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

BLAST Search on Internet

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

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

BLAST Search on Internet

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

BLAST Search on Internet

BLAST Results

Structure Search

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

Structure Search

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2. Select one of Structure search tool

Structure Search

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

SiRNA Search

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-GTGGTCCTGCAACTTTATC
S=9  GC=42.1% 5'AS=-6.12 5'S-5'AS=-0.47 2160-TAGTTTGCGCAACGTTGTT
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-GTTGGCCGCAGTGTTATCA
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-GGATCTTACCGCTGTTGAG
```

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< 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'-GUAGUUCGCCAGUUAAUAGdTdT
    Antisense 5'-CUAUUAACUGGCGAACUACdTdT

Score=9 GC=47.4 deltaG 5'AS=-5.69 kcal/mol 5'S-5'AS=-4.13 kcal/mol
 Target Seq 2081-AAGTGGTCCTGCAACTTTATCCG
        Sense 5'-GUGGUCCUGCAACUUUAUCdTdT
    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-AATAGTTTGCGCAACGTTGTTGC
        Sense 5'-UAGUUUGCGCAACGUUGUUdTdT
```

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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

RNA/DNA Secondary Structure

Predicted Secondary Structure
1. Change size of the graphic structure
2. Change orientation of the structure
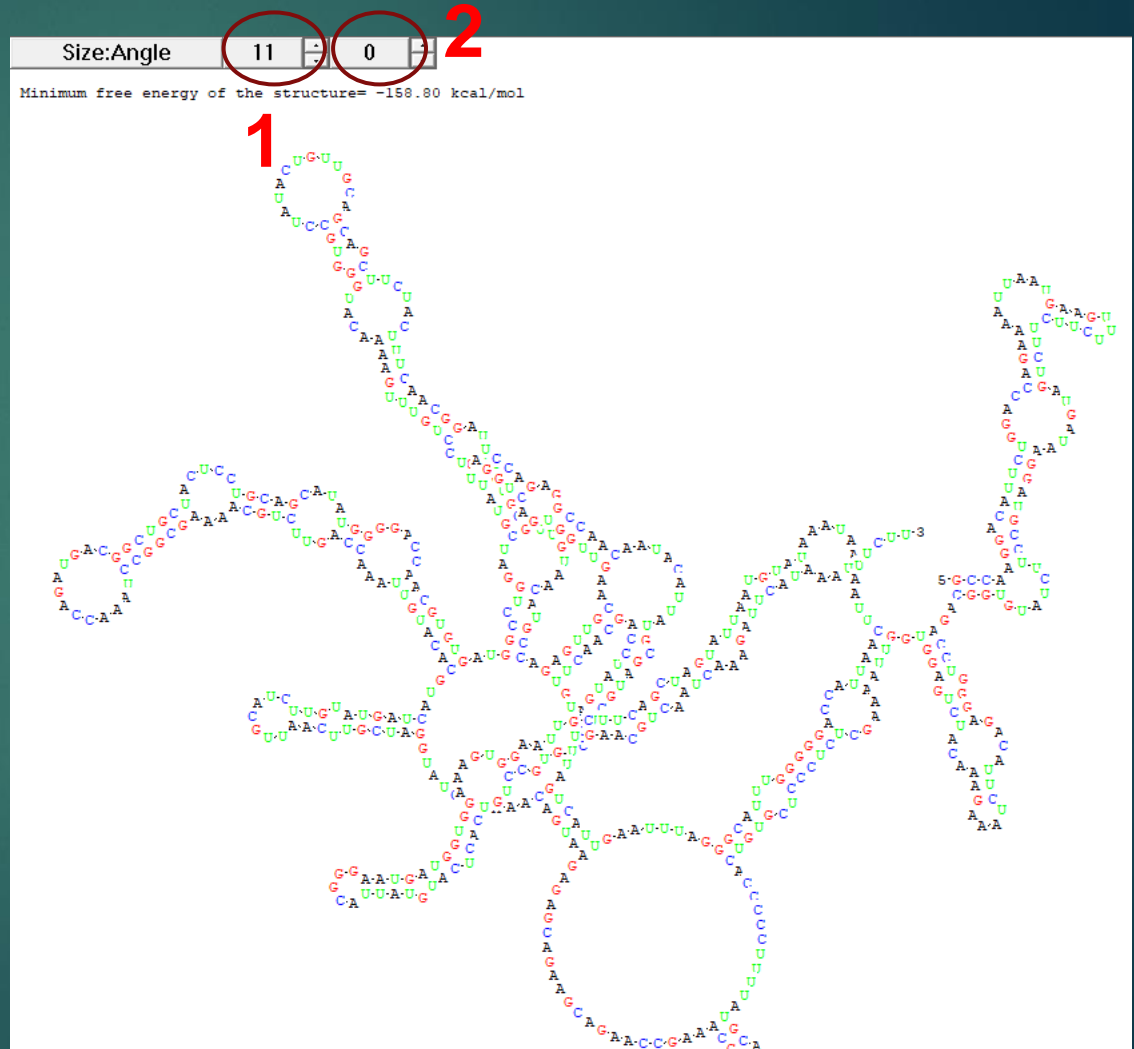
Dotplot Analysis

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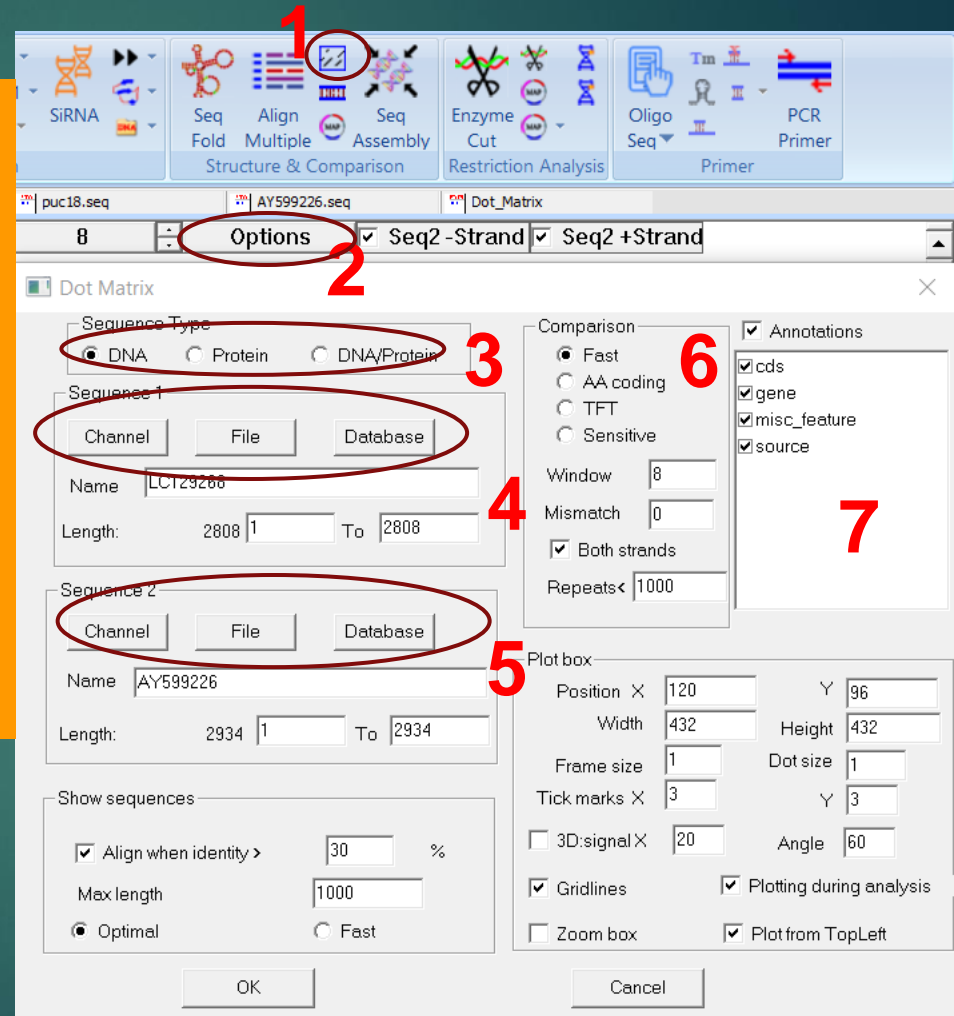4. Select First sequence
5. Select 2nd sequence for comparison
6. Select comparison methods
7. Display annotations in the plot if they are selected

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