... 941.......
P937020         744 CCTtctcccc aggccaggcg ggaaggcccc cgctCCGGCC TGGTTGAAgt
P937022         758 CCTCTCCTCT CCGAGCTACC AC-------- ----CCGGTC TGGATAAAAA
P937024         713 CCTCTCCTCT CCGGGCTACT AC-------- ----CCGGCC TGGATTAAAA
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                    ********** ********** **             ****** **********
                    ********** ********** **             ****** **********
                    ***

alignment position  951....... 961....... 971....... 981....... 991.......
P937020         794 aggggaacgG GTCCCAACGC GGGGCCGACT CCCTtgaccc tctgacttgc
P937022         796 ct-AAC---G GTCCCAACTC CAGGCTGACG ATGTCCAGtC CA--------
P937024         751 atgAGC---G GTTCCAACTC GGGACTGATG CTCTCCGG-C CA--------
                       ***   * ********** ********** ******** * **
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                                                              * **

alignment position  1001...... 1011...... 1021...... 1031...... 1041......
P937020         844 tgGCTTCCCT TGTTTTACAG TCCTCGGCCT GGCGG-AAGT TTTGCAGGTT
P937022         834 --GCTACTCT TGTTTTAACA ACCCCGTCTT GGGGTgAGGG TTTGCAGGTG
P937024         789 --GCCTCTCT TGTTTTAACA ACCTCGTCCT AGGGT-AAGG TTTGCAGGTT
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alignment position  1051...... 1061...... 1071...... 1081...... 1091......
P937020         893 GTGAAGACCC CTAGtctttc a-TTCTCTCC TTGTCACAGC CTTGTAGGGC
P937022         882 TTGAGGCGTC TTAGATAATC TGTTATTTCT TCCTCGCAGC CCTACCGGGT
P937024         836 TTGAGGCATC TTAGCTAGTC TGTgttnctn ctncgcagnc tttcngnnnn
                    ********** ********** ********** ********** **********
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alignment position  1101...... 1111...... 1121...... 1131...... 1141......
P937020         942 GTGAagGGGT CATTGCCCCA TTTagg---- ---------- ----------
P937022         932 ATCA--GGGT CTTCGCCCCA TTTcaaagtt cagaaaacag ttttgaaAAA
P937024         886 ncggnnntnn ccccnnntgn ngtnncagaa nncanntnng n------AAA
                    ****  **** ********** ***                          ***

alignment position  1151...... 1161...... 1171...... 1181...... 1191......
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P937020      968 GATGCGCACC TCCTGAT-TT CCCGTCCACT gctct----- ----------
P937022      980 GATGTGTATC TCCTCAA-CC CCCCGACAGT ATTTTGCTTC CAGTAGTGa-
P937024      930 AATGTGTATC CCCTCAnnCC CCCCGACAGT GTTCTGGTTC CTGTAGTGgc
                 ********** ********  ** ********** ********** ********
                                     ** ********** ********** ********

alignment position 1201...... 1211...... 1221
P937020     1002 ---------- ---------- --
P937022     1028 ---------- ---------- --
P937024      980 cagaaagcgc ttttgtgatc cc
```

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.

	P937022 (1027 bp)	P937024 (1001 bp)
P937020 (1001 bp)	0.270 45 %	0.281 42 %
P937022 (1027 bp)		1.000 67 %

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

Extract alignment region	
Positions in alignment	from: to:
Output file	dialign.seq

Extract aligned sequences

For comments, questions or bug reports, please contact support@genomatix.de

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GEMS Launcher 4.1.1

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

[Alignment] [Pairwise similarities]

DiAlign professional TF Release 3.1 December 2004 **Wed Jun 8 04:29:52 2005**

Solution parameters:

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

Aligned Sequences:

No.	Sequence Name	Sequence Description	Length
1	P964855	sym=NDUFV2|loc=Loc4729|taxid=9606|spec=Homo sapiens|chr=18|ctg=NT_010859|str=(+)|start=9092225|end=9093225|len=1001| tss=501| comm=NADH dehydrogenase (ubiquinone) flavoprotein 2, 24kDa; (NM_021074/522/silver;)	1001 bp
2	P964858	sym=Ndufv2|loc=Loc72900|taxid=10090|spec=Mus musculus|chr=17|ctg=NT_039657|str=(-)|start=9606486|end=9607493| len=1008|tss=501,508| comm=NADH dehydrogenase (ubiquinone) flavoprotein 2; (AK078351/508/gold;AK013511/501/gold;)	1008 bp
3	P964862	sym=Ndufv2|loc=Loc81728|taxid=10116|spec=Rattus norvegicus|chr=9|ctg=NW_047818|str=(-)|start=8001731|end=8002731| len=1001|tss=501| comm=24-kDa subunit of mitochondrial NADH dehydrogenase; (XM_343638/508/silver;)	1001 bp

Alignment (DiAlign format):

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

V$STAF V$NRF1 U$NRF1 V$ZF5F V$P53F V$GREF V$HNF4 V$EGRF

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alignment position 1.........  11........  21........  31........  41........
P964855          1 ----------  ----------  ----------  ----------  ----------
P964858          1 ----------  --------AT  CATTTCTACC  TCCCACTCAC  TGGCATCCCG
P964862          1 cgcgtagcat  cgacagtcAT  CATTTCTACC  TCCCACTTCC  TGGCATTCCG
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alignment position 51........ 61........ 71........ 81........ 91........
P964855          1 ---------- ---------- ---------- ---------- ----------
P964858         33 AAGTCAATtc cagttTAGCC TGTCGTTTTA CAGACTCTAA cgca-AAGGC
P964862         51 AAGTCAATtc cagc-TAGCC TATCCTTTTA CAGACTCTAA aagcgAAGTC
                   ********        ***** ********** **********      *****
                   ********        ***** ********** **********      *****
                   ********                                         *****
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alignment position 101....... 111....... 121....... 131....... 141.......
P964855          1 ---GGAACCA AGACATTTGG TGTCTATGGC tagcaCACTG GATAGCAGCC
P964858         82 TTGGGAGCCA AGGCACTTGC TGTCCAAGTC -----CACTA GGTGGCAGCC
P964862        100 TTGGAAGACA AGGCACTTGC TGTTCAGGTC -----CACTA AGTGGCAGCC
                   ********** ********** **********      ***** **********
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                   ********** ********** **********      *****  *********
                      ******* ********** **********      *****  *********

alignment position 151....... 161....... 171....... 181....... 191.......
P964855         48 CTCTGTGTct tgaattcgta acatgtagaa taagatttat agtgggttgc
P964858        127 CTTTAAATAC GATCGTATGT AAGAAAAGAC TCAACCAAAC GAATTTTGAA
P964862        145 CTTTAAGTAC GATCGGGTGT AAGATAAGTC TCAGCCGACC GGATTGTGCA
                   ********** ********** ********** ********** **********
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alignment position 201....... 211....... 221....... 231....... 241.......
P964855         98 aacccgactt tatttttAAC TAACAGCAAT ATAAGAGGAG GTGGctaatc
P964858        177 AG-------- -------AAA TAACTGCAAT ACCAGAGGAG GTGTTTGACA
P964862        195 GG-------- -------AAG TAACTGCAAT ACCAGAAGAG GTGTTTGACA
                   **                *** ********** ********** **********
                   **                *** ********** ********** **********
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                                     *** ********** ****** *** **********
                                                           *** ****
                                                           *** ***

alignment position 251....... 261....... 271....... 281....... 291.......
P964855        148 ct-----CAC AAGGCTCTCC ATG------- ---------- ----------
P964858        212 GAACAAACAC AAGATCCCCC AGaaggtacg cctcgtcctc aacaaacaca
P964862        230 GAACAAACAC AAGATCCTCC AGG------- ---------- ----------
                   ********** ********** ***
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                          *** ********** **

alignment position 301....... 311....... 321....... 331....... 341.......
P964855        166 ---------- --AGGGAAGC Tcacccctat aaatccaggc gggcgcttcg
P964858        262 agagcctcga gaAGGCGAGC CTCGTCC--- ---------- ----------
P964862        253 ---------- --AGGCCCGC TTCGTCC--- ---------- ----------
                                ******** *******
                                ******** *******
                                ******** *******
                                ******** *

alignment position 351....... 361....... 371....... 381....... 391.......
P964855        204 ttacccagga gcccaaggtg cagctccggg acgcttcttt TCAAGGCCGG
P964858        289 ---------- ---------- ---------- ---------- TCAGGGCGGG
P964862        268 ---------- ---------- ---------- ---------- TCAGGGCCGG
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alignment position 401....... 411....... 421....... 431....... 441.......
P964855        254 GACccctgca gcggcccgta ggacacctcC CTTTCCGAGC ACGGACTGGT
P964858        299 GACTCAGCTG GCCCAaccgg GCCGG----C CTTTTAGGGA CTGGGCTGTT
P964862        278 GACTCAGCTT GCCCA----- GCCGG----C CTTTTAGGGA TTGGGCTGTT
                   ********** *****      *****    * ********** **********
                   ********** *****      *****    * ********** **********
                   ********** *****      *****    * ********** **********
                   ***

alignment position 451....... 461....... 471....... 481....... 491.......
P964855        304 CCCCGCCCCT CCCCCGGgaa gtctccgccc acagggcCCC AGCAGCCCCC
P964858        345 TCGGGCCCGC CCACCGGt-- ---------- -------CCC AGCAGCCCTC
P964862        319 ---------- ---------- ---------- --------CC AGCAGGCCAC
                   ********** *******                    *** **********
                                                         *** **********
                                                          ** **********
                                                          ** **********

alignment position 501....... 511....... 521....... 531....... 541.......
P964855        354 GCGCGCCCTC GCtccctccc gtcagccccc gccCCTCGGC GAAGGGAGCG
P964858        376 GCGCGCCgct ---------- ---------- --------GC GTCAGGAACG
P964862        331 GCGCGCCCTC GCgcg----- ---------- ---CCCGGGC GCCTGGAGCT
                   ********** **                     ******* **********
                   ********** **                          ** **********
                   *******                                       ******
                   *******                                       ******

alignment position 551....... 561....... 571....... 581....... 591.......
P964855        404 GCGTGCCGTC CGGGTCGCCT AGG------- ---------- ----------
P964858        398 GCGTACCGTT CGGGACGCCC AGG------- ---------- ----------
P964862        363 GCGCACTCTT CCAGACGCCC AGGctcgggc tcgtgagcgt gcgccgtgcg
                   ********** ********** ***
                   ********** ********** ***
                   ********** ********** ***
                   ********** ********** ***

alignment position 601....... 611....... 621....... 631....... 641.......
P964855        427 -CCTGGGGTC GGGA--GCGC GCACGCTGTG CGCCCTGGGC GCGctcggga
P964858        421 -CCAGGGCTC GTGAgcGCGC GCGCGCCGTG CGTCCTGGGC GCGGGGCCGC
P964862        413 tCCCGGGCTC GTGA--GCGC GCGCGCCGTG CGTCCTGGGC TCGGGGCCGC
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                    ********* ****  **** ********** ********** **********
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                    ********* *     **** ********** **********  *********
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alignment position 651....... 661....... 671....... 681....... 691.......
P964855        474 ttctcgcctg gc-------- ---------- ---------- ---GCGGCTG
P964858        470 GCGCGCCGGG CCTCCGGGCT CGTTCGTTCC CaGTCAGCCT AGAGCGGCCG
P964862        461 GCCCGCCGGG CCTCCAGGCT CGTTCGTTCC CtGTCAGCCT AGAGCGGCCA
                   ********** ********** ********** * ******** **********
                   ********** ********** ********** * ******** **********
                   ********** ********** ********** * ******** **********
                   ********** ********** ********** *             *******
                   ********** ********** ********** *             *******
                                                                  *******

alignment position 701....... 711....... 721....... 731....... 741.......
P964855        493 GGGAAGGTGA ACAGTGTGGC CCGCCATGTT CTtctccgcG GCGCTCCGGG
P964858        520 GGGTCGGAGC ATCGCGTACC CCGCCATGTT CTCCTT---G GCGCTGCGGG
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P964862        511 GGGTCGGAGA ACCGCGTACC CCGCCATGTT CTCCTT---G GCGCTGCGGG
                   ********** ********** ********** ******   * **********
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                   ********** ********** ********** ******   * **********
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                                   ***** ********** **       * **********
                                   ***** ********** **       * **********
                                                             * **********

alignment position 751....... 761....... 771....... 781....... 791.......
P964855        543 CCCGGGCGGC TGGCCTCACC GCCCACTGGg taAGGAGGCT CAAGCTGAG-
P964858        567 CCAGGGCGAC CGGCCTCGCT GCTCAGTGGG T-AAGAGGCT CGGGGTGAAc
P964862        558 CCAGGGCGTC CGGCCTCACC GCTCAGTGGG T-AAGAGGCT CGGGGTGAA-
                   ********** ********** ********** * ******** *********
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alignment position 801....... 811....... 821....... 831....... 841.......
P964855        592 -CCCGGCGCT GCCGCCGCcc tTCTCTTGCT CTCCGTGTCT CCCTTAGTTT
P964858        616 cCCGGGCACT GTCGCCACAG -TCTCCCGCT CTTCGTGCCT CCCTTAGCTT
P964862        606 -GCGGGCACT GTCGCCATAG -TCg-CCGCT CTTTATGTTT CTCTTAGCTT
                    ********* **********  ********* ********** **********
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                                          **  ***** ********** **********
                                                *** ********** **********

alignment position 851....... 861....... 871....... 881....... 891.......
P964855        641 TG-GGCGCAG GAGAGCCCTG GGCTCTGCAC GGGCCTGCAG GCGGCGGCAA
P964858        665 TTaGTCCTCG GAGACCCCTA GGCGCTGGAC AGGTCAGCTG GCGGCGGCGG
P964862        653 TG-GTACCCG GAGACCCCAG GGTGCTGGAT AGGTCAGCTG GCGATGGCGG
                   ** ******* ********** ********** ********** **********
                   ** ******* ********** ********** ********** **********
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                   *  ******* ********** ********** ********** ***  *****
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                            * ********                     **** ***  ***
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alignment position 901....... 911....... 921....... 931....... 941.......
P964855        690 GGACACTGCG GCCTTAGCCC TCttagggag gccgctgcag ccccaCCGTG
P964858        715 GGACGCCGCG GCCTTCGTCC TCAGTGCCTC CGGGAtgctc cg-------C
P964862        702 AGACGCCGCG GCCTTCGTCC TGGGTGCCTC CGGGAtgc-- -----CCCTC
                   ********** ********** ********** *****           *****
                   ********** ********** ********** *****               *
                   ********** ********** ********** *****               *
                   ********** ********** ********** *****               *
                   ********** ********** **                             *
                   ********** ********** *

alignment position 951....... 961....... 971....... 981....... 991.......
P964855        740 AGAAGCCCCG AGGGAGGGTT GCCata---- ---------- CTGGGAAGTG
P964858        758 AGCTGCGGTG GCGGCGGGTG GCGGGCCGCC CGCACCGGGc CGGGGAAAGT
P964862        745 AGCTGCGGCG GCGGCGGGTG GCCGGCCGCC CGCACCGGGc cc-GGAAAGT
                   ********** ********** ********** *********  **********
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                   ********** ********** ********** *********

alignment position 1001...... 1011...... 1021...... 1031...... 1041......
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P964855        776 TACTCCTAGT TTGGTCGAGG aggaca---- ---------- ----------
P964858        808 CACCCCTAAC TTAGTCAAGG TCAGGAAGGC GaTTGTCATT TATCCTGGTG
P964862        794 CA-CCCTAAC TTAGTCAAGG TCAGGAAGGC GgTTGTCATT TGTCCCGGTG
                   ********** ********** ********** * ******** **********
                      ******* ********** ********** * ******** **********
                      ******* ********** ********** * ******** **********
                      ******* ********** ********** *

alignment position 1051...... 1061...... 1071...... 1081...... 1091......
P964855        802 ---------- ---------- ---------- ---------- ----------
P964858        858 CGGAAGCTAG TGgggggcCC TGGCGGCCCG CTGCTTCCAG GATCCTAGCA
P964862        843 CGGAACCTAG TGagat--CC TGGCGGCCTG CTGCTTCCAG GAACCCGGCA
                   ********** **      ** ********** ********** **********
                   ********** **      ** ********** ********** **********
                   ********** **      ** ********** ********** **********
                                      ** ********** ********** **********

alignment position 1101...... 1111...... 1121...... 1131...... 1141......
P964855        802 --GAAAAGAG GGGCTGCTTG gtgatatata tatatatgtt tgtttgtttt
P964858        908 GCGAAGcttt GGGCTGCTTG TC-------- ---------- ----------
P964862        891 GCGAAGAAAG GGGCTTCTTG TC-------- ---------- ----------
                   ********** ********** **
                   ******     ********** **
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                   ******

alignment position 1151...... 1161...... 1171...... 1181...... 1191......
P964855        850 tgctgttttg ctgtagcgca gaatctaggc ctgctctggc cagatcagtt
P964858        930 ---------- ---------- ---------- ---------- ----------
P964862        913 ---------- ---------- ---------- ---------- ----------

alignment position 1201...... 1211...... 1221...... 1231...... 1241......
P964855        900 tcgaagaccg tcgctccgaa ggaggcacct ctcgTTTCAA GCCTAGTGAC
P964858        930 ---------- ---------- ---------- ----TGTCAG GCATAGCGGC
P964862        913 ---------- ---------- ---------- ----TGTCAG ACTTAGCGGC
                                                        ****** **********
                                                        ****** **********
                                                        ****** **********

alignment position 1251...... 1261...... 1271...... 1281...... 1291......
P964855        950 CTCGATGCTT ttaggttgc- AGCATACTGG AGAg--CTCT GGCTTGCTTC
P964858        946 TGCGCTGCAT cggatttaaa AGCATGCTGG AGAAAACGCT GATAGGCTTG
P964862        929 AACGCTGCAa cagaattaaa gGCATGCTGG AGAAAACGCT GATGTGCTTG
                   **********            ********** ********** **********
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                   *********              ********* ********** **********
                                          ********* ********** **********
                                          ********* ***

alignment position 1301...... 1311...... 1321
P964855        997 GTGAA----- ---------- ---
P964858        996 GTAAAGGCTT Gcc------- ---
P964862        979 GTGAAGGCTT Gccgagttcc ttc
                   ********** *
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                   ********** *
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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.

	P964858	P964862

	(1008 bp)	**(1001 bp)**
P964855 (1001 bp)	0.194 40 %	0.166 34 %
P964858 (1008 bp)		1.000 79 %

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

Extract alignment region	
Positions in alignment	from: ☐ to: ☐
Output file	dialign.seq

Extract aligned sequences

For comments, questions or bug reports, please contact support@genomatix.de

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GEMS Launcher Task: *DiAlign TF*: Multiple alignment plus TF sites
working on C1-NDUFV3.seq (3 seq.)

[Alignment] [Pairwise similarities]

DiAlign professional TF Release 3.1 December 2004 **Wed Jun 8 05:00:37 2005**

Solution parameters:

Sequence file:	C1-NDUFV3.seq (3 seq.)
Type of sequences:	nucleotide sequences
Threshold T:	0.00
'*' signs below alignment denote:	diagonal similarity (max. similarity is represented by 10 '*' signs)
Alignment output:	complete alignment is shown # nucleic acids per line: 50
TF output:	common TF matches located in aligned regions (common to 3 (100.0 %) sequences)
Family matches:	yes
MatInspector library:	Matrix Family Library Version 5.0 (February 2005)
Selected groups (core/matrix sim):	ALL user_defined.lib (0.75/Optimized) ALL vertebrates.lib (0.75/Optimized)

Aligned Sequences:

No.	Sequence Name	Sequence Description	Length
1	hNDUFV3	hNDUFV3 sym=NDUFV3|loc=Loc4731|taxid=9606|spec=Homo sapiens|chr=21|ctg=NT_030188|tss=761	1547 bp
2	mNDUFV3	mNDUFV3 sym=1500032D16Rik|loc=Loc78330|taxid=10090|spec=Mus musculus|chr=17|ctg=NT_039649|str=(+)|tss=455	1471 bp
3	rNDUFV3	rNDUFV3 sym=Mipp65|loc=Loc64539|taxid=10116|spec=Rattus norvegicus|chr=20|ctg=NW_047598|str=(+)|tss=420	966 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$PCAT V$ZBPF V$ZF5F

```
alignment position  1.........  11........  21........  31........  41........
hNDUFV3          1  ggaatcccta  cacaatccat  ttaaatgact  gtggcagggc  ctcttcccct
mNDUFV3          1  tttgaactag  c---------  ----------  ----------  ----------
rNDUFV3          1  ctcatt----  ----------  ----------  ----------  ----------

alignment position  51........  61........  71........  81........  91........
hNDUFV3         51  gtggaagctg  aaggtggcac  gtccatctcc  gatgaaatgc  gaatggggct
mNDUFV3         12  ----------  ----------  ----------  ----------  ----------
rNDUFV3          7  ----------  ----------  ----------  ----------  ----------
```

```
alignment position 101....... 111....... 121....... 131....... 141.......
hNDUFV3        101 ctgggcacgc ggcggaaggc agagaagagg cagagAAAGA AGCTAATAAC
mNDUFV3         12 ---------- ---------- ---------- ---------- ----------
rNDUFV3          7 ---------- ---------- ---------- -----AATGA ATTTATCTAC
                                                        ***** **********
alignment position 151....... 161....... 171....... 181....... 191.......
hNDUFV3        151 TAATTACACC gactccacaa ttacgactaa cgttggggac gaactctttg
mNDUFV3         12 ---------- ---------- ---------- ---------- ----------
rNDUFV3         22 TGATTAATCC ttaca----- ---------- ---------- ----------
                   **********
alignment position 201....... 211....... 221....... 231....... 241.......
hNDUFV3        201 ctaaataaac atttaggtga aacaaagctt ccatttccaa tcggcctaac
mNDUFV3         12 ---------- ---------- ---------- ---------- ----------
rNDUFV3         37 ---------- ---------- ---------- ---------- ----------

alignment position 251....... 261....... 271....... 281....... 291.......
hNDUFV3        251 tctggtatta gcgttggcag gggccatgca ggaggggcag tgagcagtgg
mNDUFV3         12 ---------- ---------- ---------- ---------- ----------
rNDUFV3         37 ---------- ---------- ---------- ---------- ----------

alignment position 301....... 311....... 321....... 331....... 341.......
hNDUFV3        301 tggccgcGTT GCCGACAGAG GGTGAGGGAG CTGGGCGCGT ggtgtgggcg
mNDUFV3         12 ---------- -CCTACTGCT GGTATGGTAG GTGGGCACCT CCAtgCCCAG
rNDUFV3         37 -------GTT GCCTAGTGCT GGTAAGGTAG GTGGGCACCA CCActCCCAG
                          *** ********** ********** ********** ***  *****
                               ********* ********** ********** ***  *****
                               ********* ********** ********** ***  *****
                               ********* ********** *******         *****
alignment position 351....... 361....... 371....... 381....... 391.......
hNDUFV3        351 ccgaggtccc gagctgaaga gcttt----- ---------- ----------
mNDUFV3         51 CTTCTGGTTT GTTTGTTCAA GACCACGCCC CTActgGGCA AGCGCACTAC
rNDUFV3         80 CTTCCGGTTT GTTTGTGCAA GGCCACGCCC CTAttaGGCA AACGCCCTAC
                   ********** ********** ********** ***   **** **********
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                   ********** ********** ********** ***   **** **********
                   ********** ********** ********** ***
alignment position 401....... 411....... 421....... 431....... 441.......
hNDUFV3        376 ---------- ---------- ---------- ------AAAA CCTCTCAAAA
mNDUFV3        101 CACCGAGTTG TATCTCCAAG AAACAACAAA CTCACAAAGA TCTCACCAAA
rNDUFV3        130 CACCTAGTTG TATCTCCAAG AAACAACAAA CTCACAAAAA TCTCACCAAA
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                                      ** ********** ********** **********
                                                          **** **********
alignment position 451....... 461....... 471....... 481....... 491.......
hNDUFV3        390 CACAGAACTA TCaaTCAAGT AGGACCAGAc tgtgccccca gggaaggtcg
mNDUFV3        151 CACAGAAGTC TC--TCAAGT CGAACCAGAA ACGCAAAGGA CATGATTCTA
rNDUFV3        180 CACAGAAGaC TC--TCAAGA CGAACCAGAA ACGCAAAGGA CACGATCCTA
                   ********** **  ****** ********** ********** **********
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                   *******
alignment position 501....... 511....... 521....... 531....... 541.......
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hNDUFV3        440 ---------- ---------- -------CAG ATTTAAGGCT GCGAggacaa
mNDUFV3        199 GctgtgCAAT TTTGGTAGGT TACAGACCAG AGTTAAGGGC GAGATCAGGG
rNDUFV3        228 GttgcaCAAC TTTAGTAGGT TGCAGACTAG AGTTAAGGGT GAGATCAGGG
                   *     **** ********** ********** ********** **********
                   *     **** ********** ********** ********** **********
                   *     **** ********** ********** ********** **********
                   *     **** ********** ********** ********** **********
                   *

alignment position 551....... 561....... 571....... 581....... 591.......
hNDUFV3        463 gggcaaagaa gtgcgaagcg ttcgGGTGGA CATGCaagcc ggcccagcgc
mNDUFV3        249 CAA------- ---------- ----GGTGGG CAGGCCCAAA TCGGAGGG--
rNDUFV3        278 CAA------- ---------- ----GGTGGA CAGGCCCAGA TCGCAGGG--
                   ***                       ****** ********** ********
                   ***                       ****** ********** ********
                   ***                       ****** ********** ********
                   ***                       ****** ********** ********

alignment position 601....... 611....... 621....... 631....... 641.......
hNDUFV3        513 agacgcctga gaggggtgcc cagcagcccc cGCAGGTCTC CGCCGCGCCC
mNDUFV3        276 ---------- ---------- ---------- -GCGGGACTT tcagcgggat
rNDUFV3        305 ---------- ---------- ---------- -GCAGGACTT CCACCCAGAC
                                                     ********* **********
                                                     *********
                                                     *********
                                                     *********

alignment position 651....... 661....... 671....... 681....... 691.......
hNDUFV3        563 CCGCCACAGC GCCcaggcgc ccgcagggca cagggatcgg caccagccgg
mNDUFV3        295 cta-CCCAGG GGAGGACCCC ACGCTTTCCC gaA------- ----------
rNDUFV3        324 CTGCCCAAGG GGCGGGCACC AAGCACTCTC --A------- ----------
                   ********** ********** **********   *
                                                      *
                                                      *
                                                      *

alignment position 701....... 711....... 721....... 731....... 741.......
hNDUFV3        613 tgacgtgtcc ctcacgctgc tgCCTGTGAT TGGTGGTCCC GATCCGGGGC
mNDUFV3        327 ---------- ---------- --CCCGGAAT TGGTGGACTC AGTTAGGGGC
rNDUFV3        355 ---------- ---------- --CCCGGGAT TAGTGGACTC AGTCAGAGGC
                                           ******** ********** **********
                                           ******** ********** **********
                                           ******** ********** **********
                                           ******** ********** **********
                                           ******** ********** **********

alignment position 751....... 761....... 771....... 781....... 791.......
hNDUFV3        663 GTGGCCCCAA GGgaggcact tagccctact ggggatgcgc gcgcagaccc
mNDUFV3        355 GTGGCCTTAA GGAGCCCTCC CAGAA----- ---------- ----------
rNDUFV3        383 GTGGCCTctg GGAGCCCGCC CAGAA----- ---------- ----------
                   ********** ********** *****
                   ********** ********** *****
                   *******    ********** *****
                   *******    ********** *****
                   *******    **

alignment position 801....... 811....... 821....... 831....... 841.......
hNDUFV3        713 acggcctctg ctccgccccc agctggcctg taattggcgc agtcggccca
mNDUFV3        380 ---------- ---------- ---------- ---------- ----------
rNDUFV3        408 ---------- ---------- ---------- ---------- ----------

alignment position 851....... 861....... 871....... 881....... 891.......
hNDUFV3        763 aggggcggct gttcaggcgc gggTGCGCGC GCAGCTGCTG TGGCCCTGCT
mNDUFV3        380 ---------- ---------- ---TGCGCGC GCAAACGCTT GGGTCCACCA
rNDUFV3        408 ---------- ---------- ---TGCGCGC GCAAGCGCTT GGCCCCACCC
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alignment position 901....... 911....... 921....... 931....... 941.......
hNDUFV3        813 TGGTGCGCcc gctgtcacc- ---------- ---------- ----------
mNDUFV3        407 TGGTGTGCGA TTGGTGAACG TGgACGCGGG GCGGAGCCTG GGGTGGTGCG
rNDUFV3        435 TGGTGTACGA TTGGCGAACG TG-ACGCGGG GCCGAGCCTC GGGTTGTGCG
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alignment position 951....... 961....... 971....... 981....... 991.......
hNDUFV3        832 ---------- ---------- ---------- ---------- ----------
mNDUFV3        457 TGTGCACaag tAGGTCACGT ACCTAAGTGC GACCTCCGCT CTTGGCATTT
rNDUFV3        484 GGTGCACgct cAGGTTACGT ACCTAGGTGC GACCTCGGCG CTGGGCGTCT
                   *******     ********* ********** ********** **********
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alignment position 1001...... 1011...... 1021...... 1031...... 1041......
hNDUFV3        832 --GCCATGGC tgccccgtgt tTGCTGCGGC AAGGACGAGC CGGGGCGCTG
mNDUFV3        507 GtGCCATGGC GGTCTCTCTC CTCCTGCGGG GAGGACGGAT CCGGGCGCTG
rNDUFV3        534 GtaCCATGGC GGTCTCTCTC CTGCTGCGGG GAGGACGAAT CCGGGCGCTG
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alignment position 1051...... 1061...... 1071...... 1081...... 1091......
hNDUFV3        880 AAGGTAAAGG aggagccagc ctgggctggc tgcgcggccc cgagcctacg
mNDUFV3        557 AAGGTAAAGG GCTAACGGGC GGGA------ ---------- ----------
rNDUFV3        584 AAGGTAAAAA GCGAACGGGA GAGA------ ---------- ----------
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alignment position 1101...... 1111...... 1121...... 1131...... 1141......
hNDUFV3        930 taggggatgg ggtgaggggg cgcggtgctg gtcaggtccg ggcctgtccg
mNDUFV3        581 ---------- ---------- ---------- ---------- ----------
rNDUFV3        608 ---------- ---------- ---------- ---------- ----------

alignment position 1151...... 1161...... 1171...... 1181...... 1191......
hNDUFV3        980 cgacctctag ccgtcctagt tgggccgctg accccgctcc ctgggcccag
mNDUFV3        581 ---------- ---------- ---------- ---------- ----------
rNDUFV3        608 ---------- ---------- ---------- ---------- ----------

alignment position 1201...... 1211...... 1221...... 1231...... 1241......
hNDUFV3       1030 gactgaccgc cacggggcca ggcccggatg tggccagcga gcgtcccgcg
mNDUFV3        581 ---------- ---------- ---------- ---------- ----------
rNDUFV3        608 ---------- ---------- ---------- ---------- ----------
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alignment position 1251...... 1261...... 1271...... 1281...... 1291......
hNDUFV3       1080 gttcccCCGA GCCGGTCCgc cgccgccgct gcccgaggcc caggccgagg
mNDUFV3        581 ------CATA CCGGGcCCTT AGCCTGACCC TTA------- ----------
rNDUFV3        608 ------CCTA CCCGGTCCTT AGTCTGGCCC TTA------- ----------
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alignment position 1301...... 1311...... 1321...... 1331...... 1341......
hNDUFV3       1130 ctggcgtgcc ccgtgccgac gggcgctccc gaggGCTGCA TGCCTGGGCg
mNDUFV3        608 ---------- ---------- ---------- ----ACTGCA CCCGTGGGCC
rNDUFV3        635 ---------- ---------- ---------- ----GCTGCA CGCGTGGGCT
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alignment position 1351...... 1361...... 1371...... 1381...... 1391......
hNDUFV3       1180 gcagactcgg gtggacgttc ccaggtgatg ctgccgcgcg gctggggtca
mNDUFV3        624 CGGTGCGgag -AGGGGTCCT AGGGCCTGTG CTCACCTGAC CCggacAGAA
rNDUFV3        651 CGGTGCGgta aAGAGGTCCC AGGGCCTGTG CTCACCTGAC CCcaagAGAA
                   *******     ********* ********** ********** **    ****
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alignment position 1401...... 1411...... 1421...... 1431...... 1441......
hNDUFV3       1230 gccgctgtgc ggctcccgca cGGCTTCTCT GAAGGAcagt gacttctcca
mNDUFV3        673 GG-------- ---------- -GTTTTCTCT GCAGGAGTGA AACCGAGtca
rNDUFV3        701 GT-------- ---------- -GGTTTCTCT GCAGGAGCGA AGCCAAGgct
                   **                     ********* ********** *******
                   **                     ********* ********** *******

alignment position 1451...... 1461...... 1471...... 1481...... 1491......
hNDUFV3       1280 tttagccaag agaggaaatg agggaacttt cagggacctg gttaacttgg
mNDUFV3        704 ctgaGGCTGT TTTTAAAACG AAACCTGGCT TTCTCTGCAA AActAGTATT
rNDUFV3        732 ccttGGCTGT TTAAAAAGCA AAACCCGACT TTCTCTGCAA AAtcAGTGTT
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alignment position 1501...... 1511...... 1521...... 1531...... 1541......
hNDUFV3       1330 taacttactg acagccgttg a--------G AAGCCAGCTG ACATGACCTG
mNDUFV3        754 GGGTTTTGTT TGGGTTGGGT TCGGTGGATG GAACCTAGGG CCCTGCGCTT
rNDUFV3        782 GGGGTTTGTT TGGGTTGGGT TCGGTGGATG AAACCTAGGG CCCTGCGCTT
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alignment position 1551...... 1561...... 1571...... 1581...... 1591......
hNDUFV3       1372 ACCTGTGAAA AGgag----- ---------- --AAGAAGGG CTTTCTTTTC
mNDUFV3        804 GCTTGTCAAG AGCTGTCATT GAACtGGCCC CAAAGCAGGA AATGCTCACA
rNDUFV3        832 GCTTGTCAAG AGCTGTCATT GAACcGGCCC CAAAGTAGGA AATGCTCAAA
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alignment position 1601...... 1611...... 1621...... 1631...... 1641......
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hNDUFV3      1405 GGCAAATAAA AAGCTAAGGC CAaggccggg cgcggacact ttgggatttt
mNDUFV3       854 GCAATATAAA ATACAggTGA CAGAGGGCTC CCGTCGTCAA ATGGGCACTg
rNDUFV3       882 GCAAAATAAA ATACAGATGA CAGAGGGCCG CCATCGTCAG ATGAACACTa
                  ********** ********** ********** ********** **********
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alignment position 1651...... 1661...... 1671...... 1681...... 1691......
hNDUFV3      1455 gcctgt---- ---------- ---------- ---------- ----------
mNDUFV3       904 tttaaTTATT CCTTCAGGTA TAttgCTCCC AGCGATTTTT Ttccagcgtg
rNDUFV3       932 g----TTACT CCTTCAGGTA TAa--CTTCC AGCGATTTTT T---------
                       ***** ********** **   ***** ********** *

alignment position 1701...... 1711...... 1721...... 1731...... 1741......
hNDUFV3      1461 ---------- ---------- ---------- ---------- ----------
mNDUFV3       954 tatcggtaca cataatttgt acacacacgg agaatcatca gtataaatag
rNDUFV3       967 ---------- ---------- ---------- ---------- ----------

alignment position 1751...... 1761...... 1771...... 1781...... 1791......
hNDUFV3      1461 ---------- ---------- ---------- ---------- ----------
mNDUFV3      1004 aagttttccg gttcttttgc tccacccccc aaccccctcc ctagcatgaa
rNDUFV3       967 ---------- ---------- ---------- ---------- ----------

alignment position 1801...... 1811...... 1821...... 1831...... 1841......
hNDUFV3      1461 ---------- ---------- ---------- ---------- ----------
mNDUFV3      1054 gcatcctagg atctaacaca taccttagcg gttgccggct gaattacaat
rNDUFV3       967 ---------- ---------- ---------- ---------- ----------

alignment position 1851...... 1861...... 1871...... 1881...... 1891......
hNDUFV3      1461 ---------- ---------- ---------- ---------- ----------
mNDUFV3      1104 aagattcttc tcaaattgta acacttctga agcaattatc tacatcctat
rNDUFV3       967 ---------- ---------- ---------- ---------- ----------

alignment position 1901...... 1911...... 1921...... 1931...... 1941......
hNDUFV3      1461 ---------- ---------- ---------- ---------- ----------
mNDUFV3      1154 ttactagtag atagtgtttc tgcaacttta ctaactgtag ggagataatt
rNDUFV3       967 ---------- ---------- ---------- ---------- ----------

alignment position 1951...... 1961...... 1971...... 1981...... 1991......
hNDUFV3      1461 ---------- AATCCCAGTA CTTTGGAAGG ccgagccagg cggatcgctt
mNDUFV3      1204 ttgcaaaaag AAACATAGTA TTTTGTAAAG taacaaaata gccagt----
rNDUFV3       967 ---------- ---------- ---------- ---------- ----------
                             ********** **********

alignment position 2001...... 2011...... 2021...... 2031...... 2041......
hNDUFV3      1501 gagttcagga gttcgAGACT AGCCTGGCCA ACATGTCGAA ACCCCgt---
mNDUFV3      1250 ---------- -----AGAGT AAACTGGCTG CCCTGTATTA AGACCcagga
rNDUFV3       967 ---------- ---------- ---------- ---------- ----------
                                  ***** ********** ********** *****

alignment position 2051...... 2061...... 2071...... 2081...... 2091......
hNDUFV3      1548 ---------- ---------- ---------- ---------- ----------
mNDUFV3      1285 gtcttgggct gagagccaac tgggccttgc atccaggatc caggcctgag
rNDUFV3       967 ---------- ---------- ---------- ---------- ----------

alignment position 2101...... 2111...... 2121...... 2131...... 2141......
hNDUFV3      1548 ---------- ---------- ---------- ---------- ----------
mNDUFV3      1335 tgttacagcc ggcatgatgg ctgccatcca gaggccagca cttccctccc
rNDUFV3       967 ---------- ---------- ---------- ---------- ----------
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alignment  position  2 1 5 1 . . . . . .   2 1 6 1 . . . . . .   2 1 7 1 . . . . . .   2 1 8 1 . . . . . .   2 1 9 1 . . . . . .
hNDUFV3       1548 - - - - - - - - - -   - - - - - - - - - -   - - - - - - - - - -   - - - - - - - - - -   - - - - - - - - - -
mNDUFV3       1385 c c c t c c c c c a   t g c t a a c a c a   g g c t c c c c c c   c t c c c c c c a a   c a c a g g t c t g
rNDUFV3        967 - - - - - - - - - -   - - - - - - - - - -   - - - - - - - - - -   - - - - - - - - - -   - - - - - - - - - -

alignment  position  2 2 0 1 . . . . . .   2 2 1 1 . . . . . .   2 2 2 1 . . . . . .   2 2 3 1 . . .
hNDUFV3       1548 - - - - - - - - - -   - - - - - - - - - -   - - - - - - - - - -   - - - - - - - -
mNDUFV3       1435 t c t a a c t g a g   g c t t t g c a g g   a c a c g t g a c a   g c a a g a g
rNDUFV3        967 - - - - - - - - - -   - - - - - - - - - -   - - - - - - - - - -   - - - - - - - -
```

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.

	mNDUFV3 (1471 bp)	rNDUFV3 (966 bp)
hNDUFV3 (1547 bp)	0.063 14 %	0.074 24 %
mNDUFV3 (1471 bp)		1.000 80 %

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

Extract alignment region	
Positions in alignment	from: ☐ to: ☐
Output file	dialign.seq

Extract aligned sequences

For comments, questions or bug reports, please contact support@genomatix.de

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