

DNAMAN

Sequence Analysis Software

*Sequence
Search and
Comparison*

BIOINFORMATICS PLATFORM

Sequence Search and Comparison

- ▶ Blast Search on the Internet
- ▶ Structure Search
- ▶ SiRNA Search
- ▶ RNA/DNA Secondary Structure
- ▶ Dotplot Comparison

BLAST Search on Internet

1. Double click Example.seq file from File control

2. Click Blastn tool

An Internet browser window pops out and shows BLAST server page

The screenshot shows the DNAMAN software interface. The title bar reads "DNAMAN - [EXAMPLE1.SEQ]". The menu bar includes "Home", "Sequence", "Protein & Database", and "View". The toolbar contains various tools, with "Blastn" circled in red and a red number "2" next to it. The "File" control shows a list of files, with "EXAMPLE1.SEQ" circled in red and a red number "1" next to it. The main window displays sequence data for "example1.seq" (886 bp) with composition and molecular weight information. The "FEATURES" section shows an intron at 31..161 and a cds at 163..601. The "ORIGIN" section shows the raw sequence data.

```
SEQ example1.seq: 886 bp;
Composition 256 A; 159 C; 195 G; 276 T; 0 OTHER
Percentage: 28.9% A; 17.9% C; 22.0% G; 31.2% T; 0.0%OTHER
Molecular Weight (kDa): ssDNA: 274.14 dsDNA: 546.13
COLOURS
sequence = 1
features = 0

FEATURES
intron          31..161
                /name="Unknown"
cds             163..601
                /name="PBS"

ORIGIN
1      TTTGACTGCC ACTTCCTCGA TGAAGGTTT ACTGCCAAGG ACATTCGGGA CCAGAAAATT
61     AATGAAGTIT CTTCTTCTGA TGATAAGGAT GCCTTCTATG TGGCAGACCT GGGAGACATT
121    CTAAGAAGAA ATCTGAGGTG GTTAAAAGCT CTCCTCTGTG TCACCCOCTT TTATGCAGTC
181    AAATGTAATG ATAGCAAAGC CAAGACGAAG ACGAGAGAAAT GACAAAACAC TCATGTATTA
241    CGGGRAATGAT GGTGTCTATG GATCGTTCAA TTGCATCTTG TATGATCATG CACATGTTRA
301    ACCAGTTC TG CAAAAGCGGC CTAARACCAGA TGACGGCTGC TACTCCTGCA GCATATGGGG
361    ACCAACGTGT GATGGCCTGG ATCGTATTGT TGTGGTGTGT AACATGCCAG AGTTGCAAGT
421    TGGTGACTGG ATCCTGTTTG AAAACATGGG TGCCTATACT GTTGCAGCAG CTTCTACTTT
481    CAACGGATT CAGAGGCCAA CAATACATTA TGCGATGCTC GTTGTGCCTGT GAAAGTGGAA
541    TTGAGTATCC AGCAACTTGT GCTTCAGCTA GTATTAAATG ATAAATAATA AATACTTAGA
601    AACTAACTGC AAGTTTAGTC ATTGAATTTA GGGCATTGGG GGGACCATTA ACTTAAITCT
661    TGCTAGAATT TTTTAAGTGT TTTTTAAAAA GTTTAGGTTT GGCATAAACA CGACAAAAAA
721    ATGACTAGGA GATGGGTCAC ATTTATCTGT GTTCCTATGG AAACATTTTG AATATTGTTT
781    TTTTGGCTTT TTTTGGCTTT TTTTGGCTTT TTTTGGCTTT TTTTGGCTTT TTTTGGCTTT
```

BLAST Search on Internet

The screenshot shows the DNAMAN software interface for performing a BLAST search. The main window displays the 'Standard Nucleotide BLAST' setup. The 'Enter Query Sequence' field contains the following text:

```
>Sequence example1(1-886)
TTTGACTGCCACTTCCTCGATGAAGGTTTACTGCCAAGGACATTCTGGACCAGAAAATTAATGAAGT
TTCTTCTTCTGATGATAAAGGATGCCTTCTTGTGGCAGACCTGGGAGACATTCTAAAGAAACATCTGA
GGTGGTTAAAAGCTCTCCCTCGTGTACCCCTTTTATGCAGTCAAATGTAATGATAGCAAAGCCAAG
ACGAAGACGAGAGAATGACAAAACACTCATGTATTACGGGAATGATGGTGTCTATGGATCGTTCAATT
```

A red number '1' is positioned over the first line of the sequence. Below the sequence input, the 'Job Title' field is filled with 'Sequence example1(1-886)'. The interface also includes a 'Browse...' button for uploading a file and a 'Job Title' input field. The top navigation bar shows 'Home', 'Recent Results', 'Saved Strategies', and 'Help'. The left sidebar shows a file list with names like 'AJ40:', 'AY59', 'erwin', 'EXAN', 'fasta_', and 'facta_'.

1. Edit the query sequence and title if needed
The address of BLAST server can be set in DNAMAN configurations for a local site or NIH web page.

BLAST Search on Internet

The screenshot shows the DNAMAN software interface. The title bar reads "DNAMAN - [Nucleotide BLAST: Search nucleotide databases using a nucleotide query]". The interface includes a ribbon with tabs for "Home", "Sequence", "Protein & Database", and "View". The "Sequence" tab is active, showing various tools like "Load Seq", "Display", "Define", "Random", "Blastn", "TBlastn RF1", "Blastp Pro", "SIRNA", "Seq Fold", "Align Multiple", "Dotplot", "Align Pairwise", "Seq Map", "Seq Assembly", "Enzyme Cut", "Oligo Seq", and "PCR Primer".

The main window displays the "Program Selection" dialog. Under "Optimize for", the following options are listed:

- Highly similar sequences (megablast)
- More dissimilar sequences (discontiguous megablast)
- Somewhat similar sequences (blastn)

Below these options is a link: "Choose a BLAST algorithm".

The "BLAST" button is highlighted with a red "1". The search parameters are:

- Search database: **Nucleotide collection (nr/nt)** using **Blastn (Optimize for somewhat similar sequences)**
- Show results in a new window

Below the search parameters is a link: "+ Algorithm parameters".

At the bottom of the window, there is a footer with the text: "BLAST is a registered trademark of the National Library of Medicine". Logos for NCBI, NIH, and USA.gov are also present.

The browser address bar shows the URL: <https://blast.ncbi.nlm.nih.gov/Blast.cgi>

1. Press BLAST button to start
It may take a few minutes to complete the search

BLAST Search on Internet

DNAMAN - [NCBI Blast:cds]

Home Sequence Protein & Database View

Display Define Random Blastn Tblastn RF1 Blastp Pro SIRNA Seq Fold Align Multiple Seq Map Seq Assembly Enzyme Cut Restriction Analysis Oligo Seq PCR Primer

EXAMPLE1.SEQ NCBI Blast:cds

DNAM

Descriptions

Sequences producing significant alignments:

Select: All None Selected:0

Alignments Download GenBank Graphics Distance tree of results

	Description	Max score	Total score	Query cover	E value	Ident	Accession
<input type="checkbox"/>	PREDICTED: Gallus gallus ornithine decarboxylase 1 (ODC1), transcript variant X2	342	399	98%	4e-90	97%	gi 97139024 X NM_015
<input type="checkbox"/>	PREDICTED: Gallus gallus ornithine decarboxylase 1 (ODC1), transcript variant X1	342	399	98%	4e-90	97%	gi 971390222 X NM_015
<input type="checkbox"/>	Gallus gallus ornithine decarboxylase 1 (ODC1), mRNA	342	399	98%	4e-90	97%	gi 268370109 NM_001

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

1. Click Accession ID to browse the target sequence
2. Or click Description to visualize alignment for the search

BLAST Search on Internet

DNAMAN - [NCBI Blast:cds]

Home Sequence Protein & Database View

Display Define Random Blastn Blastp RF1 TBlastn RF1 Blastp Pro SiRNA Seq Fold Align Multiple Seq Map Dotplot Align Pairwise Seq Map Seq Assembly Enzyme Cut Restriction Analysis Oligo Seq PCR Primer

File EXAMPLE1.SEQ NCBI Blast:cds

Download GenBank Graphics Sort by: E value

PREDICTED: Gallus gallus ornithine decarboxylase 1 (ODC1), transcript variant X2, mRNA
Sequence ID: [gi|971390224|XM_015276042.1](#) Length: 1714 Number of Matches: 2

Range 1: 1108 to 1313 GenBank Graphics

Score	Expect	Identities	Gaps	Strand	Related Information
342 bits(378)	4e-90	200/206(97%)	1/206(0%)	Plus/Plus	Gene - associated gene det
Query 68	GACGAAGACGA-GAGAATGACAAAACACTCATGTATTACGGGAATGATGGTGTCTATGGA				126
Sbjct 1108	GATGAAGATGATGTGAATGACAAAACACTCATGTATTACGTGAATGATGGTGTCTATGGA				1167
Query 127	TCGTTCAATTGCATCTTGTATGATCATGCACATGTTAAACCAGTTCTGCAAAAAGCGGCCT				186
Sbjct 1168	TCGTTCAATTGCATCTTGTATGATCATGCACATGTTAAACCAGTTCTGCAAAAAGCGGCCT				1227
Query 187	AAACCAGATGACGGCTGCTACTCCTGCAGCATATGGGGACCAACGTGTGATGGCCTGGAT				246
Sbjct 1228	AAACCAGATGACGGCTGCTACTCCTGCAGCATATGGGGACCAACGTGTGATGGCCTGGAT				1287
Query 247	CGTATTGTTGTGCGTTGTAACATGCC		272		
Sbjct 1288	CGTATTGTTGAGCGTTGTAACATGCC		1313		

Channel 1:DNA example1 886bp CAP NUM/SCBI

BLAST Results

Structure Search

1. Double click a Sequence file in File control
2. Select one of Structure search tool

The screenshot displays the DNAMAN software interface. The 'File' menu is open, showing a list of files in the 'DNAMAN Files' folder. The file 'AY599226.seq' is selected, and its details are shown in the right-hand pane. The 'Structure' menu is also open, showing options for 'Repeats', 'Peptide', 'Nucleotide', and 'Seq Fold'. The 'Inverted' option is highlighted, and a red '2' is placed next to it. A red '1' is placed next to the 'AY599226.seq' file in the file list.

Name	Size	Type
AJ403983.seq	8 KB	DN
AY599226.seq	1 KB	DN
erwinia_genom...	8,101 KB	DN

AY599226.seq

SEQ AY599226.seq 2934
Composition 746 A; 742 T; 0 OTHER
Percentage 25.4% A; 24.8% C; 24.4% G; 25.3% T;
MW (kDa) 905.64 ssDNA 1808.79 dsDNA
KEYWORDS CIRCULAR
COLOURS
sequence = 1
features = 0

FEATURES
source 1..2934
/source="Cloning_vector"
misc_feature 582..671
/attributes="MCS;_multiple_c
gene complement(1874..2734)
/name="bla"
cds complement(1874..2734)
/name="beta-lactamase"

ORIGIN
1 TCGCGCGTTT CGGTGATGAC GGTGAAAACC TCTGACA
61 CAGCTTGTCT GTAAGCGGAT GCCGGGAGCA GACAAGC
121 TTGGCGGGTG TCGGGGCTGG CTTAACTATG CGGCATC
181 ACCATATGCG GTGTGAAATA CCGCACAGAT GCGTAAG

Structure Search

1. Double click a Sequence file in File control
2. Select one of Structure search tool

The screenshot shows the DNAMAN software interface. The 'File' menu is open, displaying a list of files in the 'DNAMAN Files' folder. The file 'AY599226.seq' is selected, indicated by a red '1'. The 'Structure' menu is also open, showing options like 'Repeats', 'Direct', 'Inverted', 'Mirror', and 'Stem Loop'. The 'Inverted' option is highlighted with a red '2'. The main window displays the sequence details for 'AY599226.seq', including composition, keywords, and features.

Name	Size	Type
AJ403983.seq	8 KB	DN
AY599226.seq	5 KB	DN
erwinia_genom...	8,101 KB	DN

AY599226.seq

SEQ AY599226 2934
Composition 746 A; 742 T; 0 OTHER
Percentage 25.4% A; 24.8% C; 24.4% G; 25.3% T;
MW (kDa) 905.64 ssDNA 1808.79 dsDNA
KEYWORDS CIRCULAR
COLOURS
sequence = 1
features = 0

FEATURES
source 1..2934
/source="Cloning_vector"
misc_feature 582..671
/attributes="MCS;_multiple_c
gene complement(1874..2734)
/name="bla"
cds complement(1874..2734)
/name="beta-lactamase"

ORIGIN
1 TCGCGCGTTT CGGTGATGAC GGTGAAAACC TCTGACA
61 CAGCTTGTCT GTAAGCGGAT GCCGGGAGCA GACAAGC
121 TTGGCGGGTG TCGGGGCTGG CTTAACTATG CGGCATC
181 ACCATATGCG GTGTGAAATA CCGCACAGAT GCGTAAG

Structure Search

The image displays three windows from the Structure Search software, each showing search results for a specific sequence. The windows are titled 'Search' and contain the following data:

Window 1: Direct repeats in AY599226(1-2934)

Size	Pos1	Pos2	Repeat Sequence
19	390	431	GACAATAAAGTCTTAAACT (
13	1061	1072	AGCAAAAAGGCCAG (N-2)
12	706	826	AACTATTTTTGTC (N108)
11	1690	1787	AAAAGGATCT (N86)
11	752	816	CCCAGTCCCA (N53)
11	708	764	CTATTTTGTC (N45)
10	1058	2663	GTGAGCAAAA (N1595)
10	196	222	AAATACCGCA (N16)
10	764	828	CTATTTTGTC (N54)
9	968	1343	GGTCGTTTCG (N366)
9	1790	2570	AAGGATCTT (N771)
9	820	2242	GTTCCCAAC (N1413)
9	1748	2559	CGAAAATC (N802)
9	1706	1804	AGATCCTTT (N89)
9	2038	2763	ATTTATCAG (N716)
9	403	464	TAAACTGAA (N52)
9	872	925	TTGGGCGCT (N44)
9	2284	2691	GCAAAAAAG (N398)
9	113	376	AGCGGGTGT (N254)
8	1693	2570	AAGGATCT (N869)
8	71	373	GTBAGCGG (N294)

Window 2: Inverted repeats in AY599226(1-2934)

Size	Pos1	Pos2	Repeat Sequence
13	382	833	TGTGGGCGGACAA (N438)
13	716	1814	TCATTTTAATT (N1085)
11	1633	1647	AAACCACCGCT (N3)
11	1704	1789	GAAGATCCTTT (N74)
11	411	762	ACAAAATAGAT (N340)
10	1691	1804	AAAAGGATCT (N103)
10	1788	1804	AAAAGGATCT (N6)
10	1258	1405	TTACCGGATA (N137)
10	960	2071	CTGCGCTCGG (N1101)
9	347	2427	GGTIGAGTA (N2071)
9	1994	2364	CAGTGCTGC (N361)
9	1695	2586	GGATCTCAA (N882)
9	28	1165	ACCTCTGAC (N1128)
9	411	708	ACAAAATAG (N288)
9	532	1820	CTTCATTT (N1279)
9	1570	2073	TCTGCGCTC (N494)
9	411	828	ACAAAATAG (N408)
9	63	89	GCTTGTCTG (N17)
9	859	2672	CTCCTGTT (N1804)
9	987	2005	GCGGTATCA (N1009)
9	1692	1706	AAAAGGATCT (N5)

Window 3: Complementary sequence in AY599226(1-2934)

Pos	Size (bp)	Complementary Sequence
476	8	AGTCCAGTtatgctc
1692	9	AAAGGATCTcaaga
63	9	GCTTGTCTGtaagcc
1788	10	AAAAGGATCTtcacc
1633	11	AAACCACCGCTggt

1. Direct Repeats
2. Inverted Repeats
3. Potential Stem-Loop Structures

siRNA Search

The screenshot shows the DNAMAN software interface. The 'File' control on the left lists several files, with 'AY599226.seq' selected (1). The 'SiRNA Selector' dialog box is open, showing various filter settings (2). The 'SiRNA' tool icon in the 'Search' menu is highlighted (3).

SiRNA Selector

GC content score

30-35%	4	41-50%	6	56-60%	4
36-40%	5	51-55%	5	60-65%	-10

Score

Start by A	End by TT
3	1

Penalty in CDS

<100bp from ATG	<100bp from Stop
-2	-2

-deltaG 5'AS must < 9.8 -deltaG 5'S- 5'AS must > 0.1

Start with AA End with TT Probes for Pol III expression vectors
 Y at position 21 R at position 3 No sequence with polyN(>3)

Target sequence length: 19 CDS defined

< Back Next > Cancel Help

1. Double click a file in File control to load sequence into channel
2. Click SiRNA search tool
3. Set filters for siRNA selection

siRNA Search

1. Target sequence list
2. A report window displays search results
3. BLAST search against target organism is required for avoid unwanted sequences

siRNA Target Sequences

7 seq Order Score Position deltaG 5'AS deltaG 5'S-5'AS

```
S=10 GC=42.1% 5'AS=-5.46 5'S-5'AS=-2.48 2144-GTAGTTCGCCAGTTAATAG
S=9 GC=47.4% 5'AS=-5.69 5'S-5'AS=-4.13 2081-GTGGTCTGCAACTTTATC
S=9 GC=42.1% 5'AS=-6.12 5'S-5'AS=-0.47 2160-TAGTTTGCACGTTGTTC
S=9 GC=47.4% 5'AS=-6.77 5'S-5'AS=-1.31 2248-CGATCAAGGCGAGTTACAT
S=8 GC=52.6% 5'AS=-6.84 5'S-5'AS=-1.63 2331-GTTGGCCGAGTGTATCA
S=8 GC=36.8% 5'AS=-5.69 5'S-5'AS=-2.63 2432-CCAAGTCATTCTGAGAATA
S=8 GC=52.6% 5'AS=-7.38 5'S-5'AS=-1.64 2570-GGATCTTACCCTGTTGAG
```

1

< Back Next > Cancel Help

AY599226.seq Untitled

siRNA sequences for AY599226
Selection parameters:
Target sequence length: 19
Start with A: Yes
End with TT: Yes
R at position 3: No
Y at position 21: No
No polyN(>3) seq: Yes
PolIII expression vectors: No
CDS region defined: Yes
delatG of pentamer at 5'AS must >: -9.8 kcal/mol
delatG difference of pentamer 5'S - 5'AS must <: -0.1 kcal/mol

BLAST search of the target sequences must be performed to avoid unwanted similar sequences.

Score=10 GC=42.1 deltaG 5'AS=-5.46 kcal/mol 5'S-5'AS=-2.48 kcal/mol
Target Seq 2144-AAGTAGTTCGCCAGTTAATAGTT
Sense 5'-GUAGUUCGCCAGUUAUAGdTdT
Antisense 5'-CUAUUACUGGCGAACUACdTdT

Score=9 GC=47.4 deltaG 5'AS=-5.69 kcal/mol 5'S-5'AS=-4.13 kcal/mol
Target Seq 2081-AAGTGGTCTGCAACTTTATCCG
Sense 5'-GUGGUCCGCAACUUUAUCdTdT
Antisense 5'-GAUAAAGUUGCAGGACCACdTdT

Score=9 GC=42.1 deltaG 5'AS=-6.12 kcal/mol 5'S-5'AS=-0.47 kcal/mol
Target Seq 2160-AATAGTTTGCACGTTGTTC
Sense 5'-UAGUUUGCGCACGUUGUdTdT

3

2

RNA/DNA Secondary Structure

With a DNA sequence loaded into channel

1. Click Seq Fold tool
2. Choose sequence type for secondary structure analysis
3. Edit sequence if needed

The screenshot shows the DNAMAN software interface. The title bar reads "DNAMAN - EXAMPLE1.SEQ". The "Seq Fold" tool icon is circled in red and labeled with a red "1". A dialog box titled "Secondary Structure" is open, with the "RNA" radio button selected and circled in red, labeled with a red "2". The dialog box shows a DNA sequence with a position of 886. The "OK" and "Cancel" buttons are visible at the bottom of the dialog box, with a red "3" next to the "OK" button.

DNAMAN - EXAMPLE1.SEQ

Home Sequence Protein & Database View

Seq Fold

Secondary Structure

RNA DNA

Position = 886

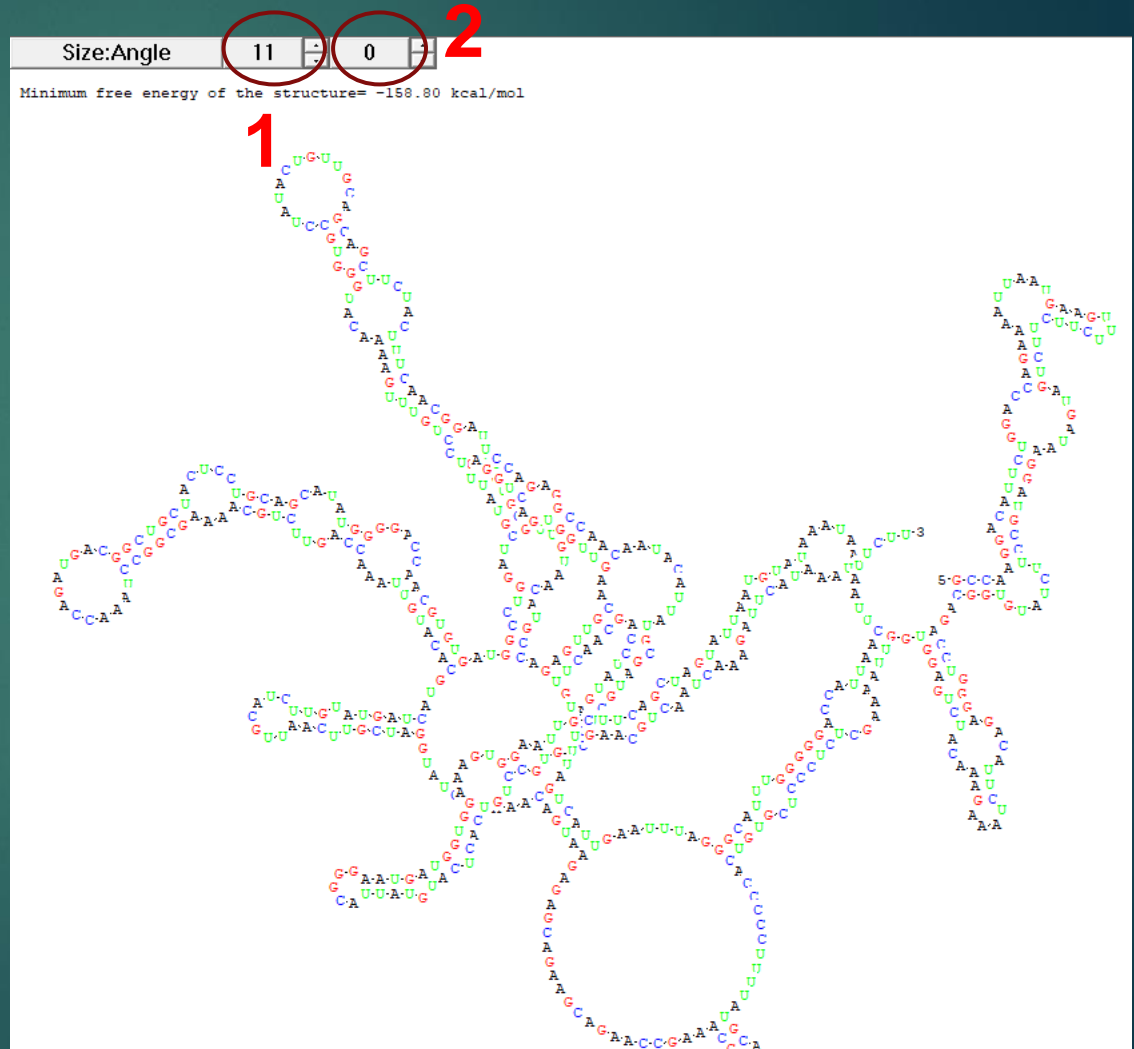
00001 ATGACTGCCACTTCCTGGAAGAGGTTTTACTGCCAAGGACATTCTGGACCAGAAAATTAATGAAGTTTCTTCTCTG
00080 ATGATAAGGATGCCTTCTATGTGGCAGACCTGGGAGACATTCTAAAGAAACATCTGAGGTGGTTAAAAGCTCCCTCG
00159 TGTCAACCCCTTTTATGCAGTCAAAATGTAATGATAGCAAAGCCAAAGCAGAGAGAAATGACAAAACACTCATGTA
00238 TTACGGGAATGATGGTGTCTATGGATCGTTCAATTGCATCTTGTATGATCATGCACATGTTAAACCAGTTCTGCAAAAG
00317 CGGCCTAAACCAGATGACGGCTGCTACTCCTGCAGCATATGGGGACCAACGTGTGATGGCCTGGATCGTATTGTTGTGC
00396 GTTGTAAACATGCCAGAGTTGCAAGTTGGTACTGGATCCTGTTGAAAACATGGGTGCTATACTGTTGCAGCAGCTTC
00475 TACTTTCAACGGATTCCAGAGGCCAACAATACATTATGCGATGCTCCTGTGCCTGTGAAAGTGGAAATTGAGTATCCAGC
00554 AACTTGTGCTTCAGCTAGTATTAAATGATAAATAATAAATACTTAGAAACTAACTGCAAGTTTAGTCATTGAATTTAGG
00633 GCATTTGGGGGACCATAACTTAATCTTGTAGAAATTTTTAAGTGTTTTTTAAAAGTTTAGGTTTGGCATAAACAC
00712 GACAAAAAATGACTAGGAGATGGGTACATTTATCTGTGTTCCATGAAACTATTTGAATATTGTTTTATATGGATT
00791 TTTATTCACITTTTCATGATGCTAACTAAAGACTGACCCCTCAGCTGTCAAACAAGTATTTGTAGCTTGTGTATGCCAGA
00870 ATGGGCTAAGCTTAGTG

OK Cancel

RNA/DNA Secondary Structure

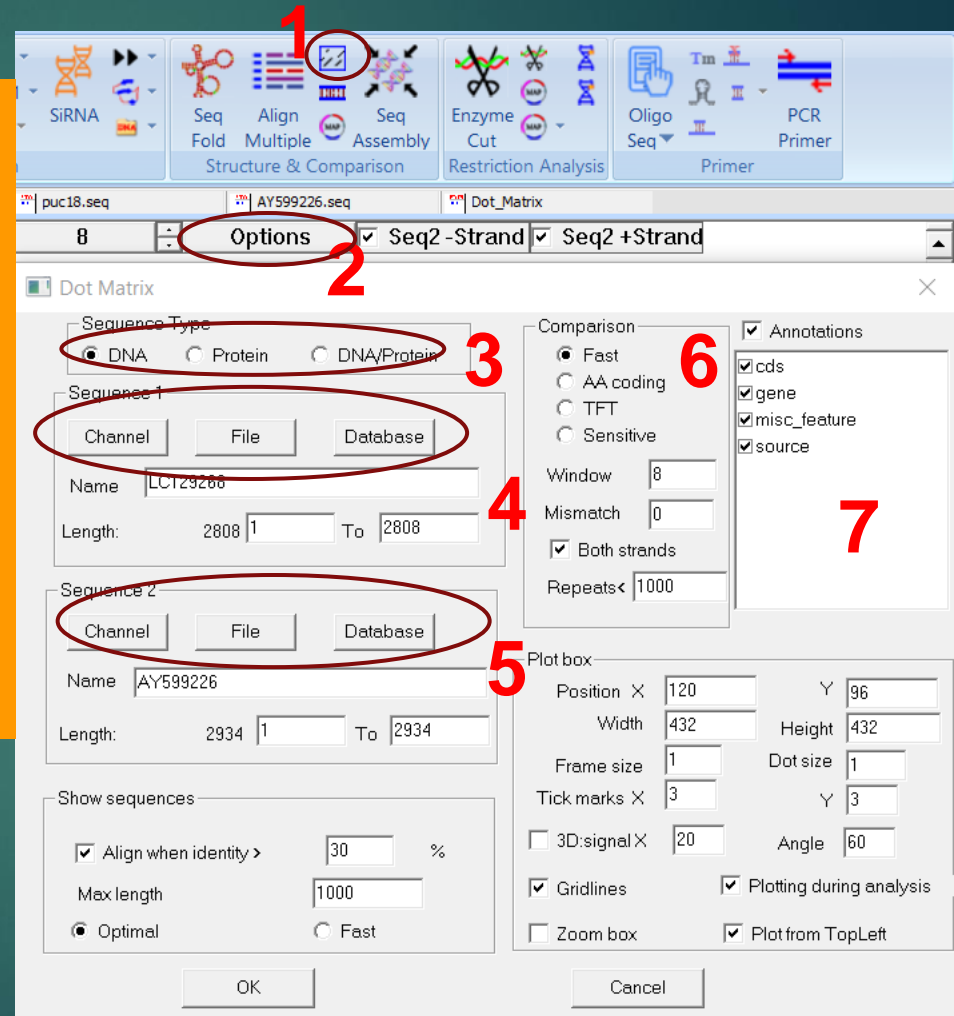
Predicted Secondary Structure

1. Change size of the graphic structure
2. Change orientation of the structure



Dotplot Analysis

1. Click Dot Matrix tool for Structure & Comparison tab
2. Click Option button to set up dot plot
3. Choose plot type
4. Select First sequence
5. Select 2nd sequence for comparison
6. Select comparison methods
7. Display annotations in the plot if they are selected



Dotplot Analysis

1. Name of Sequence 1
2. Name of Sequence 2
3. Annotations of Sequence 1
4. Annotations of Sequence 2
5. Threshold of dot size
6. Options for the plot
7. Sequence 2 strand controls
 - Any area of the plot can be zoom in/out by drag&drop with mouse left button
 - Homologous sequences can be aligned by drag&drop with right mouse button

