

アラインメントと系統樹作成

出席と宿題の提出 [提出方法](#)

リンク集

データベース検索：

1. [PubMed](#): 論文検索
2. [Entrez](#): 総合データベース
3. [Google Scholar](#): 文献データベース
4. [特許データベース](#)

ホモロジー検索：

1. [BLAST](#) [GenomeNET]
2. [FASTA](#) [GenomeNET]

配列解析：

1. [DNA → AA](#) : DNA配列をアミノ酸配列に変換
2. [Spidey](#) : DNAとcDNAのマッチング
3. [BLAST\(NCBI\)](#) : 遺伝子のホモロジー検索
4. [BLAST\(DDBJ\)](#) : 遺伝子のホモロジー検索
5. [Softberry/FGENESH](#) : 遺伝子の予測
6. [GeneMark](#) : 遺伝子の予測
7. [GENESCAN](#) : 遺伝子の予測
8. [clustalW](#) : アライメント
9. [SSPN](#) : スプライシングの予測
10. [ORF Finder](#) : ORFの予測
11. [TFSEARCH](#) : 転写因子結合部位の予測
12. [MOTIF](#) : タンパク質モチーフ検索
13. [pI/Mw](#) : 等電点、分子量の予測

解析用配列

[ある遺伝子AのgenomeDNA配列](#)

Safari ファイル 編集 表示 履歴 ブックマーク ウィンドウ ヘルプ

BLAST: Basic Local Alignment Search Tool

http://blast.ncbi.nlm.nih.gov/Blast.cgi

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BLAST Basic Local Alignment Search Tool

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BLAST finds regions of similarity between biological sequences. [more...](#)

New Designing or Testing PCR Primers? Try your search in **Primer-BLAST**.

BLAST Assembled Genomes

Choose a species genome to search, or [list all genomic BLAST databases](#).

- [Human](#)
- [Mouse](#)
- [Rat](#)
- [Arabidopsis thaliana](#)
- [Oryza sativa](#)
- [Bos taurus](#)
- [Danio rerio](#)
- [Drosophila melanogaster](#)
- [Gallus gallus](#)
- [Pan troglodytes](#)
- [Microbes](#)
- [Apis mellifera](#)

Basic BLAST

Choose a BLAST program to run.

nucleotide blast	Search a nucleotide database using a nucleotide query <i>Algorithms: blastn, megablast, discontinuous megablast</i>
protein blast	Search protein database using a protein query <i>Algorithms: blastp, psi-blast, phi-blast</i>
blastx	Search protein database using a translated nucleotide query
tblastn	Search translated nucleotide database using a protein query
tblastx	Search translated nucleotide database using a translated nucleotide query

Specialized BLAST

Choose a type of specialized search (or database name in parentheses.)

- Make specific primers with [Primer-BLAST](#)
- Search [trace archives](#)
- Find [conserved domains](#) in your sequence (cds)
- Find sequences with similar [conserved domain architecture](#) (cdart)
- Search sequences that have [gene expression profiles](#) (GEO)
- Search [immunoglobulins](#) (IgBLAST)
- Search for [SNPs](#) (snp)
- Screen sequence for [vector contamination](#) (vecscreen)
- [Align](#) two sequences using BLAST (bl2seq)
- Search [protein](#) or [nucleotide](#) targets in PubChem BioAssay

News

[Align Sequences with BLAST](#)

A new BL2seq functionality has been added to the standard BLAST pages that allows you to align a query against a set of subject sequences.
2008-09-04 12:56:52

[More BLAST news...](#)

Tip of the Day

How to Search Custom Databases in Web-Blast Using Entrez Queries.

A powerful feature of the BLAST Web interface is the ability to limit BLAST searches to a subset of any database using a standard Entrez query. Skillful use of Entrez queries allows the equivalent of on-the-fly construction of databases of exact composition.

[More tips...](#)

Protein BLAST: Align two or more sequences using BLAST

http://blast.ncbi.nlm.nih.gov/Blast.cgi?PROGRAM=blastp&BLAST_PROGRAMS=bla

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Protein BLAST: Align two o...

BLAST Basic Local Alignment Search Tool

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NCBI/ BLAST/ blastp suite

blastn **blastp** blastx tblastn tblastx

BLASTP programs search protein subjects using a protein query. [more...](#) [Reset page](#) [Bookmark](#)

Enter Query Sequence

Enter accession number, gi, or FASTA sequence Clear

Query subrange From

```
MAAIYLLIAALIASSHALAAHGAGGGVPLAAAAPLPFGDLAASGKLRTPNATVPASMDFGNIT
AALPAAVLFPGPSGDVAELLRAAYAAPGRPFTVSRFRGHSTMGQALAAAGVVVHMQSMGGG
GAPRINVSADGAYVDAGGEQLWVDVLRALARGVAPRSWTDYLHLTVGGTLSNAGVSGQTYR
HGPQISNVLELDVITGHGETVYCSKAVNSDLFDAVLGGLGQFGVITRVARVAVEPAPARARWVRLV
YADFAAFSADQERLVAARPDGSHGPWSYVEGAVYLAGRGLAVALKSSGGFFSDADAARVVALA
```

Or, upload file

Job Title

Enter a descriptive title for your BLAST search

Align two or more sequences

Enter Subject Sequence

Enter accession number, gi, or FASTA sequence Clear

Subject subrange From

```
MAVLLMLNCFVKATAPPPWPPSASSASFLDDLGLGIAPLIRADEAGTARASADFGNLSVAG
VGAPRLAAAAVLYPSRPADIAALLRASCARPAPFAVSARGCGHSHVHGQASAPDGVVDM
ASLGRLLQGGGARRLAVSVEGRYVDAGGEQLWVDVLRASMAHGLTPVSWTDYLHLTVGGT
LSNAGISGQAFRHGQISNVLELDVITGVGEMVYCSKEKAPDLFDAVLGGLGQFGVITRARI
LAPAPARARWVRFVYTTAAAMTADQERLIAVDRAGGAGAVGGLMDYVEGSVHLNQLVE
```

Or, upload file

Program Selection

Algorithm blastp (protein-protein BLAST)

Choose a BLAST algorithm

BLAST Search protein sequence using Blastp (protein-protein BLAST)

Show results in a new window

Algorithm parameters

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NCBI | NLM | NIH | DHHS

B1遺伝子のアミノ酸配列

B1遺伝子のアミノ酸配列

NCBI Blast:Protein Sequence (532 letters)

http://blast.ncbi.nlm.nih.gov/Blast.cgi

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NCBI Blast:Protein Sequenc...

BLAST Basic Local Alignment Search Tool

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▶ NCBI/ BLAST/ blastp suite-2sequences/ Formatting Results - HTSSZ2DY113

[Edit and Resubmit](#) [Save Search Strategies](#) ▶ [Formatting options](#) ▶ [Download](#)

Blast 2 sequences

Protein Sequence (532 letters)

Query ID	lcl 52017	Subject ID	52019
Description	None	Description	None
Molecule type	amino acid	Molecule type	amino acid
Query Length	532	Subject Length	658
		Program	BLASTP 2.2.22+ ▶ Citation

Other reports: ▶ [Search Summary](#) [[Taxonomy reports](#)]

▼ **Graphic Summary**

Distribution of 2 Blast Hits on the Query Sequence

Mouse over to see the define, click to show alignments

Color key for alignment scores

<40	40-50	50-80	80-200	>=200
-----	-------	-------	--------	-------

Query 0 100 200 300 400 500

▼ **Dot Matrix View**

▼ **Descriptions**

Sequences producing significant alignments:	Score (Bits)	E Value
lcl 52019 unnamed protein product	<u>481</u>	3e-140

▼ **Alignments** Select All [Get selected sequences](#) **NEW**

```
>lcl|52019 unnamed protein product
Length=658

Score = 481 bits (1239), Expect = 3e-140, Method: Compositional matrix adjust.
Identities = 289/519 (55%), Positives = 341/519 (65%), Gaps = 36/519 (6%)
```

NCBI Blast:Protein Sequence (532 letters)

http://blast.ncbi.nlm.nih.gov/Blast.cgi

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NCBI Blast:Protein Sequenc...

>lcl|52019 unnamed protein product

▼ Alignments Select All [Get selected sequences](#) **NEW**

>lcl|52019 unnamed protein product
Length: 532

Score = 481 bits (1239), Expect = 3e-140, Method: Compositional matrix adjust.
Identities = 289/519 (55%), Positives = 341/519 (65%), Gaps = 36/519 (6%)

Query 39 GDLAASGKLRTPDNATVPASMDFGNITAA-----LPAAVLFPSPGDVAELLRAAYA 90
GDL + +R D T AS DFGN++ A AAVL+P P D+A LLRA+ A
Sbjct 33 GDLGIAPLIRADEAGTARASADFGNLSVAGVAGAPRLAAAAAVLYPSRPADIAALLRASCA 92

Query 91 APGRPFVTSFRGRGHSTMGQALAAGGVVHMQSMG---GGGAPRINVSADGAYVDAGGEQ 147
P PF VS RG GHS GQA A GVVV M S+G GGG R+ VS +G YVDAGGEQ
Sbjct 93 RPA-PFAVSARGCGSHVHGQASAPDGVVDMASLGRLLQGGARRLAVSVEGRYVDAGGEQ 151

Query 148 LWVDVLRaalARGVAPRSWTDYLHLTVGGTLSNAGVSGQTYRHGPQISNVLELDVITGHG 207
LWVDVLR+AA G+ P SWTDYLHLTVGGTLSNAG+SQQ +RHGPQISNVLELDVITG G
Sbjct 152 LWVDVLRASMAHGLTPVSWTDYLHLTVGGTLSNAGISGQAFRHGPQISNVLELDVITGVG 211

Query 208 ETVTCISKAVNSDLFDVAVLGGGQFGVITRARVAVEPAPARARWVRLVYADFAAFSADQER 267
E VTC SK DLFDVAVLGGGQFGVITRAR+ + PAPARARWVR VY AA +ADQER
Sbjct 212 EMVTCSEKAPDLFDVAVLGGGQFGVITRARIPLAPAPARARWVRFVYTTAAAMTADQER 271

Query 268 LVAA----RPDGSHPWSYVEGAVYLAGRGLAVALKS-----SGGFFSDADAAR 312
L+A G YVEG+V+L +GL ++ S FFSADAR
Sbjct 272 LIAVDRAGGAGAVGLMDYVEGSVHL-NQGLVETWRTQPSPSSSSSSSSFFSDADEAR 330

Query 313 VVALAAARNATAVYSIEATLNYAANATPSS--VDAVAALGDLHFEGFSSFRSDVYEE 370
V ALA +Y +E + + A PS+ VD + +L E GF F+DV Y
Sbjct 331 VAALAKEAGGV-LYFLEGAIFGGAAGPSAADVKRMDVLRREL RHERGFVFAQDVAYAG 389

Query 371 FLDRVYEEEEALEKAGLRVPHFWLNLFPVPSRIADFRGVFKGILQTATDIAGPLIYIP 430
FLDRV+ E L AGLW VPHFWLNLFP S + F GVF GIL + T GP++IYP
Sbjct 390 FLDRVHDGELKRAAGLWDVPHFWLNLFLPRSGVLAFAADGVFHGIL-SRTPAMGPVLIYIP 448

Query 431 VNKSKWDAAMSAV-TPEGEEVFYVVSLLFS-AVANDVAALEAQNRRILRFCDLAGIGYK 488
+N++KWD+ MSAV T + +EVFY V +L S A A DV LE QN IL FC++AGI YK
Sbjct 449 MNRNKWDSNMSAVITDDDDGDEVFYTVGILRSAAAAGDVGRLQNDLILGFCEVAGIAYK 508

Query 489 AYLHYDSRGDWV-RHFGAK-WDRFVQRKDYDPKLLS 525
YL +Y S+ +W RHFGA W RFVQRK KYDPK +LS
Sbjct 509 QYLPYYSQAEWQKRHFGANLWPRFVQRKSKYDPKAILS 547

Score = 20.8 bits (42), Expect = 0.17, Method: Compositional matrix adjust.
Identities = 17/47 (36%), Positives = 26/47 (55%), Gaps = 6/47 (12%)

Query 8 IAALIASS-----HALAAHGAGGGVPLAAAAPLFPFGDLAASGKLR 48
IAAL+ +S A++A G G V A+AP D+A+ G+L+
Sbjct 83 IAALLRASCARPAPFAVSARGCGSHVHGQASAPDGVVDMASLGRLLQ 129

Select All [Get selected sequences](#) **NEW**

▼ **Alignments** Select All [Get selected sequences](#) NEW

Identities: 同じアミノ酸を1とカウント/全体
Positives: 類似アミノ酸を1とカウント/全体
Similarity: 類似アミノ酸を0.5とカウント/全体

>lcl|52019 unnamed protein product
Length=658

Score = 481 bits (1239), Expect = 3e-140, Method: Compositional matrix adjust.
Identities = 289/519 (55%), Positives = 341/519 (65%), Gaps = 36/519 (6%)

```
Query 39  GDLAASGKLRTPNATVPASMDFGNITAA-----LPAAVLFPSPGDVAELLRAAYA 90
          GDL + +R D T AS DFGN++ A AAVL+P P D+A LLRA+ A
Sbjct 33  GDLGIAPLIRADEAGTARASADFGNLSVAGVGAPRLAAAAAVLYPSRPADIAALLRASCA 92

Query 91  APGRPFVTVSFRGRGHSTMGQALAAAGVVVHMQSMG---GGGAPRINVSADGAYVDAGGEQ 147
          P PF VS RG GHS GQA A GVVV M S+G GGG R+ VS +G YVDAGGEQ
Sbjct 93  RPA-PFAVSARGCGHSVHGQASAPDGVVVDMASLGRLOGGGARRLAVSVEGRYVDAGGEQ 151

Query 148 LWVDVLRAALARGVAPRSWTDYLHLTVGGTLSNAGVSGQTYRHGPQISNVLELDVITGHG 207
          LWVDVLRA++A G+ P SWTDYLHLTVGGTLSNAG+SGQ +RHGPQISNVLELDVITG G
Sbjct 152 LWVDVLRASMAHGLTPVSWTDYLHLTVGGTLSNAGISGQAFRHGPQISNVLELDVITGVG 211

Query 208  ETVTCSKAVNSDLFDAVLGGLGQFGVITRARVAVEPAPARARWVRLVYADFAAFSADQER 267
          E VTCSK DLFDAVLGGLGQFGVITRAR+ + PAPANARWVR VY AA +ADQER
Sbjct 212  EMVTCSKEKAPDLFDAVLGGLGQFGVITRARIPLAPAPANARWVRFVYTTAAAMTADQER 271

Query 268  LVAA----RPDGSHPWSYVEGAVYLAGRGLAVALKS-----SGGFFSDADAAR 312
          L+A G YVEG+V+L +GL ++ S FFSADAD AR
Sbjct 272  LIAVDRAGGAGAVGGLMDYVEGSVHL-NQGLVETWRTQPQPPSPSSSSSSFFSDADEAR 330

Query 313  VVALAAARNATAVYSIEATLNYAANATPSS--VDAAVAAALGDLHFEEGFSFSRDVITYEE 370
          V ALA +Y +E + + A PS+ VD + +L E GF F++DV Y
Sbjct 331  VAALAKEAGGV-LYFLEGAIYFGGAAGPSAADVDRMDVLRRELRRHERGFVFAQDVAYAG 389

Query 371  FLDRVYEEEEALEKAGLWRVPHWLNLFVPGSRIADFDRGVFKGILQTATDIAGPLIYYP 430
          FLDRV+ E L AGLW VPHWLNLF+P S + F GVF GIL + T GP++IYP
Sbjct 390  FLDRVHDGELKLRAGLWDVPHWLNLFVPRSGVLAFAFGVFGIL-SRTPAMGPVLIYP 448

Query 431  VNKSKWDAAMSAV-TPEGEEVFYVVSLLFS-AVANDVAALEAQNRRILRFCDLAGIGYK 488
          +N++KWD+ MSAV T + +EVFY V +L S A A DV LE QN IL FC++AGI YK
Sbjct 449  MNRNKWDSNMSAVITDDDGDEVFYTVGILRSAAAAGDVGRLEEQNDEILGFCEVAGIAYK 508

Query 489  AYL AHYDSRGDWV-RHFGAK-WDRFVQRKDYDPKLLS 525
          YL +Y S+ +W RHFGA W RFVQRK KYDPK +LS
Sbjct 509  QYLPYYGSQAEWQKRHFGANLWPRFVQRKSKYDPKAILS 547
```

Score = 20.8 bits (42), Expect = 0.17, Method: Compositional matrix adjust.
Identities = 17/47 (36%), Positives = 26/47 (55%), Gaps = 6/47 (12%)

アミノ酸20種類

水になじむもの
(親水性)
(極性を持つもの)

電荷を持つもの

酸性

アスパラギン酸(D), グルタミン酸(E)

塩基性

アルギニン(R), リシン(K), ヒスチジン(H)

電荷を持たないもの

グリシン(G), セリン(S), トレオニン(T), システイン(C)
アスパラギン(N), グルタミン(Q), チロシン(Y)

水になじまないもの
(疎水性)
(非極性のもの)

アラニン(A), バリン(V), ロイシン(L), イソロイシン(I)
メチオニン(M), トリプトファン(W), フェニルアラニン(F)
プロリン(P)

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4. [特許データベース](#)

ホモロジー検索：

1. [BLAST](#) [GenomeNET]
2. [FASTA](#) [GenomeNET]

配列解析：

1. [DNA → AA](#) : DNA配列をアミノ酸配列に変換
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6. [GeneMark](#) : 遺伝子の予測
7. [GENESCAN](#) : 遺伝子の予測
8. [clustalW](#) : アライメント
9. [SSPN](#) : スプライシングの予測
10. [ORF Finder](#) : ORFの予測
11. [TFSEARCH](#) : 転写因子結合部位の予測
12. [MOTIF](#) : タンパク質モチーフ検索
13. [pI/Mw](#) : 等電点、分子量の予測

解析用配列

[ある遺伝子AのgenomeDNA配列](#)



Multiple Sequence Alignment by CLUSTALW

CLUSTALW

MAFFT

PRRN

[Help](#)

General Setting Parameters:

Output Format:

Pairwise Alignment: FAST/APPROXIMATE SLOW/ACCURATE

Enter your sequences (with labels) below (copy & paste): PROTEIN DNA

Support Formats: FASTA (Pearson), NBRF/PIR, EMBL/Swiss Prot, GDE, CLUSTAL, and GCG/MSF

Or give the file name containing your query

ファイルが選択されていません

More Detail Parameters...

Pairwise Alignment Parameters:

For FAST/APPROXIMATE:

K-tuple(word) size: , Window size: , Gap Penalty:

Number of Top Diagonals: , Scoring Method:

For SLOW/ACCURATE:

Gap Open Penalty: , Gap Extension Penalty:

Select Weight Matrix:

(Note that only parameters for the algorithm specified by the above "Pairwise Alignment" are valid.)

Multiple Alignment Parameters:

Gap Open Penalty: , Gap Extension Penalty:

Weight Transition: YES (Value:) , NO

Hydrophilic Residues for Proteins:


Hydrophilic Gaps: YES NO

Multiple Sequence Alignment - CLUSTALW

http://align.genome.jp/

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Multiple Sequence Alignme...



Multiple Sequence Alignment by CLUSTALW

CLUSTALW MAFFT PRRN

Help

General Setting Parameters:

Output Format: CLUSTAL

Pairwise Alignment: FAST/APPROXIMATE SLOW/ACCURATE

Enter your sequences (with labels) below (copy & paste): PROTEIN DNA

Support Formats: FASTA (Pearson), NBRF/PIR, EMBL/Swiss Prot, GDE, CLUSTAL, and GCG/MSF

```
>B1
MAAIYLLIAALIASHALAAHGAGGGVPLAAAAPLPPFGDLAASGKLRTDPNATVPASMD
FGNITAAALPAAVLFGSPGDVAELLRAAYAAPRPFVTSFRGRGHSTMGQALAAGGVV
HMQSMGGGGAPRINVSADGAYVDAGGEQLWVDVLAALARGVAPRSWTDYHLHTVG
GTLNAGVSGQTYRHGPQISNVLELDVITGHGETVTCISKAVNSDLFDVGLGQFGVIT
```

Or give the file name containing your query
ファイルを選択 ファイルが選択されていません

Execute Multiple Alignment Reset

More Detail Parameters...

Pairwise Alignment Parameters:

For FAST/APPROXIMATE:
K-tuple(word) size: 1, Window size: 5, Gap Penalty: 3
Number of Top Diagonals: 5, Scoring Method: PERCENT

For SLOW/ACCURATE:
Gap Open Penalty: 10.0, Gap Extension Penalty: 0.1
Select Weight Matrix: BLOSUM (for PROTEIN)

(Note that only parameters for the algorithm specified by the above "Pairwise Alignment" are valid.)

Multiple Alignment Parameters:

Gap Open Penalty: 10, Gap Extension Penalty: 0.05

Weight Transition: YES (Value: 0.5), NO

Hydrophilic Residues for Proteins: GPSNDQERK

Hydrophilic Gaps: YES NO

B1遺伝子のアミノ酸配列

B2遺伝子のアミノ酸配列

CLUSTALW Result

http://align.genome.jp/sit-bin/clustalw

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CLUSTALW Result

[\[clustalw.aln\]](#)[\[clustalw.dnd\]](#)[\[readme\]](#)

CLUSTAL W (1.81) Multiple Sequence Alignments

Sequence type explicitly set to Protein
 Sequence format is Pearson
 Sequence 1: B1 532 aa
 Sequence 2: B2 658 aa
 Start of Pairwise alignments
 Aligning...

Sequences (1:2) Aligned. Score: 47.5564
 Sequences (2:2) Aligned. Score: 100
 Guide tree file created: [\[clustalw.dnd\]](#)
 Start of Multiple Alignment
 There are 1 groups
 Aligning...
 Group 1: Sequences: 2 Score:4053
 Alignment Score 1571
 CLUSTAL-Alignment file created [\[clustalw.aln\]](#)

[clustalw.aln](#)

CLUSTAL W (1.81) multiple sequence alignment

```

B1      MAIYLLIAALIASSHAAHAGGGVPLAAAAPLFPFGDLAASGKLRTPNATVPASMD
B2      -----MAVLLMLNCFVKATAPPPWPPSASSASFLDDLGLGIAPLIRADEAGTARASAD
          : . * : . . . . * : . . : : * : * * * . : : * * . * * *
B1      FGNITAALP-----AAVLFPSPGDVAELLRAAYAAPGRPFTVSRFRGRHSTMGQAL
B2      FGNLSVAGVGAPRLAAAAVLYPSRPADIAALLRASCARP-APFAVSARGCGHSVHGQAS
          ***:!.*          ***:*. *.:* *****: * * **:* ** * ** . ***
B1      AAGGVVHMQSMG---GGGAPRINVSADGAYVDAGGEQLWVDVLRRAALARGVAPRSWTDY
B2      APDGVVDMASLGRLQGGGARRLAVSVEGRYVDAGGEQLWVDVLRASMAHGLTPVSWTDY
          *.***** *:* * * * * * : * .: * *****: : * : : * * * * *
B1      LHLTVGGTLSNAGVSGQTYRHGPQISNVLELDVITGHGETVTCSEKAVNSDLFPAVLGGLG
B2      LHLTVGGTLSNAGISGQAFRHGPQISNVLELDVITGVGEMVTCSEKAPDLFPAVLGGLG
          *****: : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
B1      QFGVITRARVAVEPAPARARWVRLVYADFAAFSADQERLVAARPDGSHGFPW---YVEG
B2      QFGVITRARIPLAPAPARARWVRFVYTTAAAMTADQERLIAVDRAGGAGAVGGLMDYVEG
          *****: : : : : : : : : : : : : : : : : : : : : : : : : : :
B1      AVYLAG-----RGLAVALKSSGGFFSDADARVVALAARNATAVYSIEATLN-Y
B2      SVHLNQLVETWRTQPQPPSPSSSSSSFFSDADEARVAALAKEAGGVLYFLEGAIYFGG
          : : * : : : : : : : : : : : : : : : : : : : : : : : : : :
B1      AANATPSSVDAVAALGDLHFEEGFSFSRDVYEEFLDRVYEEEALEKAGLWRVPHPW
B2      AAGPSAADVDRMDVLRRELRLHERGFVFAQDVAYAGFLDRVHDGELKLRAGLWDVPHPW
          **..: : : * * : : : : : : : : : : : : : : : : : : : : : :

```

Multiple Sequence Alignment - CLUSTALW

http://align.genome.jp/

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Multiple Sequence Alignment by CLUSTALW

CLUSTALW MAFFT PRRN

Help

General Setting Parameters:

Output Format:

Pairwise Alignment: FAST/APPROXIMATE SLOW/ACCURATE

Enter your sequences (with labels) below (copy & paste): PROTEIN DNA

Support Formats: FASTA (Pearson), NBRF/PIR, EMBL/Swiss Prot, GCG, CLUSTAL, and GCG/MSF

```
TKWDNRISVVIPDEEIFYLVGFLSSAPSSSGHGSVEHAMNLNKIXDFCEKNGVGMKQYL  
ARYITQKQWKAHEGAX  
>B5  
MMLAYMDHAAAAAEPDAGAEPVAVAVDAAEFAAAMDFGGLVSARPAAVRPASSDD  
VASAIRAAARTAHLTVAARGNGHVSAGQAMARGGLVDMRALPRRMLVVPSPGKFK
```

Or give the file name containing your query

ファイルが選択されていません

More Detail Parameters...

Pairwise Alignment Parameters:

For FAST/APPROXIMATE:

K-tuple(word) size: , Window size: , Gap Penalty:

Number of Top Diagonals: , Scoring Method:

For SLOW/ACCURATE:

Gap Open Penalty: , Gap Extension Penalty:

Select Weight Matrix:

(Note that only parameters for the algorithm specified by the above "Pairwise Alignment" are valid.)

Multiple Alignment Parameters:

Gap Open Penalty: , Gap Extension Penalty:

Weight Transition: YES (Value:), NO

Hydrophilic Residues for Proteins:

Hydrophilic Gaps: YES NO

Select Weight Matrix:

Type additional options (delimited by whitespaces) below:

B1~B5遺伝子のアミノ酸配列

CLUSTALW Result

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CLUSTALW Result

Group 2: Sequences: 2 Score:3854
Group 3: Sequences: 4 Score:3342
Group 4: Sequences: 5 Score:3508
Alignment Score 12129
CLUSTAL-Alignment file created [clustalw.aln]

clustalw.aln

CLUSTAL W (1.81) multiple sequence alignment

```
B1      MAAIYLLIAALIASHALAAHGAGGGVPLAAAAPLFFPGDLAASGKLRTPDPNATVPASMD
B2      -----MAVLLMLNCFVKATAPPWPSPASSASSFLDDLDLGIAPLIRADEAGTARASAD
B3      -----MAWCLVFMVFLIYCLISTVGLFVAPADEAAMQLGGVGGRLSVEPSDVMSEASLD
B4      --MRGAMKPSIVHCLKLLMLLALGGVTMHVPEDEDDVVASLGALRLDGHFSFDDAHAHAARD
B5      -----MMLAYMDHAAAAAEFDAGAEPAVAAVDAAEFAAAMD
                                         *: *

B1      FGNITAAALP-----AAVLFPGSPGDVAELLR--AAYAAPGRPFTVSRFRGRGHSMTGQA
B2      FGNLSVAGVAGPRLAAAAAVLYPSRPADIAALLR-ASCARP-APFAVSARGCGHSVHGQA
B3      FGRLTSAEP-----LAVFHPRGAGDVAALVK--AAYGSASGIRVSARGHGHISGQA
B4      FGNRCSLLP-----AAVLFHFGSVSDVAATVRRVFLQGRSSPLTVAARGHGHISLLGQS
B5      FGGLVSARP-----AAVVRPASSDDVASAIR---AAARTAHLTVAARGNGHSVAGQA
**          ** *   *: *  : :          : * : ** ** * :

B1      LAAGGVVHMQSMG---GGGAPRINVSADG--AYVDAGGEQLWVDVLRALARG-VAPRS
B2      SAPDGVVDMASLGRLOGGGARRLAVSVEG--RYVDAGGEQLWVDVLRASMAHG-LTPVS
B3      QAAGGVVDMSHGWRAEAERTLPVYSPALGGHYIDVWGGELWIDVLNWTLAHGGLAPRS
B4      QAAGGIVVMES---LAAAAARAVRVHGGASPHVDAPGGELWINVLHETLKHG-LAPRS
B5      MARGGLVDMRALP-----RRMQLVVAPSGEKFADVPGGALWEVLEHWAVSKHGLAPAS
 * .*: : . *          . * . * ** : ** . : : : : ** *

B1      WTDYLHLTVGGTSLNAGVSGQTYRHGPQISNVLELDVITGHGETVTCSEKAVNSDLFPAVL
B2      WTDYLHLTVGGTSLNAGISGQAFRHGPQISNVLELDVITGVGEMVTCSEKAPDLFPAVL
B3      WTDYLHLTVGGTSLNAGISGQAFRHGPQISNVLELDVITGVGEMVTCSESNNDLFFGAL
B4      WTDYLHLTVGGTSLNAGVSGQAFRHGPQISNVLELDVITGRGEVVTCSHEVNSDLFYAAL
B5      WTDYLRHLTVGGTSLNAGVSGQAFRYGPQISNVLELDVITGDGECHVCSRSADPDLFFAVL
***** : : ***** : : ***** : : ***** : : ***** : : ***** : : ***** : :

B1      GGLGQFGVITRARIPLAPAP-----ARARWVRLVYAD
B2      GGLGQFGVITRARIPLAPAP-----ARARWVRFVYTT
B3      GGLGQLGITRARIPLAPAP-----HRVRWIRALYSN
B4      GGLGQFGVITRARIPLAPAP-----KMVRWIRVLYSD
B5      GGLGQFGVITRARIPLAPAPQTVSTTPPPNRRNRRPNRPAADRRELALQVRWTRVLYAS
***** : : ***** : : ***** : : ***** : : ***** : : ***** : :

B1      FAAFSADQERLVAARPDGSHCPWS---YVEGAVYLAC-----RGLAVALKSSGG
B2      AAAMTADQERLIAVDRAGGAGAVGLMDYVEGSHVHLNQLVETWRTQPQPPSPSSSSSSS
B3      FTEFTADQERLISLQHGRR-----FDYVEGFVVAEG-----LINNRSS
B4      FETFTEDQEKLIASEKT-----FDYIEGFVIINRT-----GILNWRWT
B5      FADYAADAEWLVTRPHEA-----FDYVEGFVFRSD-----DPVNGWPTV
 : * * * : :          * : * .

B1      FFSDADAARVVALAAARN-ATAVYSIEATLN-YAANATPSSVDAVAALGDLHFEFGFS
B2      FFSDAEARVAALAKEAG-GVLYFLEGAIYFGGAAGPSAADVVKRMDVLRRELRRHGRFV
B3      FFSQNPVKLSSLKHHSG-VLYCLEVTMNFN---DSTAVTVDQDVEALLGELNFIPTV
B4      SFPQDPVQASQFQSDGR-VLYCLEVTMNFN---HDEADIMEQEVGALLSRLRYISSTL
B5      PIPDGAHFDSL PANAGPVLVLYCLEVALYQGGGGGGDDMDKRVGEMMRQLKYVRGLE
 :          :          : :          : * . .

B1      FSRDVTYEEFLDRVYEEEEALEKAGLWRVPHWLNLFVPSGRIADFDRGVFKGLQTATD
B2      FAQDVAYAGFLDRVHDGELKRAAGLWDVPHWLNLFVPSGRIADFDRGVFKGLQTATD
B3      FTTDLPIYDFLDRVHKAELKRGKMWVPHWLNLFVPSGRIADFDRGVFKGLQTATD
B4      FYTDVTYEFLDRVHTSELKRAAGLWDVPHWLNLFVPSGRIADFDRGVFKGLQTATD
B5      FTTDLPIYDFLDRVHKAELKRGKMWVPHWLNLFVPSGRIADFDRGVFKGLQTATD
```

CLUSTALW Result

http://align.genome.jp/sit-bin/clustalw

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CLUSTALW Result

```
B2 AAAMTADQERLIIVDRAGGAGAVGGLMDYVEGSHLNQGLVETWRTQPFPSPSSSSSS
B3 FTEFTADQERLISLQHGGR-----FDYVEGFVAAEG-----LINNWRSS
B4 FETFTEDQEKLIASEKT-----FDYIEGFVIINRT-----GILNWRRT
B5 FADYAADAEWLVTRPPHEA-----FDYVEGFVFRSD-----DPVNGWPTV
   : * * * : : * * * .

B1 FFSADAARVVALAAARN-ATAVYSIEATLN-YAANATPSSVDAVAAALGDLHFEEGFS
B2 FFSADAARVVALAAAKEAG-GVLYLEGAIYFGAAGPSAADVDRKMDVLRRELHERGFV
B3 FFSQPQPVKLSLKHHSGLVLYCLEVTKNYD----DSTAVTVDQDVEALLGELNFIPTV
B4 SFKQDPVQASQFQSDGR-VLYCLELTMNFN----HDEADIMEQEVGALLSRLRYISSTL
B5 PIPDGAHFASLLPANAGPVLYCLEVALYQRGGGGDDMDKRVGEMMRQLKYVRGLE
   :           :           : : * * * .

B1 FSRDVTYEEFLDRVYEEEEALEKAGLWRVPHWLNLFVPGSRIADFDRGVFKGILQTATD
B2 FAQDVAYAGFLDRVHDGELKLRAGLWDVPHWLNLFVPSGVLAADGVFHGILSRTPA
B3 FTDDLPIYVDFLDRVHKAELKLRGKGMWEVPHWLNLFVPSRIADFDRGVFRGVLGSR-T
B4 FYTDVTYELFLDRVHSELKLRAGLWVPHWLNLLIPRSTVHKFAKEVFGKILKD--S
B5 FAAGVGVYDFLSRVNRVEDEARRNGSWAAPHWLNLFISRRDIAAFDRAVLNGLADG--
 * . : * * * . * * * . * * * . * * * . * * * . * * * . * * * . *

B1 IAGPLIIPVNKSKWDAAMSAVTPEGE-EEVFYVVSLLF--SAVAN-DVAALEAQNRRI
B2 MG-PVLIYPMNRKWDNSMSAVITDDDGDEVFYTVGILR--SAAAAGDVGRLEQNDL
B3 AGGPILYPMNRHKWDRSSVVTPEEDVFYLVAFVLSAVPGSTDPAQSLAALERQNRIL
B4 NNGPILYPMNRHKWDRNRTSVVTPDEEIFYLVGFLSSAP--SSSGHGSVEHAMLNKIV
B5 VDGPMLIYPMKSKWDPATSVLNPGEIFYLVALLRFRCP-YPGGGPPVDELVAQNNAI
   * * * * : * * * * . * * * . : . : . : . : * * *

B1 RFCDLAGIGYKAYLAHYDSRGDWVRHFG--AKWDRFVQRKDKYDPKLLSPGQDIFN---
B2 GFCEVAGIAYKQYLPYYSQAQWQKRHFANLWPRFVQRKSKYDPKALLSLQYVLLVYY
B3 EFCDEAGIGAKQYLPNHKAQREWEAHFG--ARWARFARLKAEPDPRAMLATGQGFDSPP
B4 DFCEKNGVMKQYLPYTTQKQWKAHFG--AX-----
B5 DACRSNGYDYKIYFPSYHAQSDWSRHFG--AKWSRFVDRKARYDPLAILAPQNI FARTP
   * * * * * : : : : * * .

B1 -----
B2 QPICMHWMPSYACRSQTYGMECIMMHIYRRLIFHIQHVLCKPELTARSIDVSQSSER
B3 LLAES-----
B4 -----
B5 SSVAAAAAIV-----

B1 -----
B2 QLTTTANDTGDSSHHRITWITTTLLVAFELANLCLVPTTT
B3 -----
B4 -----
B5 -----
```

clustalw.dnd

```
(
(
B1:0.25377,
B2:0.27066)
:0.04462,
(
B3:0.25219,
B4:0.27805)
:0.02580,
B5:0.34051);
```

Select tree menu Exec

CLUSTALW Result

http://align.genome.jp/sit-bin/clustalw

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CLUSTALW Result

```

B2 AAAMTADQERLITAVDRAGGAGAVGGLMDYVEGSHLNQGLVETWRTQPQPPSPSSSSSSS
B3 FTEFTADQERLISLQHGRR-----FDYVEGFVVAAG-----LINNRWS
B4 FETFTEDQEKLIASEKT-----FDYIEGFVLIINRT-----GILNNWRT
B5 FADYAADAEWLVTRPPHEA-----FDYVEGFVFRSD-----DPVNGWPTV
   : * * * * :          * : * * .

B1 FFSDADAARVVALAAARN-ATAVYSIEATLN-YAANATPSSVDAVAALGDLHFEEGFS
B2 FFSDADEARVAALAKEAG-GVLYFLEGAIYFGGAAGPSAADVKRMDVLRRELRRHERGFV
B3 FFSPQNPVKLSSLKHHSG-VLYCLEVTKNYD----DSTAVTVDQDVEALLGELNFIPTV
B4 SFKPDQPVQASQFQSDGR-VLYCLELTMNFN----HDEADIMEQEVGALLSRLRYISSTL
B5 PIPDGAHFDAALLPANAGPVLYCLEVALYQRGGGGGGDDMDKRVGEMMRQLKYVRGLE
   :           :           : : : * . .

B1 FSRDVTYEEFLDRVYEEEEALEKAGLWRVPHWLNLFVPGSRIADFRGVFKILQTATD
B2 FAQDVAYAGFLDRVHDGELKLRAGLWDVPHWLNLFVPRSGVLAADGVFHGILSRTPA
B3 FTDDLPHYVDFLDRVHKAELKLRGKGMWEVPHWLNLFVPASRIADFRGVFRGVLGSR-T
B4 FYTDVTYLEFLDRVHTSELKLRAGLWEVPHWLNLLIPRSTVHKFAKEVFGKILKD--S
B5 FAAGVGYVDFLSRVNRVEDEARRNGSWAAPHWLNLFISSRDIAAFDRAVLNGMLADG--
   * . : * * * . * * . * * . * * * . * * * . * * * . * * * . * * : *

B1 IAGPLIIPVNSKWDAAAMSAVTPEGE-EEVFYVVSLLF--SAVAN-DVAALEAQNRRIL
B2 MG-PVLIYPMNRKWDNSMSAVITDDGGDEVFYTVGILR--SAAAAGDVGRLEEQNDEIL
B3 AGGPLIIPMNRHKWDRSSVVTPEEDVYLVAFVLSAVPGSTDPAQSLAALERQNRIL
B4 NNGPILLYPVNRTKWDNRNRTSVVTPDEEIFYLVGFLSSAP--SSSGHGSVEHAMLNKIV
B5 VDGPMIIPMLKSKWDPATSVLNPGEIFYLVALLRFRCP-YPGGGPPVDELVAQNNAII
   * : : * * : * * * * . . : : . : . : . : * * :

B1 RFCDLAGIGYKAYLAHYDSRQDWRHFG--AKWDRFVQRKDKYDPKLLSPGQDIFN---
B2 GFCDEVAGIAYKQYLPYYSQAQWQKRHFANLWPRFVQRKSKYDPKALLSLQYVLLVY
B3 EFCDEAGIGAKQYLPNHKAQREWEAHFG--ARWARFARLKAEPDPRAMLATGQGIQDSSPP
B4 DFCEKNGVGMKQYLPAYTTQKQWKAHFG--AX-----
B5 DACRSNGYDYKIYFPSYHAQSDWSRHF--AKWSRFVDRKARYDPLAILAPQNI FARTP
   * * * * * . : : : * * .

B1 -----
B2 QPICMHWMPSYACRSQTYGMLECIMMHIYRRLIFHIQHVLICKPELTARSIDVSQSSER
B3 LLAES-----
B4 -----
B5 SSVAAAAIV-----

B1 -----
B2 QLTTFANDTGDSSHRYITWITTTLLVAFELANLCLVPTTT
B3 -----
B4 -----
B5 -----

```

clustalw.dnd

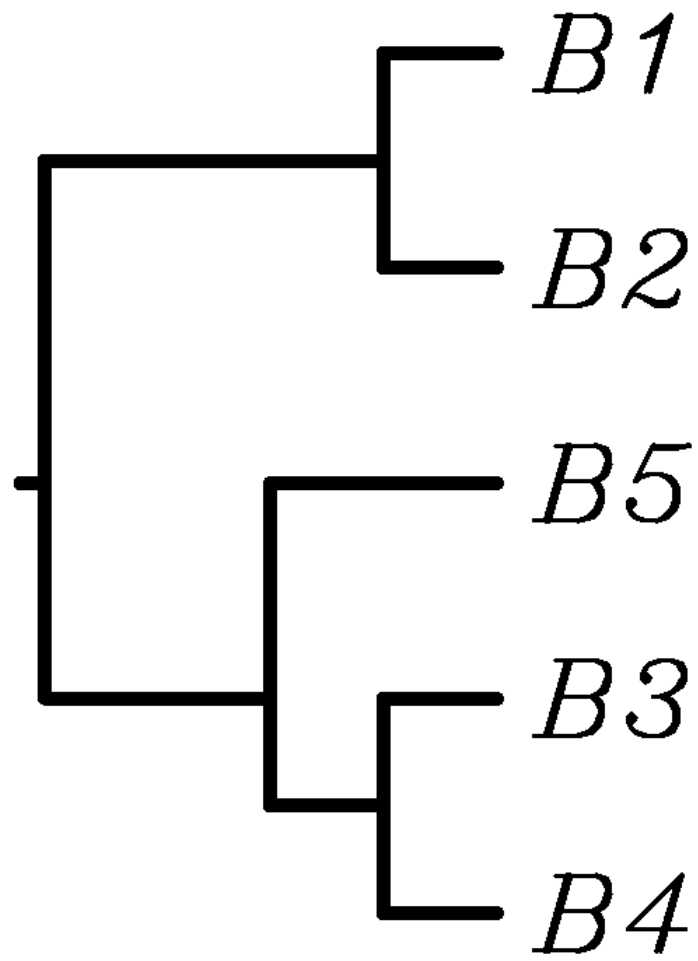
```

(
(
B1:0.25377,
B2:0.27066)
:0.04462,
(
B3:0.25219,
B4:0.22000)
:0.02580,
:0.34051);

```

N-J Tree Exec

[\[PostScript file\]](#) [\[PDF file\]](#) [\[Phylip format\]](#)



CLUSTALW Result

Start of Multiple Alignment
There are 4 groups
Aligning...

Group 1: Delayed
Group 2: Delayed
Group 3: Delayed
Group 4: Delayed

Sequence:3 Score:20157
Sequence:2 Score:19947
Sequence:4 Score:16880
Sequence:5 Score:17102
Alignment Score 61032
CLUSTAL-Alignment file created [clustalw.aln]

clustalw.aln

CLUSTAL W (1.81) multiple sequence alignment

```
B1      ATGGCGGCGATTACCTGCTGATCGCCGCGTGATCGCCTCCTCCCATGCACTCGCCGGG
B3      ---ATGGCGTGGTGTGTTTCATGGTGTCTTGATCTACTGCCTCAT-CTCGACTGT
B2      ---ATGGCAGTGCTCCTCATGCTCAACTGCTTCGTCGAAG-GCCACGGCGCCCGCCCATG
B4      ----ATGCGGGGAGCCATGAAGCCGTCGA--TCGTGCACTGCCATCAAGCTGCTCATGCTG
B5      -----

```

```
B1      CATGGCGCCGGCGGGCGGTTCCGTT----GGCGGGCGCGCG-CCTC----TCCCGTT
B3      CGGGCTGCCGGTGGCGCCGGCCGAC-----GAGCGCGGATG-CAGC----TG----
B2      GCCCGCGTCGGCTTCGTCCGCCCTCCTTCTCGACGACCTCGCGGACCTCGGCATCGCGCC
B4      CTGGCGCTCGCGGGGTCACCATGCA----CGTCCCGGACGAGGACGACGTGGTCGGCT-
B5      -----ATGATGCTCGCGTACATGGACCACCGCCGCGCGG-CCGGGAGCCG----
          *                * * * * *

```

```
B1      CCCCGGGACCTCGCCGCTCCGGCAA-GCTCCGGACCGACCCGAACGCCACCGTGCCGG
B3      ----GGCGCGTCG--GCGGTGGCG--GCTCAGCGTGAGCCGCTGATGATGGAGG
B2      GCTCATCCCGCCGACGAGGGGGCACCGCGCGGCTCCCGGACTTTGGCAACCTCTC
B4      ---CGTCCGGGGCGCTCGCCCT--CGACGGCCATTTAGCTTCGACGACGCCACGCCG
B5      ----GACCGCGCCGAGCCG-CGGTGGCCGCGTGCACGCGCCGAGTTTCGGCGCGG
          ** * * * * *

```

```
B1      CGTCGATGGACTTCGGCAACATCACGGCGCGCTGCCGGCGCGTGTTCGGGGCT
B3      CGTCCCTTGACTTTGGCGGCTCACACGCGCGAGCCGCTGGCCGTTTCCACCCGCGG
B2      CGTCGCGCGCTCGGGCGCTCGGCTCGCCCGCGCGCG-CGGTCTTACCCGTCGC
B4      CGCC-CGGGACTTCGGCAACCGGTGACGCTCCTGCCGGCGCGCTGCCACCCCTGGCT
B5      CG--ATGGACTTCGGCGCGCTGTTGAGCGCCCGCCCGCGCGCTGTCGCGCCGGCGA
          ** * * * * *

```

```
B1      CCCCGGGACGTGGCGGA-GCTCCTGCGCGCCCTACG--CCGCCCGGGGGCGGCGT
B3      GGGCCGGGACGTGCGCGC-GCTGTTGAAGGGCGGTACGGTFCGGCCAGCGCATCCG-
B2      GCCCGCCGACATGCGCGC-GCTGCTGCGCGCTGTCGCGC-ACGCCGGGGCGGTCG-
B4      CGGTGTCGACGTGCGCCACCGCTCAGCGCGCTGTTCCAGCTGGGACGAGGTCGCGC
B5      GCTCGGACGACGTGGCCAGCGCCATC-CGCGCGCG-GCG---CGCACCGCG-CACCTG-
          **** * * * *

```

```
B1      TCACCGTCTCGTTCCGGCGCCGCGGCACTCCACCATGGCCAGGCCCTCGCCGCGCGG
B3      ---CGTCTCGGCGCGGGGACGCGCATTCATCAGCGGGCAGGCCAGGCGCGCGG
B2      ---CGGTGTCGCGCGGGGTGTGCCACTCGTGCACGGCAGGCCCTCCGCGCGGAG
B4      TCACCGTCCGGCGCGGGGACGCGCACTCGCTCCTCGGCCAGTCCAGGCGCGCGG
B5      --ACCGTGGCCCGCGGAACGCGCACTCGTGGCCGGCAGGCCATGCGCCGCGCGG
          ** * * * * *

```

```
B1      GCGTCGTCGTCACATG-----CAGTCCATGGGCGCGCGCGG-----CGCCGG
B3      GGGTGGTCGTGACATGAGTCA--CGGTGGCGCGGAGGCGCGGAGAGGACGTTCG
B2      GCGTCGTCGTGACATGGCGTCTCGGCCCTGCAG-GGCGCGCG-----CGCGCG
B4      GGTGGCGCGGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTC

```

CLUSTALW Result

http://align.genome.jp/sit-bin/clustalw

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CLUSTALW Result

```
B3      GTTCGACCCGCGGGCCATGCT--CGCCACCGGCCAGGGAATCTTCGACTCGCCGCGCTC
B2      GTATGATCCAAAGGCCATCCTGTCCCTACAGTACTACGTACTACTAGTGTACTACCAGCC
B4      -----
B5      CTACGACCCGCTCGCCATCCT--CGCCCCGGCCAGAACATCTTCGCCCGGACCCCTCC

B1      -----
B3      TTGGCGGAGTCCTGA-----
B2      AATTTGCATGCATGCATGGATGCCCTTCATATGCATGTCGATCTCAAACGTACGGCATGCT
B4      -----
B5      TCCGTCGCCCGCCGCGCCCGTGATCGGTAA-----

B1      -----
B3      -----
B2      TGAATGCATCATGATGCATATCTATCGTCGTCTTATCTTCCACATCCAGCAGTACTGTG
B4      -----
B5      -----

B1      -----
B3      -----
B2      TATCAAGCCAGAATGACAGCTCGATCGATCGATGTAAGCCAATCATCAGAAAGACAATT
B4      -----
B5      -----

B1      -----
B3      -----
B2      GACGACGACGGCTAACGACACCGGAGATTCACATCATCATCGATATATCACATGGATAAC
B4      -----
B5      -----

B1      -----
B3      -----
B2      AACGACATTTGTTGGTTGCTTTTGAGCTGGCCAATCTGTGTTTAGTTCCAACAACGACTTG
B4      -----
B5      -----

B1      -
B3      -
B2      A
B4      -
B5      -
```

clustalw.dnd

```
(
(
B1:0.42869,
B3:0.43372)
:0.00691,
B2:0.43766,
(
B4:0.44037,
B5:0.44037)
:0.00958);
```

Select tree menu ▾ Exec

