PmiR-NA User Guide

The PmiR-NA has many useful miRNA-target network analysis and functions that are demonstrated in this user guide. It is a web-based tool that aids analysis of miRNA targets and its interaction network. PmiR-NA is very easy to use, and provides an user-friendly interface.

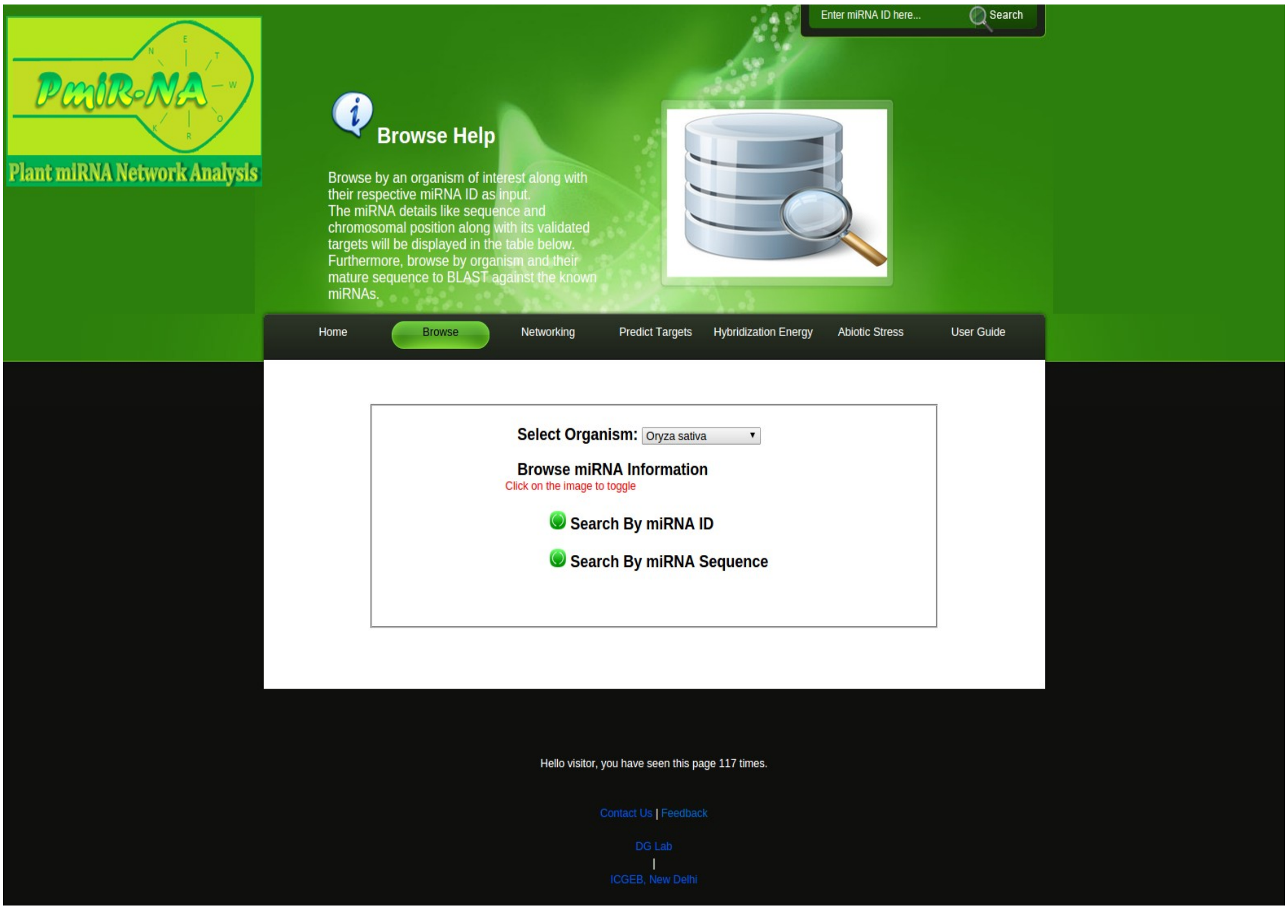
1. Prerequisite

a. Web browser with Adobe Flashplayer Plugin.

b. Input miRNA and target query sequence/files.

2. Browse

The Browse page mainly contains miRNAs information along with its experimentally validated targets, hybridization energy, abiotic stress details and its homologs. Here, the user need to first select the organism from the first dropdown menu. After organism selection, user can seen that there are two separate sections for the seach. In the first section, user can search by miRNA ID and in the second section user can search by miRNA sequence.



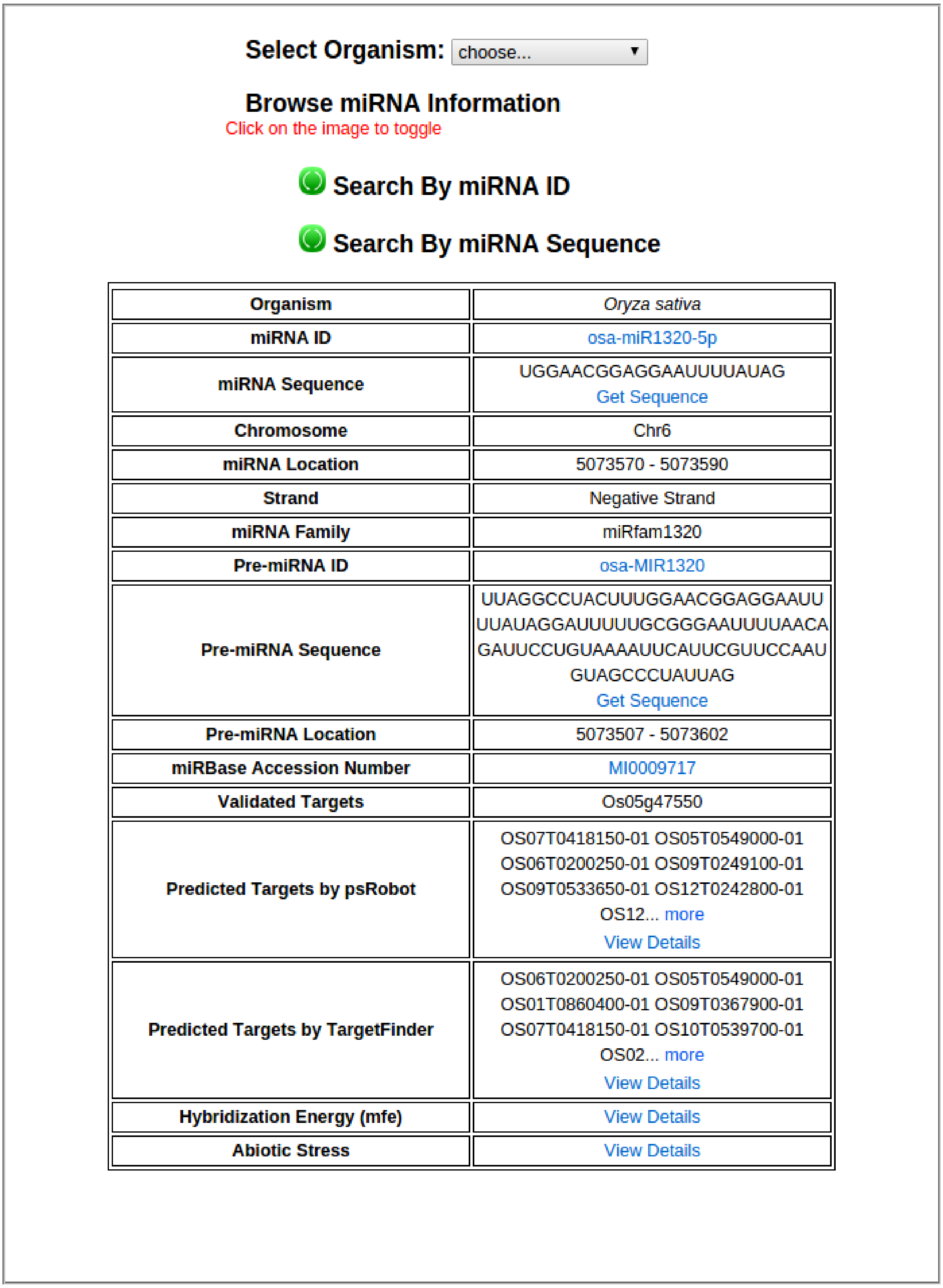
Browse Help

Browse by an organism of interest along with their respective miRNA ID as input.
The miRNA details like sequence and chromosomal position along with its validated targets will be displayed in the table below.
Furthermore, browse by organism and their mature sequence to BLAST against the known miRNAs.

Select Organism: Oryza sativa

Hello visitor, you have seen this page 117 times.

As the first toggle is clicked, user can see the dropdown menu having the list of validated miRNA IDs of the respective organism selected in the first dropdown menu. User need to select the miRNA ID to view the search results. As the miRNA ID is selected, it retrives information from the pmiR-NA database for a selected miRNA of the species of interest, and display the search results in a tabular form below the toggle option.



Select Organism: choose... ▼

Browse miRNA Information

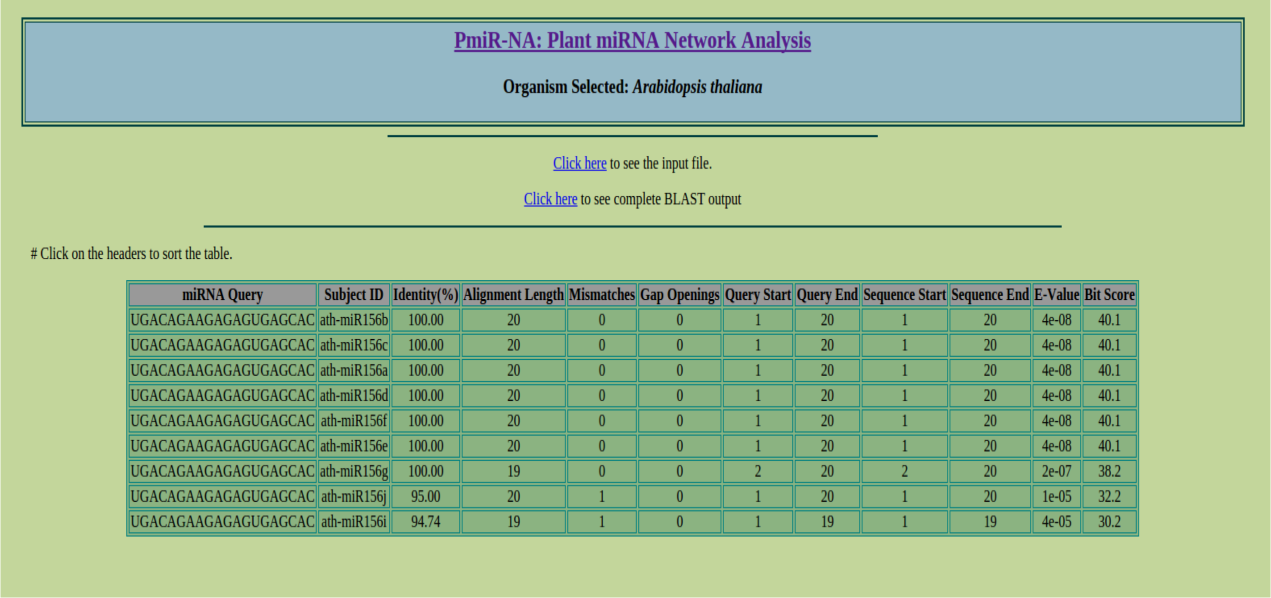
Click on the image to toggle

● **Search By miRNA ID**

● **Search By miRNA Sequence**

Organism	*Oryza sativa*
miRNA ID	osa-miR1320-5p
miRNA Sequence	UGGAACGGAGGAAUUUUAUAG Get Sequence
Chromosome	Chr6
miRNA Location	5073570 - 5073590
Strand	Negative Strand
miRNA Family	miRfam1320
Pre-miRNA ID	osa-MIR1320
Pre-miRNA Sequence	UUAGGCCUACUUUGGAACGGAGGAAUUUUAUAGGAUUUUUGCGGGAAUUUUAACAGAUUCCUGUAAAAUUCAUUCGUUCCAAUGUAGCCCUAUUAG Get Sequence
Pre-miRNA Location	5073507 - 5073602
miRBase Accession Number	MI0009717
Validated Targets	Os05g47550
Predicted Targets by psRobot	OS07T0418150-01 OS05T0549000-01 OS06T0200250-01 OS09T0249100-01 OS09T0533650-01 OS12T0242800-01 OS12... more View Details
Predicted Targets by TargetFinder	OS06T0200250-01 OS05T0549000-01 OS01T0860400-01 OS09T0367900-01 OS07T0418150-01 OS10T0539700-01 OS02... more View Details
Hybridization Energy (mfe)	View Details
Abiotic Stress	View Details

In the second section, user again have to specify the organism from the first dropdown menu. After organism selection, a name to the search sequence is to be provided by the user in the first input textbox and then user need to paste the miRNA sequence in the second input textbox. As the submit botton is clicked, the sequence homologs for the input sequence in second textbox are shown on the new result page in a tabular form. The result can also be downloaded by “click here” option to view output file.



PmiR-NA: Plant miRNA Network Analysis

Organism Selected: ***Arabidopsis thaliana***

Click here to see the input file.

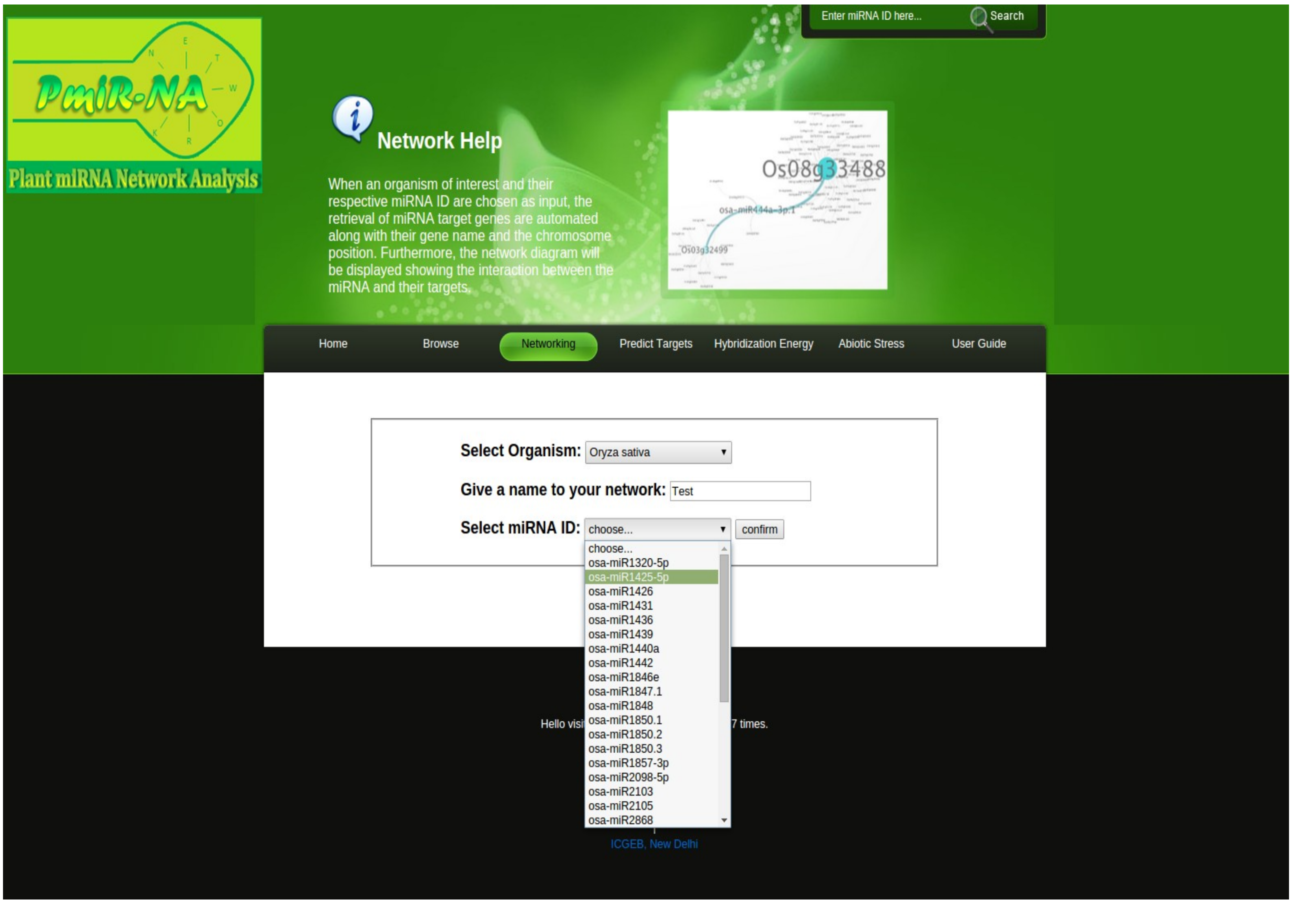
Click here to see complete BLAST output

Click on the headers to sort the table.

miRNA Query	Subject ID	Identity(%)	Alignment Length	Mismatches	Gap Openings	Query Start	Query End	Sequence Start	Sequence End	E-Value	Bit Score
UGACAGAAGAGAGUGAGCAC	ath-miR156b	100.00	20	0	0	1	20	1	20	4e-08	40.1
UGACAGAAGAGAGUGAGCAC	ath-miR156c	100.00	20	0	0	1	20	1	20	4e-08	40.1
UGACAGAAGAGAGUGAGCAC	ath-miR156a	100.00	20	0	0	1	20	1	20	4e-08	40.1
UGACAGAAGAGAGUGAGCAC	ath-miR156d	100.00	20	0	0	1	20	1	20	4e-08	40.1
UGACAGAAGAGAGUGAGCAC	ath-miR156f	100.00	20	0	0	1	20	1	20	4e-08	40.1
UGACAGAAGAGAGUGAGCAC	ath-miR156e	100.00	20	0	0	1	20	1	20	4e-08	40.1
UGACAGAAGAGAGUGAGCAC	ath-miR156g	100.00	19	0	0	2	20	2	20	2e-07	38.2
UGACAGAAGAGAGUGAGCAC	ath-miR156j	95.00	20	1	0	1	20	1	20	1e-05	32.2
UGACAGAAGAGAGUGAGCAC	ath-miR156i	94.74	19	1	0	1	19	1	19	4e-05	30.2

3. Networking

The Networking page dynamically generate biological network of miRNA and their targets. To visualize the network user first need to select the organism from the dropdown menu. As the organism is selected, user must provide a name to the network in the first input textbox. After a name is given to the network that is going to be drawn, user needs to select the miRNA ID from the second dropdown menu which is the list of validated miRNA IDs of the selected organism from the first dropdown menu.



When an organism of interest and their respective miRNA ID are chosen as input, the retrieval of miRNA target genes are automated along with their gene name and the chromosome position. Furthermore, the network diagram will be displayed showing the interaction between the miRNA and their targets.

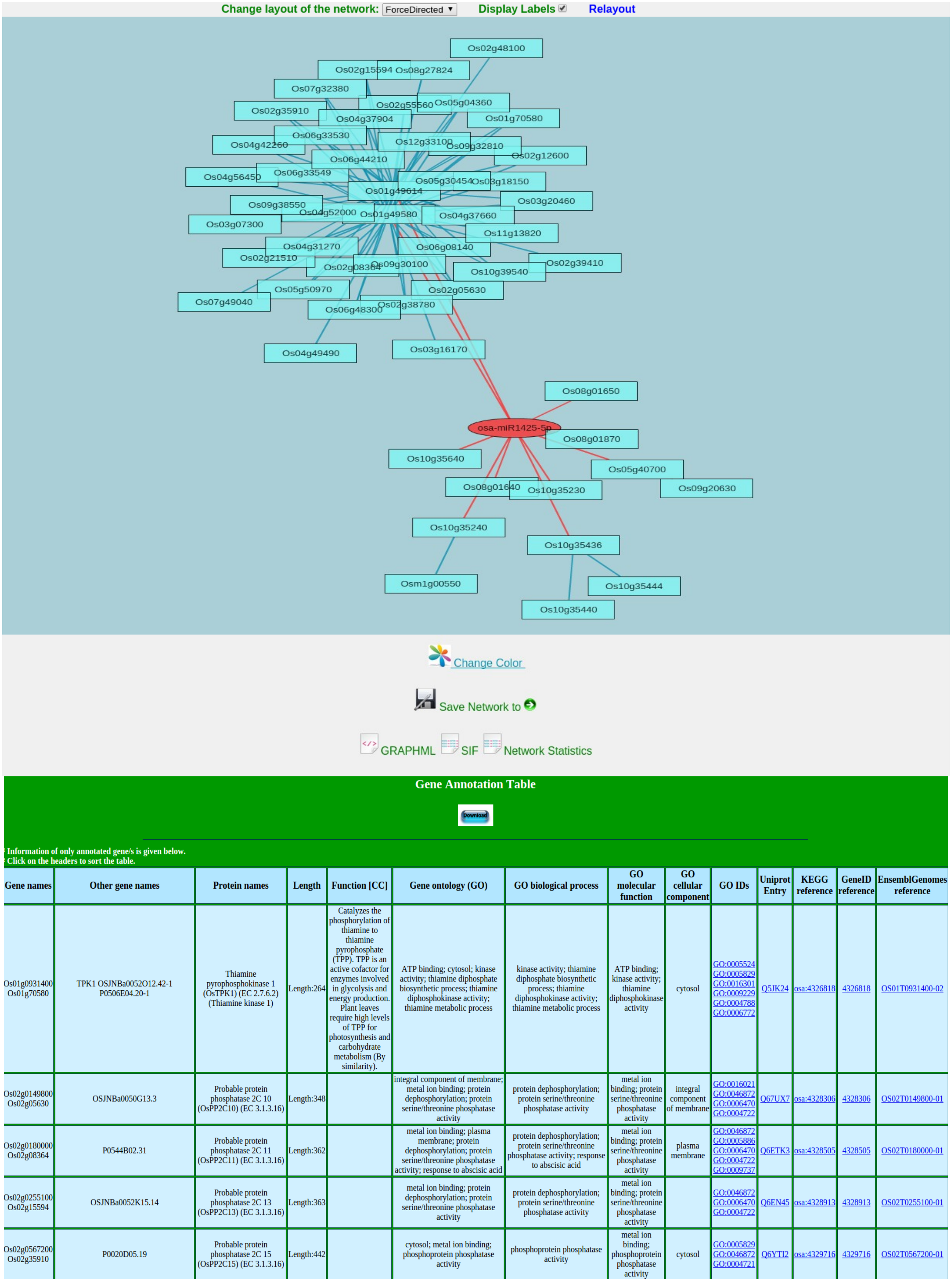
Select Organism: Oryza sativa

Give a name to your network: Test

Select miRNA ID: choose...

Hello visi 7 times.

As the miRNA ID is submitted, a new result page is shown. The result page shows a adobe flashplayer plugin network frame and below the frame, a gene annotation table having list of targets and their interacting parters in the above network are shown. The network visualization is mainly done by using Cytoscape Web (http://cytoscapeweb.cytoscape.org/). The full Cytoscape tutorial can be found here: http://www.cytoscape.org/documentation_users.html



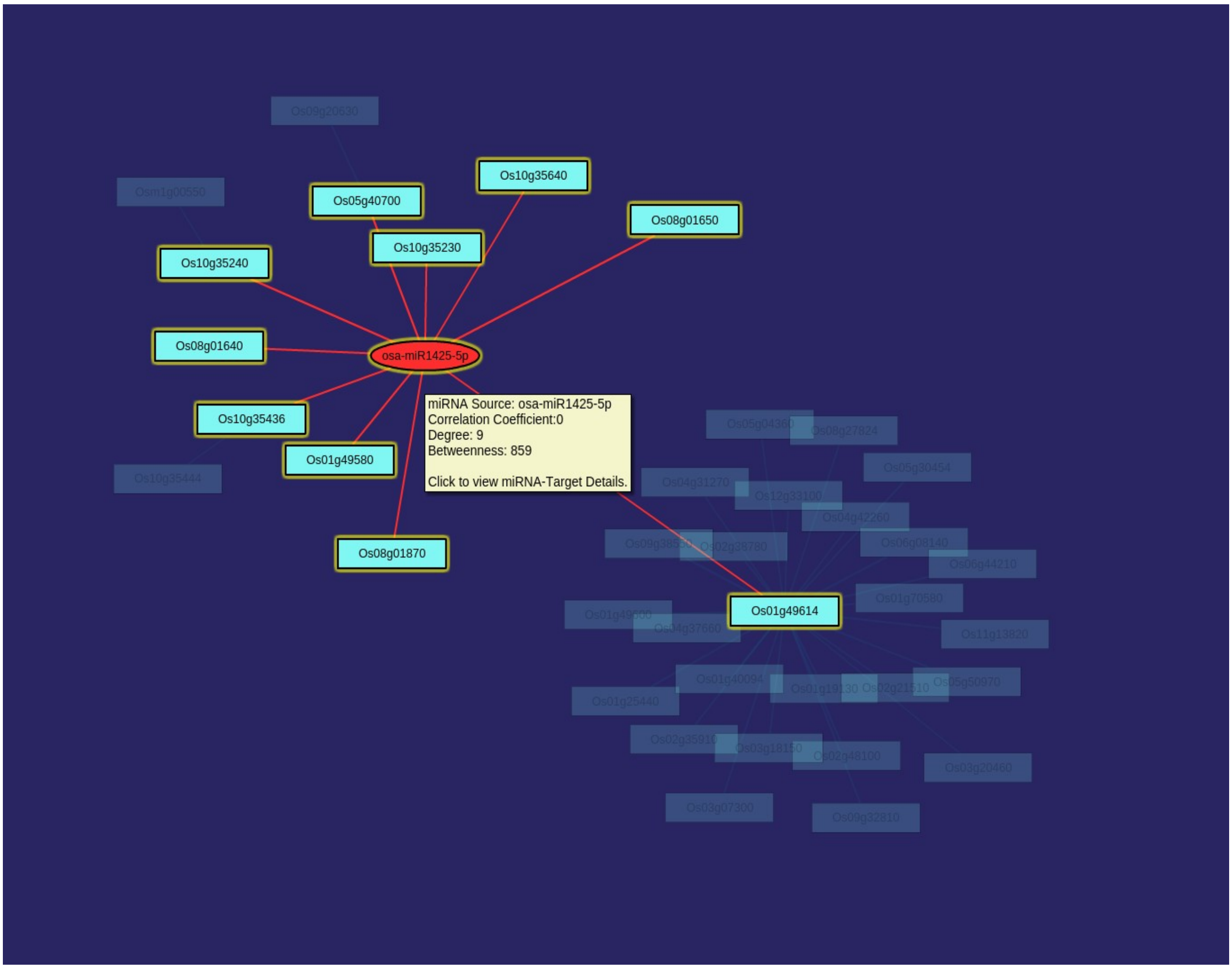
Gene Annotation Table

* Information of only annotated gene/s is given below.
* Click on the headers to sort the table.

Gene names	Other gene names	Protein names	Length	Function [CC]	Gene ontology (GO)	GO biological process	GO molecular function	GO cellular component	GO IDs	Uniprot Entry	KEGG reference	GeneID reference	EnsemblGenomes reference
Os01g0931400 Os01g70580	TPK1 OSJNBa0052O12.42-1 P0506E04.20-1	Thiamine pyrophosphokinase 1 (OsTPK1) (EC 2.7.6.2) (Thiamine kinase 1)	Length:264	Catalyzes the phosphorylation of thiamine to thiamine pyrophosphate (TPP). TPP is an active cofactor for enzymes involved in glycolysis and energy production. Plant leaves require high levels of TPP for photosynthesis and carbohydrate metabolism (By similarity).	ATP binding; cytosol; kinase activity; thiamine diphosphate biosynthetic process; thiamine diphosphokinase activity; thiamine metabolic process	kinase activity; thiamine diphosphate biosynthetic process; thiamine diphosphokinase activity; thiamine metabolic process	ATP binding; kinase activity; thiamine diphosphokinase activity	cytosol	GO:0005524 GO:0005829 GO:0016301 GO:0009229 GO:0004788 GO:0006772	Q5JK24	osa:4326818	4326818	OS01T0931400-02
Os02g0149800 Os02g05630	OSJNBa0050G13.3	Probable protein phosphatase 2C 10 (OsPP2C10) (EC 3.1.3.16)	Length:348		integral component of membrane; metal ion binding; protein dephosphorylation; protein serine/threonine phosphatase activity	protein dephosphorylation; protein serine/threonine phosphatase activity	metal ion binding; protein serine/threonine phosphatase activity	integral component of membrane	GO:0016021 GO:0046872 GO:0006470 GO:0004722	Q67UX7	osa:4328306	4328306	OS02T0149800-01
Os02g0180000 Os02g08364	P0544B02.31	Probable protein phosphatase 2C 11 (OsPP2C11) (EC 3.1.3.16)	Length:362		metal ion binding; plasma membrane; protein dephosphorylation; protein serine/threonine phosphatase activity; response to abscisic acid	protein dephosphorylation; protein serine/threonine phosphatase activity; response to abscisic acid	metal ion binding; protein serine/threonine phosphatase activity	plasma membrane	GO:0046872 GO:0005886 GO:0006470 GO:0004722 GO:0009737	Q6ETK3	osa:4328505	4328505	OS02T0180000-01
Os02g0255100 Os02g15594	OSJNBa0052K15.14	Probable protein phosphatase 2C 13 (OsPP2C13) (EC 3.1.3.16)	Length:363		metal ion binding; protein dephosphorylation; protein serine/threonine phosphatase activity	protein dephosphorylation; protein serine/threonine phosphatase activity	metal ion binding; protein serine/threonine phosphatase activity		GO:0046872 GO:0006470 GO:0004722	Q6EN45	osa:4328913	4328913	OS02T0255100-01
Os02g0567200 Os02g35910	P0020D05.19	Probable protein phosphatase 2C 15 (OsPP2C15) (EC 3.1.3.16)	Length:442		cytosol; metal ion binding; phosphoprotein phosphatase activity	phosphoprotein phosphatase activity	metal ion binding; phosphoprotein phosphatase activity	cytosol	GO:0005829 GO:0046872 GO:0004721	Q6YTI2	osa:4329716	4329716	OS02T0567200-01

The network shows the single input, miRNA node in red color and its target nodes in sky-blue color. The edges from the miRNA which are connecting it to the first target are shown in red color. Further the targets connect to the interacting targets with an edges having blue color. The nodes in the network can be draged by the user anywhere inside the network frame. User can also maximize and minimize the network inside the frame by increasing or decreasing the size using the pan zoom control panel placed on the bottom left corner of the network frame.

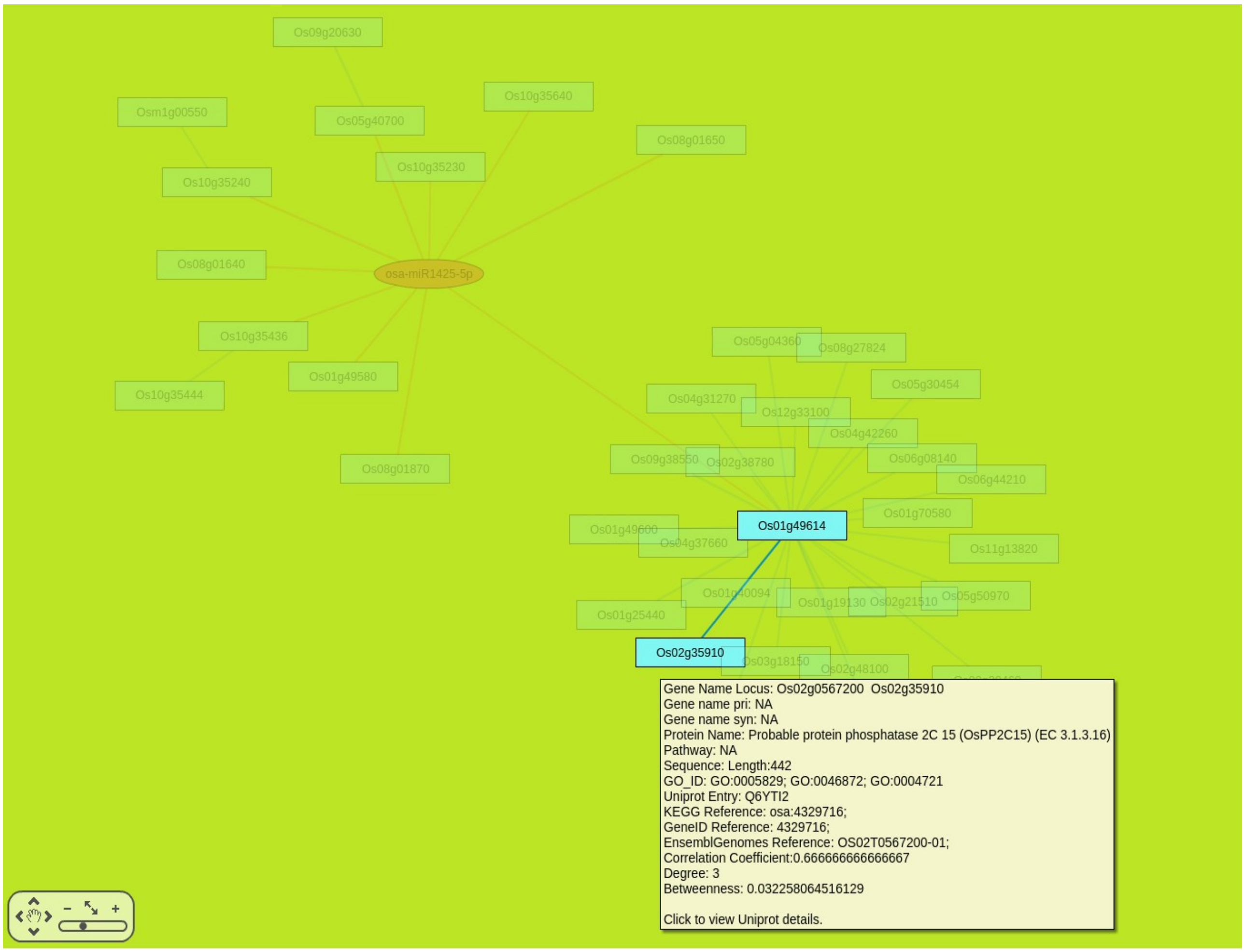
Each node (miRNA, targets and its interacting parters) can select its first neighbors by the content menu option on right click, placed for each nodes. As the "Select first neighbors" option is clicked, the first neighbors of that node are highlighted. All the selected nodes in this case can also be moved within the network frame at the same time.



miRNA Source: osa-miR1425-5p
Correlation Coefficient:0
Degree: 9
Betweenness: 859

Click to view miRNA-Target Details.

Another feature to be marked in the network drawn is to visualize the details about each node in the network frame itself. Here, user needs to move the cursor above a node to view the onmouse event feature which helps to shown the gene details along with the correlation coefficient, degree and betweenness of target nodes inside a yellow color box. As the cursor is on the node, not only the details of target node is shown in yellow box but the first neighbors of that particular nodes is also shown. Further if the user clicks on the target node, user will be linked to the webpage of UniprotKB showing the detailed information of the clicked target node. Similarly, if the user clicks on the miRNA node, one will be linked to a new webpage showing the details of miRNA-target hybridization energy (minimum free energy i.e mfe in kcal/mol) and secondary structure informations.



Gene Name Locus: Os02g0567200 Os02g35910
Gene name pri: NA
Gene name syn: NA
Protein Name: Probable protein phosphatase 2C 15 (OsPP2C15) (EC 3.1.3.16)
Pathway: NA
Sequence: Length:442
GO_ID: GO:0005829; GO:0046872; GO:0004721
Uniprot Entry: Q6YTI2
KEGG Reference: osa:4329716;
GeneID Reference: 4329716;
EnsemblGenomes Reference: OS02T0567200-01;
Correlation Coefficient:0.666666666666667
Degree: 3
Betweenness: 0.032258064516129

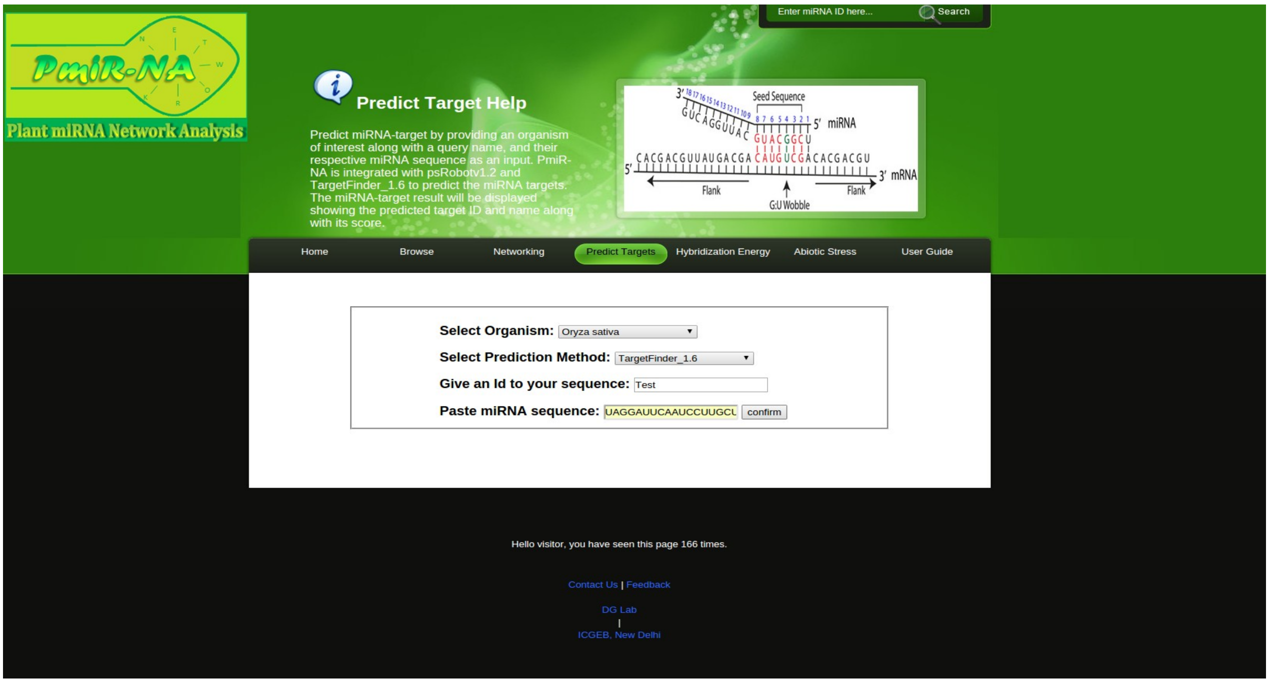
Click to view Uniprot details.

Further the network can also be customized by the user on changing the layout of the network using the dropdown menu placed at the top of the network frame. Force-directed layout is set as a default layout for the network but user can also change it to radial, circle or tree layouts. Beside the network layout dropdown menu, there are other customizable features for the user like “display labels” checkbox option to enable or disable the labels of the nodes to be viewed. User can also change the color of the network by “Change color” option placed below the network drawn. The user can download the network in output formats like SIF and GRAPHML formats. Further network statistics details can also be downloaded. In case the user customize the network using different features but wishes to revert back to the initial network, one can do so by using the “Relayout” option placed beside the “Display Labels” option. The gene annotation table shown below the network can also be downloaded in EXCEL format by clicking on the download image.

The user can also analyse the gene annotation list on the basis of target gene length by a click on the header to allow it to sort in an accending or desending order. Further the gene annotation details are linked to its reference webpages like Gene Ontology, Uniprot, KEGG, Gene ID, EnsemblGenomes.

4. Predict Targets

For Predict Target page, user need to choose an organism within the list of nine organisms (*Oryza sativa, Arabidopsis thaliana, Triticum aestivum, Zea mays, Physcomitrella patens, Hordeum vulgare, Sorghum bicolor, Populus trichocarpa* and *Medicago truncatula)* from the first dropdown menu. After organism selection, user must select a prediction method within psRobot_v1.2 or TargetFinder_v1.6 from the second dropdown menu. Further user need to provide a name to the sequence in the first input textbox and then paste the query sequence in the second input textbox.



Predict Target Help

Predict miRNA-target by providing an organism of interest along with a query name, and their respective miRNA sequence as an input. PmiR-NA is integrated with psRobotv1.2 and TargetFinder_1.6 to predict the miRNA targets. The miRNA-target result will be displayed showing the predicted target ID and name along with its score.

Select Organism: Oryza sativa

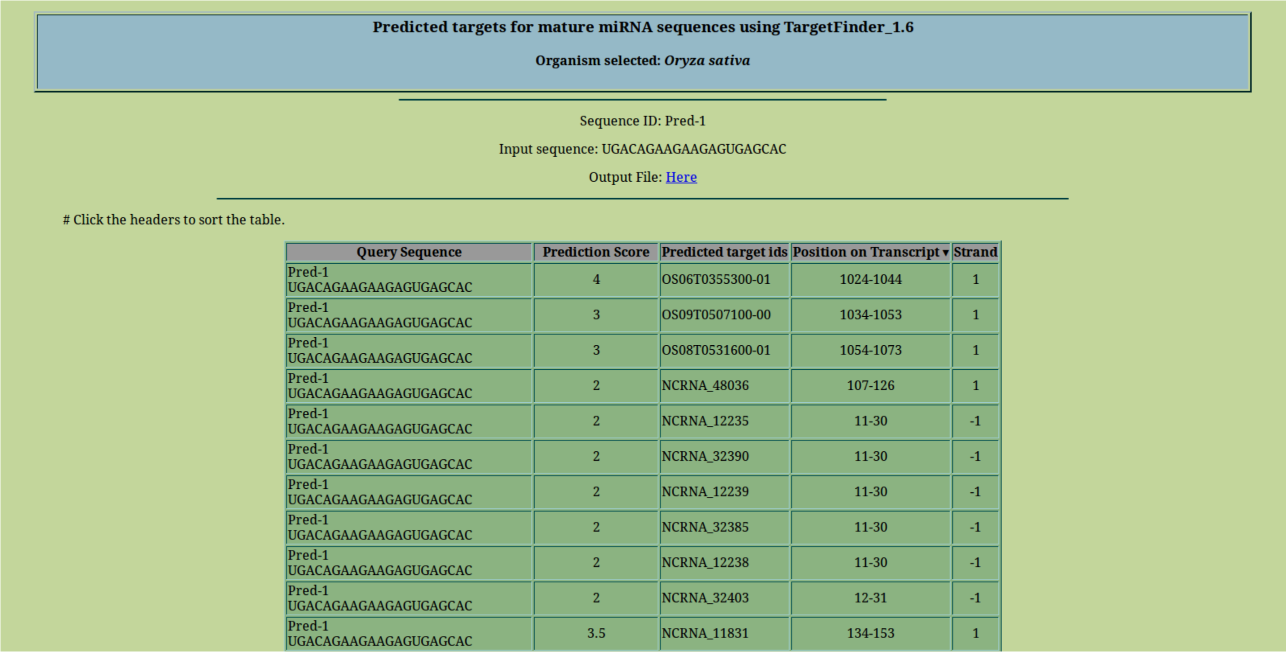
Select Prediction Method: TargetFinder_1.6

Give an Id to your sequence: Test

Paste miRNA sequence: UAGGAUUCAAUCCUUGCU

Hello visitor, you have seen this page 166 times.

On submit, a new result webpage is shown on which a table having the list of predicted targets along with the prediction score are given. The predicted targets list can be analysed by clicking on the header of the table to sort accordingly. The output can also be downloaded by the “Output File” link. Both psRobot and TargetFinder are designed to find potential small RNA targets on a large scale.



Predicted targets for mature miRNA sequences using TargetFinder_1.6

Organism selected: *Oryza sativa*

Sequence ID: Pred-1

Input sequence: UGACAGAAGAGAGUGAGCAC

Output File: Here

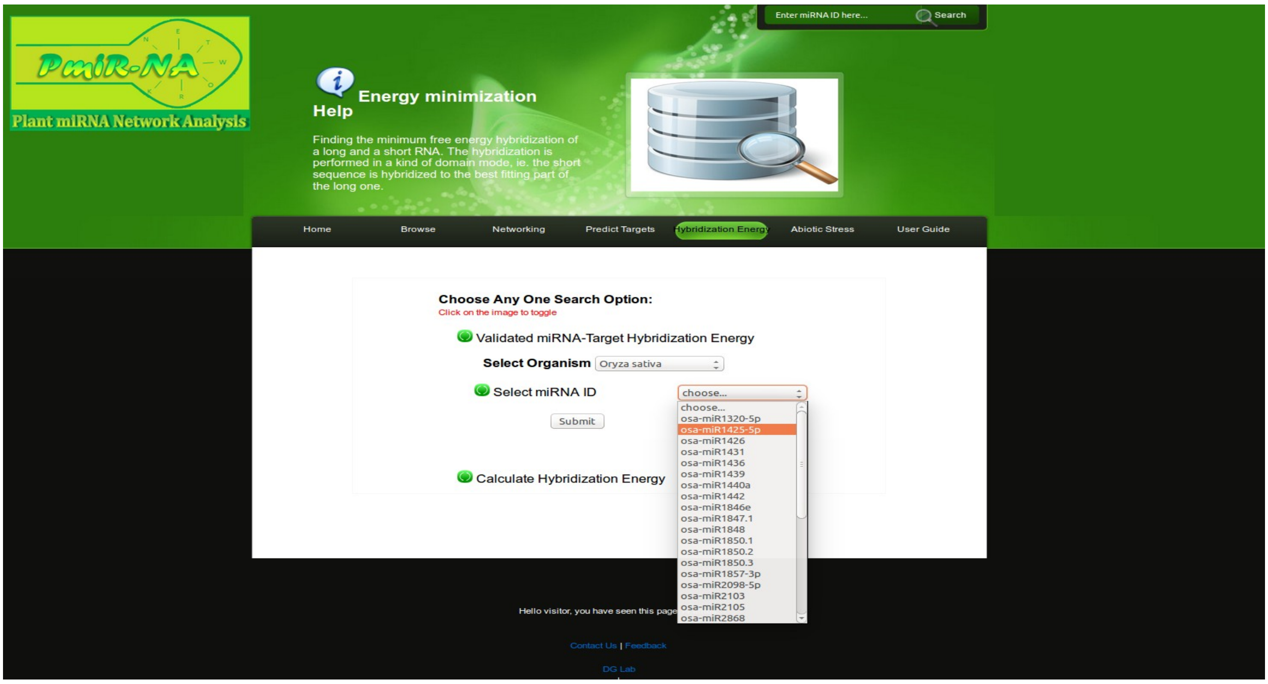
Click the headers to sort the table.

Query Sequence	Prediction Score	Predicted target ids	Position on Transcript ▾	Strand
Pred-1 UGACAGAAGAGAGUGAGCAC	4	OS06T0355300-01	1024-1044	1
Pred-1 UGACAGAAGAGAGUGAGCAC	3	OS09T0507100-00	1034-1053	1
Pred-1 UGACAGAAGAGAGUGAGCAC	3	OS08T0531600-01	1054-1073	1
Pred-1 UGACAGAAGAGAGUGAGCAC	2	NCRNA_48036	107-126	1
Pred-1 UGACAGAAGAGAGUGAGCAC	2	NCRNA_12235	11-30	-1
Pred-1 UGACAGAAGAGAGUGAGCAC	2	NCRNA_32390	11-30	-1
Pred-1 UGACAGAAGAGAGUGAGCAC	2	NCRNA_12239	11-30	-1
Pred-1 UGACAGAAGAGAGUGAGCAC	2	NCRNA_32385	11-30	-1
Pred-1 UGACAGAAGAGAGUGAGCAC	2	NCRNA_12238	11-30	-1
Pred-1 UGACAGAAGAGAGUGAGCAC	2	NCRNA_32403	12-31	-1
Pred-1 UGACAGAAGAGAGUGAGCAC	3.5	NCRNA_11831	134-153	1

5. Hybridization Energy

The Hybridization Energy page looks for the energetically favorable interaction sites between a small RNA in a large RNA by using RNAhybrid. Hybridization energy page is mainly divided in two sections. The first section is used to search for the validated miRNA-target hybridization energy, which is pre-calculated and the second section is used to calculate the hybridization energy of the users query sequences.

In the first section, user needs to click on the toggle and choose an organism from the first dropdown menu. After that user must click on the next toggle to select the miRNA ID from the second dropdown menu and submit it.



Energy minimization Help

Finding the minimum free energy hybridization of a long and a short RNA. The hybridization is performed in a kind of domain mode, ie. the short sequence is hybridized to the best fitting part of the long one.

Choose Any One Search Option:
Click on the image to toggle

● Validated miRNA-Target Hybridization Energy

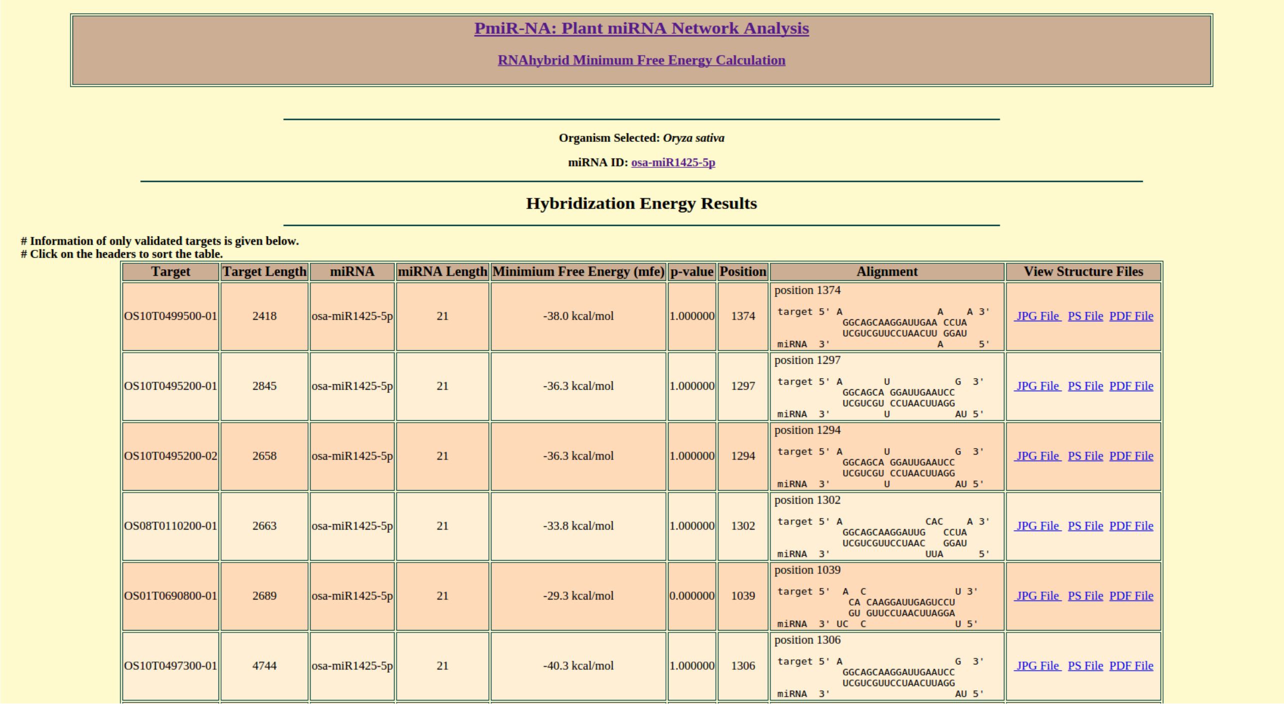
Select Organism Oryza sativa

● Select miRNA ID choose...

● Calculate Hybridization Energy

Hello visitor, you have seen this page

The result is shown on a new webpage having a list of targets along with the length of target and miRNA sequence, minimum free energy (mfe), p-value, position, alignment and its secondary structure file in three formats i.e JPG, PS and PDF. User can view the JPG image on the same webpage itself by moving the cursor on the JPG link. A small window showing the secondary structure of the respective target along with its mfe in kcal/mol is shown as a image. The list of targets can be analysed by clicking the headers to sort the respective columns like mfe and p-value in either increasing or decreasing order. The result table can also be downloaded by clicking on the download image link.



PmiR-NA: Plant miRNA Network Analysis

RNAhybrid Minimum Free Energy Calculation

Organism Selected: *Oryza sativa*

miRNA ID: osa-miR1425-5p

Hybridization Energy Results

 # Information of only validated targets is given below.
 # Click on the headers to sort the table.

Target	Target Length	miRNA	miRNA Length	Minimium Free Energy (mfe)	p-value	Position	Alignment	View Structure Files
OS10T0499500-01	2418	osa-miR1425-5p	21	-38.0 kcal/mol	1.000000	1374	position 1374	JPG File PS File PDF File
OS10T0495200-01	2845	osa-miR1425-5p	21	-36.3 kcal/mol	1.000000	1297	position 1297	JPG File PS File PDF File
OS10T0495200-02	2658	osa-miR1425-5p	21	-36.3 kcal/mol	1.000000	1294	position 1294	JPG File PS File PDF File
OS08T0110200-01	2663	osa-miR1425-5p	21	-33.8 kcal/mol	1.000000	1302	position 1302	JPG File PS File PDF File
OS01T0690800-01	2689	osa-miR1425-5p	21	-29.3 kcal/mol	0.000000	1039	position 1039	JPG File PS File PDF File
OS10T0497300-01	4744	osa-miR1425-5p	21	-40.3 kcal/mol	1.000000	1306	position 1306	JPG File PS File PDF File

OS10T0499500-01

```
target 5' A                A    A 3'
           GGCAGCAAGGAUUGAA CCUA
           UCGUCGUUCCUAACUU GGAU
miRNA  3'                  A      5'
```

OS10T0495200-01

```
target 5' A       U           G  3'
           GGCAGCA GGAUUGAAUCC
           UCGUCGU CCUAACUUAGG
miRNA  3'         U           AU 5'
```

OS10T0495200-02

```
target 5' A       U           G  3'
           GGCAGCA GGAUUGAAUCC
           UCGUCGU CCUAACUUAGG
miRNA  3'         U           AU 5'
```

OS08T0110200-01

```
target 5' A              CAC    A 3'
           GGCAGCAAGGAUUG   CCUA
           UCGUCGUUCCUAAC   GGAU
miRNA  3'                UUA      5'
```

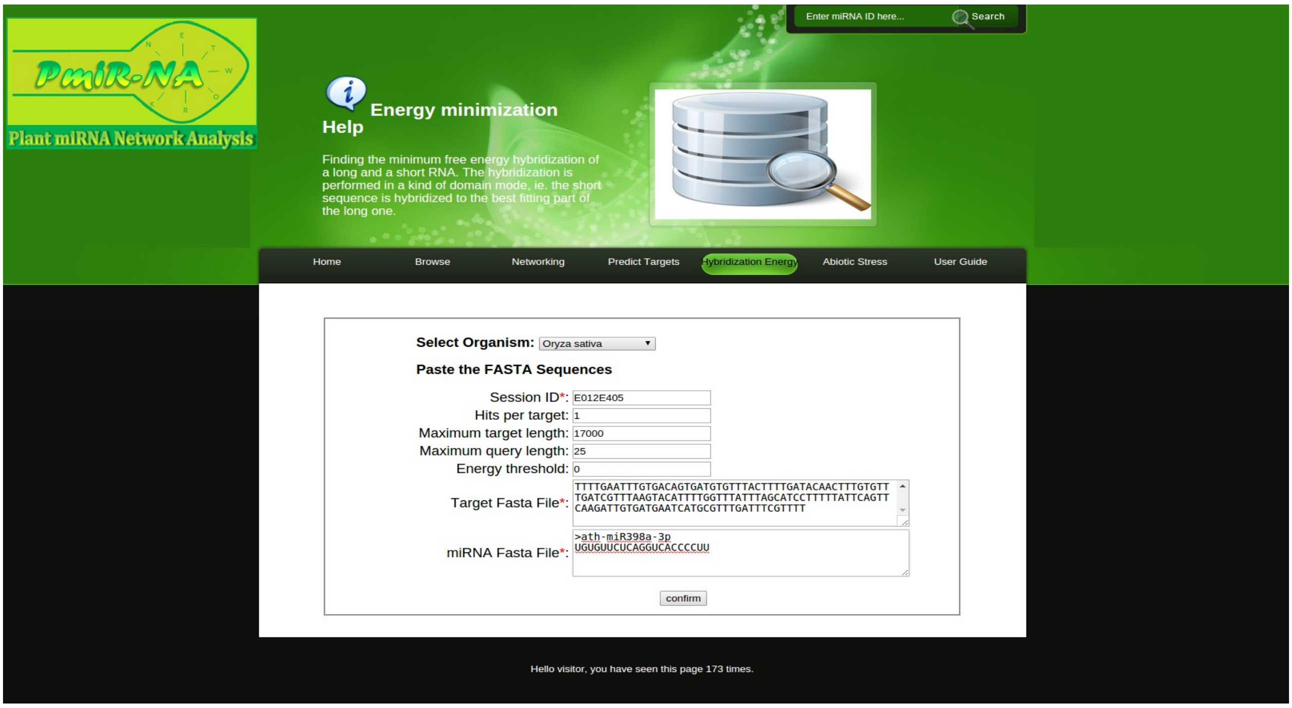
OS01T0690800-01

```
target 5'  A  C               U 3'
            CA CAAGGAUUGAGUCCU
            GU GUUCCUAACUUAGGA
miRNA  3' UC  C               U 5'
```

OS10T0497300-01

```
target 5' A                   G  3'
           GGCAGCAAGGAUUGAAUCC
           UCGUCGUUCCUAACUUAGG
miRNA  3'                     AU 5'
```

In the second section, user can choose either of the two options between "Paste the fasta sequences" or "Upload the fasta files". Depending upon the choice of user, input miRNA and target sequences/files are provided. User can also provide various parameters for each hybridization energy calculation. In case user doesnot know about the parameters, one should simply provide the default parameters already written in the input textbox and hit submit.



Finding the minimum free energy hybridization of a long and a short RNA. The hybridization is performed in a kind of domain mode, ie. the short sequence is hybridized to the best fitting part of the long one.

Select Organism: Oryza sativa

Paste the FASTA Sequences

Session ID*: E012E405
Hits per target: 1
Maximum target length: 17000
Maximum query length: 25
Energy threshold: 0
Target Fasta File*:

```
TTTTGAATTTGTGACAGTGATGTGTTTACTTTTGATACAACTTTGTGTT
TGATCGTTTAAGTACATTTTGGTTTATTTAGCATCCTTTTTATTCAGTT
CAAGATTGTGATGAATCATGCGTTTGATTTCGTTTT
```

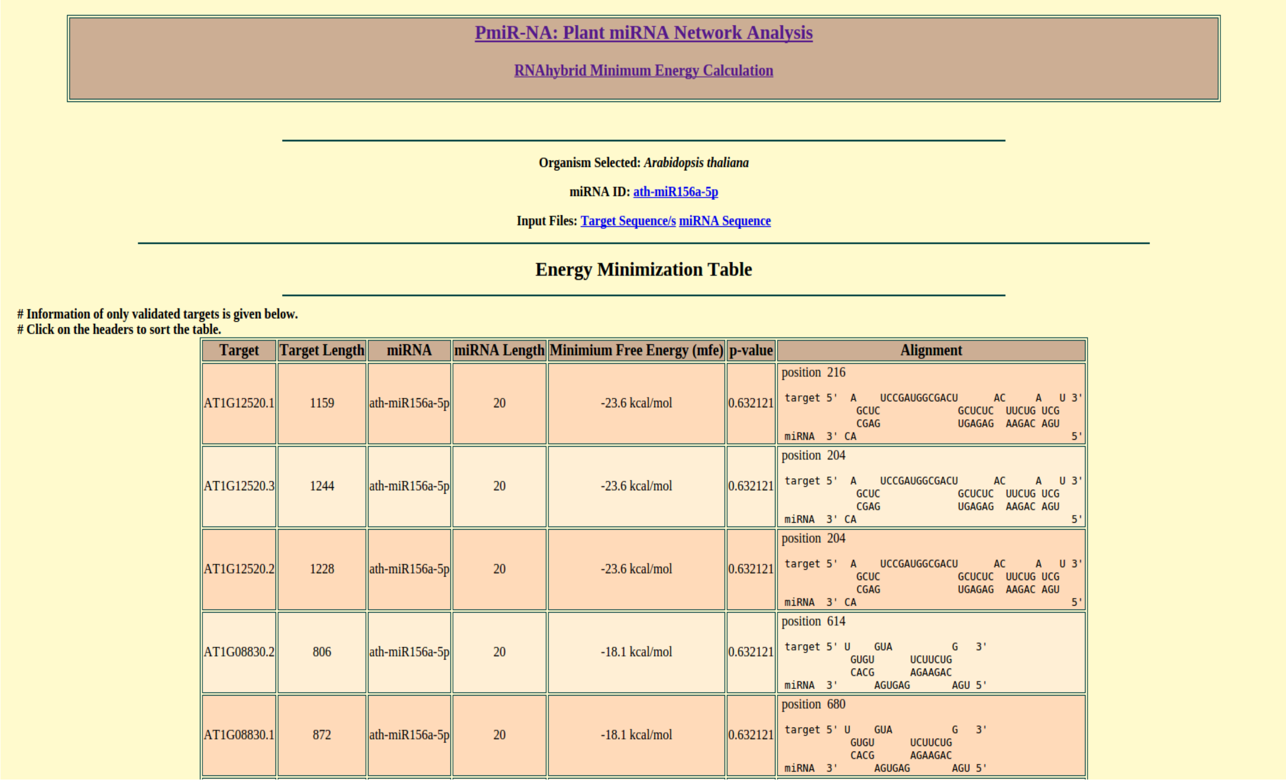
miRNA Fasta File*:

```
>ath-miR398a-3p
UGUGUUCUCAGGUCACCCCUU
```

confirm

Hello visitor, you have seen this page 173 times.

The result of hybridization energy calculation is shown on a new webpage mostly in the similar way as the result of the first section. The result can also be downloaded by clicking on the download image.



PmiR-NA: Plant miRNA Network Analysis

RNAhybrid Minimum Energy Calculation

Organism Selected: *Arabidopsis thaliana*

miRNA ID: ath-miR156a-5p

Input Files: Target Sequence/s miRNA Sequence

Energy Minimization Table

 # Information of only validated targets is given below.
 # Click on the headers to sort the table.

Target	Target Length	miRNA	miRNA Length	Minimium Free Energy (mfe)	p-value	Alignment
AT1G12520.1	1159	ath-miR156a-5p	20	-23.6 kcal/mol	0.632121	position 216
AT1G12520.3	1244	ath-miR156a-5p	20	-23.6 kcal/mol	0.632121	position 204
AT1G12520.2	1228	ath-miR156a-5p	20	-23.6 kcal/mol	0.632121	position 204
AT1G08830.2	806	ath-miR156a-5p	20	-18.1 kcal/mol	0.632121	position 614
AT1G08830.1	872	ath-miR156a-5p	20	-18.1 kcal/mol	0.632121	position 680

AT1G12520.1

```
target 5'  A    UCCGAUGGCGACU      AC     A   U 3'
            GCUC             GCUCUC  UUCUG UCG
            CGAG             UGAGAG  AAGAC AGU
miRNA  3' CA                                    5'
```

AT1G12520.3

```
target 5'  A    UCCGAUGGCGACU      AC     A   U 3'
            GCUC             GCUCUC  UUCUG UCG
            CGAG             UGAGAG  AAGAC AGU
miRNA  3' CA                                    5'
```

AT1G12520.2

```
target 5'  A    UCCGAUGGCGACU      AC     A   U 3'
            GCUC             GCUCUC  UUCUG UCG
            CGAG             UGAGAG  AAGAC AGU
miRNA  3' CA                                    5'
```

AT1G08830.2

```
target 5' U    GUA          G   3'
           GUGU      UCUUCUG
           CACG      AGAAGAC
miRNA  3'      AGUGAG       AGU 5'
```

AT1G08830.1

```
target 5' U    GUA          G   3'
           GUGU      UCUUCUG
           CACG      AGAAGAC
miRNA  3'      AGUGAG       AGU 5'
```

6. Abiotic Stress

The Abiotic Stress page provides the list of miRNA regulation in different plant abiotic stress conditions. This page is also divided in two separate sections i.e "Search by organism" and "Search by stress condition".

In the first section, user need to click the first toggle and choose the organism from the first dropdown menu. After organism selection, user need to select one choice between "Select miRNA ID" or "Select stress condition". Depending upon the user choice, one need to click the next toggle to select either miRNA ID or stress condition and hit submit.

Abiotic Stress Help

Abiotic Stress related data can be searched by either an organisms miRNA ID or stress type, or by selecting the stress condition of intrest.

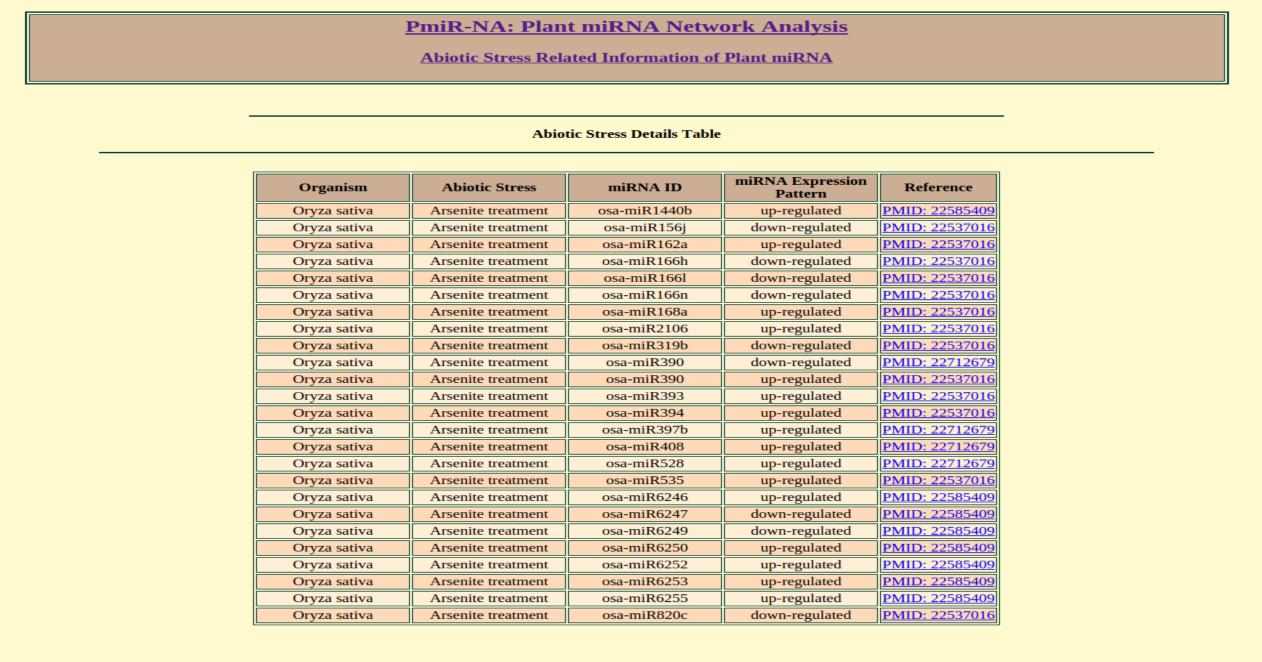
Choose Any One Search Option:

Click on the image to toggle

Select Organism: Oryza sativa

Hello visitor, you have seen this page 14 times.

After submit, user can view the results on new webpage showing the list of abiotic stress related details along with the miRNA expression pattern and the references which is hyperlinked.



PmiR-NA: Plant miRNA Network Analysis

Abiotic Stress Related Information of Plant miRNA

Abiotic Stress Details Table

Organism	Abiotic Stress	miRNA ID	miRNA Expression Pattern	Reference
Oryza sativa	Arsenite treatment	osa-miR1440b	up-regulated	PMID: 22585409
Oryza sativa	Arsenite treatment	osa-miR156j	down-regulated	PMID: 22537016
Oryza sativa	Arsenite treatment	osa-miR162a	up-regulated	PMID: 22537016
Oryza sativa	Arsenite treatment	osa-miR166h	down-regulated	PMID: 22537016
Oryza sativa	Arsenite treatment	osa-miR166l	down-regulated	PMID: 22537016
Oryza sativa	Arsenite treatment	osa-miR166n	down-regulated	PMID: 22537016
Oryza sativa	Arsenite treatment	osa-miR168a	up-regulated	PMID: 22537016
Oryza sativa	Arsenite treatment	osa-miR2106	up-regulated	PMID: 22537016
Oryza sativa	Arsenite treatment	osa-miR319b	down-regulated	PMID: 22537016
Oryza sativa	Arsenite treatment	osa-miR390	down-regulated	PMID: 22712679
Oryza sativa	Arsenite treatment	osa-miR390	up-regulated	PMID: 22537016
Oryza sativa	Arsenite treatment	osa-miR393	up-regulated	PMID: 22537016
Oryza sativa	Arsenite treatment	osa-miR394	up-regulated	PMID: 22537016
Oryza sativa	Arsenite treatment	osa-miR397b	up-regulated	PMID: 22712679
Oryza sativa	Arsenite treatment	osa-miR408	up-regulated	PMID: 22712679
Oryza sativa	Arsenite treatment	osa-miR528	up-regulated	PMID: 22712679
Oryza sativa	Arsenite treatment	osa-miR535	up-regulated	PMID: 22537016
Oryza sativa	Arsenite treatment	osa-miR6246	up-regulated	PMID: 22585409
Oryza sativa	Arsenite treatment	osa-miR6247	down-regulated	PMID: 22585409
Oryza sativa	Arsenite treatment	osa-miR6249	down-regulated	PMID: 22585409
Oryza sativa	Arsenite treatment	osa-miR6250	up-regulated	PMID: 22585409
Oryza sativa	Arsenite treatment	osa-miR6252	up-regulated	PMID: 22585409
Oryza sativa	Arsenite treatment	osa-miR6253	up-regulated	PMID: 22585409
Oryza sativa	Arsenite treatment	osa-miR6255	up-regulated	PMID: 22585409
Oryza sativa	Arsenite treatment	osa-miR820c	down-regulated	PMID: 22537016

In the second section, user need to click the second toggle i.e “Search by stress condition” and choose the aboitic stress condition from the dropdown menu and hit submit botton.

Abiotic Stress related data can be searched by either an organisms miRNA ID or stress type, or by selecting the stress condition of intrest.

Choose Any One Search Option:

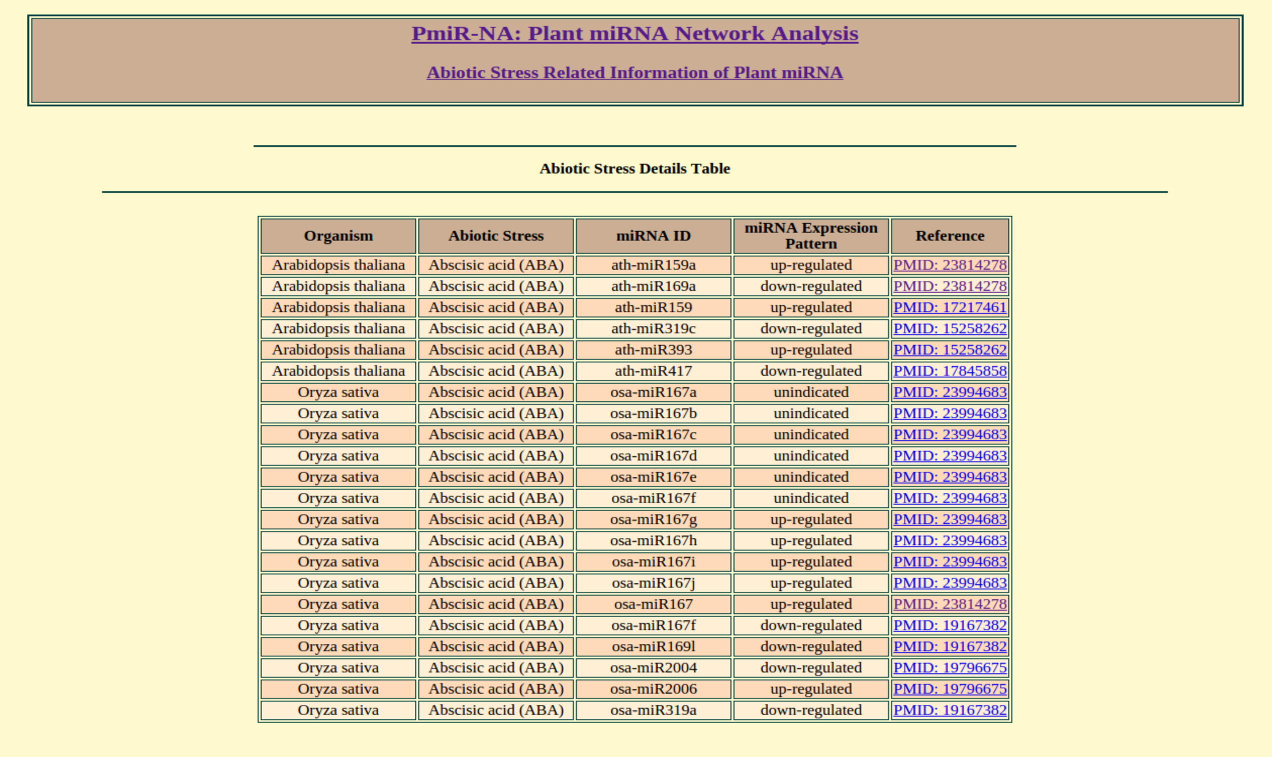
Click on the image to toggle

● Search by Organism

● Search by Stress Condition

Hello visitor, you have seen

The result is shown on a new webpage containing the list of miRNA showing the selected stress condition which was given by the user. Here also the list is provided with the miRNA expression pattern and hyperlinked references.



PmiR-NA: Plant miRNA Network Analysis

Abiotic Stress Related Information of Plant miRNA

Abiotic Stress Details Table

Organism	Abiotic Stress	miRNA ID	miRNA Expression Pattern	Reference
Arabidopsis thaliana	Abscisic acid (ABA)	ath-miR159a	up-regulated	PMID: 23814278
Arabidopsis thaliana	Abscisic acid (ABA)	ath-miR169a	down-regulated	PMID: 23814278
Arabidopsis thaliana	Abscisic acid (ABA)	ath-miR159	up-regulated	PMID: 17217461
Arabidopsis thaliana	Abscisic acid (ABA)	ath-miR319c	down-regulated	PMID: 15258262
Arabidopsis thaliana	Abscisic acid (ABA)	ath-miR393	up-regulated	PMID: 15258262
Arabidopsis thaliana	Abscisic acid (ABA)	ath-miR417	down-regulated	PMID: 17845858
Oryza sativa	Abscisic acid (ABA)	osa-miR167a	unindicated	PMID: 23994683
Oryza sativa	Abscisic acid (ABA)	osa-miR167b	unindicated	PMID: 23994683
Oryza sativa	Abscisic acid (ABA)	osa-miR167c	unindicated	PMID: 23994683
Oryza sativa	Abscisic acid (ABA)	osa-miR167d	unindicated	PMID: 23994683
Oryza sativa	Abscisic acid (ABA)	osa-miR167e	unindicated	PMID: 23994683
Oryza sativa	Abscisic acid (ABA)	osa-miR167f	unindicated	PMID: 23994683
Oryza sativa	Abscisic acid (ABA)	osa-miR167g	up-regulated	PMID: 23994683
Oryza sativa	Abscisic acid (ABA)	osa-miR167h	up-regulated	PMID: 23994683
Oryza sativa	Abscisic acid (ABA)	osa-miR167i	up-regulated	PMID: 23994683
Oryza sativa	Abscisic acid (ABA)	osa-miR167j	up-regulated	PMID: 23994683
Oryza sativa	Abscisic acid (ABA)	osa-miR167	up-regulated	PMID: 23814278
Oryza sativa	Abscisic acid (ABA)	osa-miR167f	down-regulated	PMID: 19167382
Oryza sativa	Abscisic acid (ABA)	osa-miR169l	down-regulated	PMID: 19167382
Oryza sativa	Abscisic acid (ABA)	osa-miR2004	down-regulated	PMID: 19796675
Oryza sativa	Abscisic acid (ABA)	osa-miR2006	up-regulated	PMID: 19796675
Oryza sativa	Abscisic acid (ABA)	osa-miR319a	down-regulated	PMID: 19167382