

User manual for Plant ESdb

content

01	Home Page.....	2
02	Search Features.....	3-17
03	Tools.....	18-24
04	Data Submission.....	25

User manual for Plant ESdb

Home page
With
navbar





Keyword Search And Pubmed Search with Ids

[Home](#)[Search](#)[Tools](#)[Statistics](#)[Acknowledgement](#)[Contact Us](#)[User Manual](#)[Submit Data](#)

Highlights

Update 1: <https://pubmed.ncbi.nlm.nih.gov/33069875/>

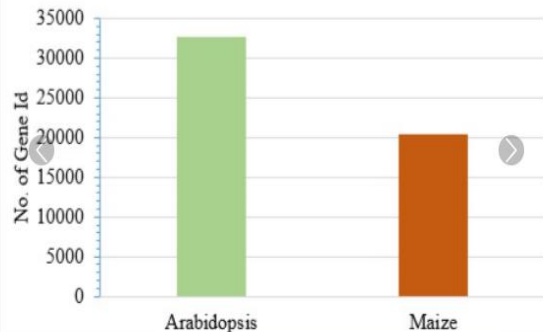
Citation 1: <https://pubmed.ncbi.nlm.nih.gov/33069875/>

Citation 2: <https://www.ncbi.nlm.nih.gov/search/all/?term=33582802>

Plant and Environment Stress

Land plants are frequently exposed to a variety of undesirable or even adverse environmental conditions due to their sessile nature. Abiotic stresses (such as salinity, drought, heat, cold, heavy metals, ozone, UV radiation, and nutritional deficits) and biotic stresses (including microbes, insects, and herbivores) are key factors that affect plant development, growth, and reproduction, posing a significant threat to plant survival. The catastrophic forecast of global warming, which is expected to have a negative impact on crop yield and thus on food production, is expected to increase the frequency, intensity, and duration of these adverse environmental conditions. The development of stress-tolerant cultivars with higher yields is at the top of the priority list for meeting future food and nutrition needs. Thus, at this juncture, the comprehensive knowledge of the molecular mechanisms underlying stress tolerance would be the initial step towards developing stress-tolerant crops.

Gene IDs



Research Focus

This image represents our research on plant stress responses.

Plant Environment Stress Database

Several databases contain information on stress-responsive genes in plants. Most of these databases lack information about genes, including details about regulatory elements, sequence (gene/CDS/Protein) information, orthology, and structural information. There are studies that have reported exploring transcriptional or post-transcriptional regulatory interactions; however, an integrated perspective of the regulatory elements is lacking. The present effort involved the construction of a highly curated, authentic database named Plant Environmental Stress Gene Database (PlantESdb), which contains comprehensive, high-quality resources for the individual, as well as combined environmental stress-responsive genes (ESR genes) and their transcriptional and post-transcriptional regulatory elements in Arabidopsis and maize with an effective knowledge-based information retrieval system.



This page is for keyword search.
Select Arabidopsis
or Maize then click
on search by species.

Plant Environment Stress Gene Database

[Home](#) [Search](#) [Tools](#) [Statistics](#) [Acknowledgement](#) [Contact Us](#) [User Manual](#) [Submit Data](#)

Welcome to PlantESdb

Select the Species :

Arabidopsis
Maize

Enter gene IDs separated by commas

Search by species

Example: (Maize V5 Gene ID - Zm00001eb103260 , Arabidopsis Gene ID - AT1G01010)

Location

Indian Agricultural Statistics Research Institute
Library Avenue, Pusa,
New Delhi - 110012
India

Contact

Email: info@iasri.icar.gov.in
Phone: +91-11-2584-xxxx

Official Website

<https://iasri.icar.gov.in/>



After entering the Ids we
gets the General
Information for
Arabidopsis

Select the Species : Arabidopsis

Enter gene IDs separated by commas

Search by species

Example: (Maize V5 Gene ID - Zm00001eb103260 , Arabidopsis Gene ID - AT1G01010)

Results for Arabidopsis:

General Information : 1

Gene Id	Entrez ID	Gene Name	Chr	Start	End	Strand	Gene Model Description	Gene Model Type	Primary Gene Symbol	All Gene Symbol
AT1G01310	839333	Na	1	120154	121130	+	CAP (Cysteine-rich secretory proteins Antigen 5 and Pathogenesis-related 1 protein) superfamily protein; (source:Araport11)	protein_coding	Na	Na

We can click any
of the button for
detailed
information.

Evidence

Gene

CDS

mRNA

Protein

PPI

Pathway

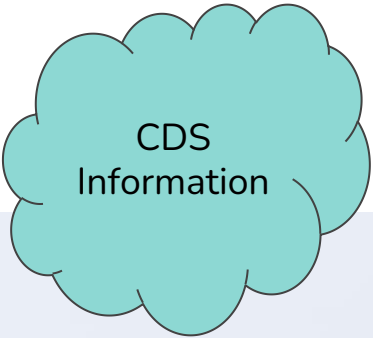
Domain

Ontology

ExternalLink

Orthologs

[Regulatory Network](#)



Evidence

Gene

CDS

mRNA

Protein

PPI

Pathway

Domain

Ontology

ExternalLink

Orthologs

[Regulatory Network](#)

Information of Gene ID: AT1G01310

Items	Information
CDS id	AT1G01310
Sequence	>AT1G01310 ATGGAGCTTCGTAACGGAAAAACGAGCTCCATTACATATCTTCGTCGGCATAACGTTCTTCCTCCTTCAGCTTTGGTC GGGAACGGCCCAATTAACCATGAAGACTCTTCACAAAACCTCCGTTAAAACTCTCCGTCAGCGACGAGTACTCGGC TTCTGTTGTCACCACCTTCGTTACCGGAAACCGATTCTCGTTCAGGTTCAAGGTGGAGGAGAATACGACGTCGTAACAGA GTCAACAGAGCGAGCAGAGAGTTTTTAATCGACATAACCTCGTAAGAGCGCGCTGGGAGAACCACCGTTTCAATGGGA CGGAAGATTAGCGCGTACGCGCACGTGGCGAATCAGCGCGTGGGTGATTGTAGGCTTGTTCACTCTAACGGGCCGT ATGGAGAAAACATATTTTGGCCGGAAAGAATAACTGGAGCCCCAGAGATATTGTTAATGTGTGGCCGATGAGGATAAA TTCTACGACGTGAAAGGTAACACGTGTGAGCCGCAACACATGTGTGGGCACTACACGCAGATCGTGTGGAGAGATAGTAC CAAGGTCGGATGCGCAAGGTGTGATTGTTGAAACGGCGCTTTATGCGATTGTGTTATAACCCACCGGAAATTACG AAGGTGAAAATCCGTTTGGAAAGTTATGATGATCAGATTGGTCTTGCCCGGATGATCCACGGCGGTGATCGGAGGAATG GCTTGA

And we can also
check the information
for pubmed ids by
clicking on the ids

Evidence

Gene

CDS

mRNA

Protein

PPI

Pathway

Domain

Ontology

ExternalLink

Orthologs

[Regulatory Network](#)

51 Evidence for Gene ID: AT1G01310

Pubmed Id	Year	Gene ID	Stress	Regulation	Technique
18684332	2008	AT1G01310	Arsenate	Down	Microarray
18684332	2008	AT1G01310	Arsenic	Down	Microarray
26941754	2016	AT1G01310	Drought	Down	Microarray
28904348	2017	AT1G01310	Salt	Down	NGS
15734908	2005	AT1G01310	Anoxia	Na	Microarray
28132837	2017	AT1G01310	Biotic	Na	NGS
18567827	2008	AT1G01310	Biotic	Na	Microarray
16972869	2006	AT1G01310	Drought	Na	Microarray

On clicks
at pubmed
ids its take
you to this
page.

Google Translate
[https://translate.google.com/?sl=hi&tl=en&text=kya kar rahe ho&op=translate](https://translate.google.com/?sl=hi&tl=en&text=kya%20kar%20rahe%20ho&op=translate)



National Library of Medicine
National Center for Biotechnology Information

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Display options ⚙

► Front Plant Sci. 2016 Feb 23;7:180. doi: 10.3389/fpls.2016.00180. eCollection 2016.

Transcriptomic Analysis of Soil-Grown Arabidopsis thaliana Roots and Shoots in Response to a Drought Stress

Sultana Rasheed ¹, Khurram Bashir ², Akihiro Matsui ², Maho Tanaka ², Motoaki Seki ³

Affiliations + expand

PMID: 26941754 PMID: PMC4763085 DOI: 10.3389/fpls.2016.00180

Abstract

Drought stress has a negative impact on crop yield. Thus, understanding the molecular mechanisms responsible for plant drought stress tolerance is essential for improving this beneficial trait in crops. In

FULL TEXT LINKS



ACTIONS

“ Cite

📖 Collections

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Gene Information

Information of Gene ID:AT1G01310

Result:

Items	Information
Entrez id	839333
Gene Name	Na
Chr	1
Start	120154
end	121130
Gene Description	CAP (Cysteine-rich secretory proteins Antigen 5 and Pathogenesis-related 1 protein) superfamily protein;(source:Araport11)
Gene Sequence	37120 ← >37120 AT1G01310
View the Location of Gene	AT1G01310 ←

We can check gene
Sequence and
location of the
gene by click on
these ids.

Protein
information

Evidence

Gene

CDS

mRNA

Protein

PPi

Pathway

Domain

Ontology

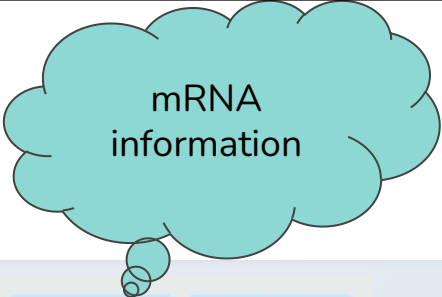
ExternalLink

Orthologs

[Regulatory Network](#)

Information of Gene ID:AT1G01310

Items	Information
Protein id	AT1G01310.1
Transcript id	AT1G01310.1
Xref id	A0A178WB87
Database name	Uniprot/SPTREMBL
Protein Sequence	<pre>>AT1G01310.1 MELRKRKIRAPLHIFVGITFFLLQLWSGTAGINHEDSSTKPSVKNSPSATSTRLLSPPSFTGNRFS FRWRRIIRRNQVWRA SREFLIAHLLVRAVGEPPFQWDGRLAAYARTWANGRVGDCLRVHSGF ENIFWAGKNNWSPRDIVNVWADEKFDVKGNTCEPQHMCGHYTQIVWRDSTKVGCASVDCSN VYAICVYNPPNGYEGENPFGSYDDQIGLARDPPAVIGGMA</pre>



Evidence

Gene

CDS

mRNA

Protein

PPI

Pathway

Domain

Ontology

ExternalLink

Orthologs

[Regulatory Network](#)

Information for Gene ID: AT1G01310

Attribute	Value
Entrez ID	839333
Gene Name	Na
Chromosome	1
Start Position	120154
End Position	121130
Gene Description	CAP (Cysteine-rich secretory proteins Antigen 5 and Pathogenesis-related 1 protein) superfamily protein;(source:Araport11)
Gene Sequence	NM_100013.2
Gene Location	AT1G01310

PPI information

General information : 1

Gene Id	Entrez ID					Strand	Gene Model Description	Gene Model Type	Primary Gene Symbol	All Gene Symbol
AT1G01310	839333	Na	1	120154	121130	+	CAP (Cysteine-rich secretory proteins Antigen 5 and Pathogenesis-related 1 protein) superfamily protein,(source:Araport11)	protein_coding	Na	Na

☒ Evidence

☐ Gene

☐ CDS

☐ mRNA

☐ Protein

☒ PPI

☐ Pathway

☐ Domain

☐ Ontology

☐ ExternalLink

☐ Orthologs

☐ [Regulatory Network](#)

Information of Gene ID:AT1G01310

Items	Information
Protein id	AT1G01310 

Click here for String Data

Location

Indian Agricultural Statistics Research Institute
Library Avenue, Pusa,
New Delhi - 110012
India

Contact

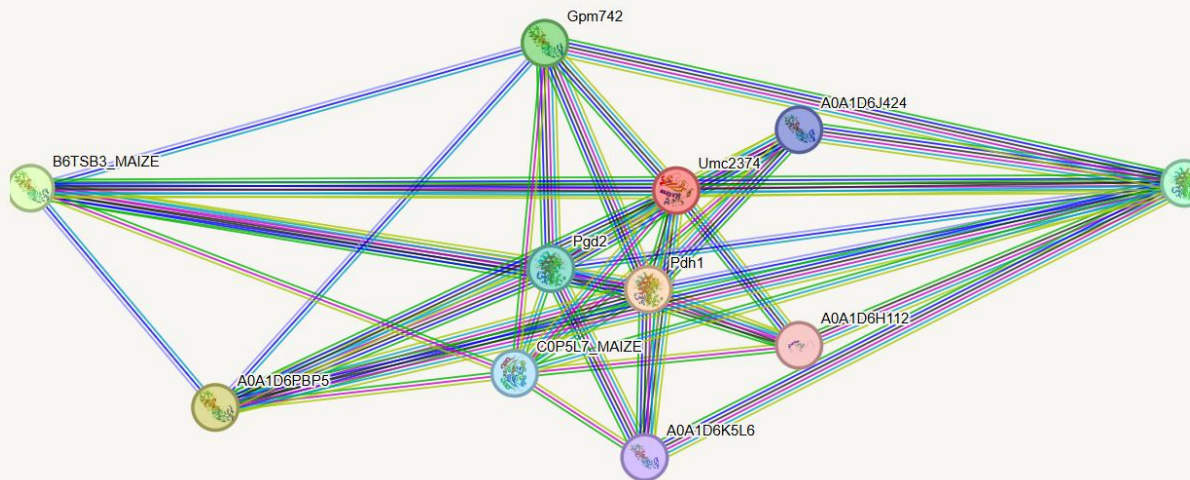
Email: info@iasri.icar.gov.in
Phone: +91-11-2584-xxxx

Official Website

<https://iasri.icar.gov.in/>



STRING Network

[Search](#)[Download](#)[Help](#)[My Data](#)[Viewers >](#)[Legend >](#)[Settings v](#)[Analysis >](#)[Exports >](#)[Clusters >](#)[+ More](#)[- Less](#)

Basic Settings

Network type:

☒ full STRING network (the edges indicate both functional and physical protein associations)

[UPDATE](#)

This page contains
Domain Information
and when we click to
the pfam ID it takes
us to the Interpro
database.

AT1G01310	839333	Na	1	120154	121130	+	CAP (Cysteine-rich superfamily protein, ... ed 1 protein)	protein_coding	Na	Na
-----------	--------	----	---	--------	--------	---	---	----------------	----	----

Evidence

Gene

Chromosome

mRNA

Protein

PPI

Pathway

Domain

Ontology

ExternalLink

Orthologs

[Regulatory Network](#)

Information of Gene ID:AT1G01310

Result:

Items	Information
pfam ID	PF00188
pfam Name	SCP
Start	139
end	268
InterPro ID	IPR001283
InterPro Name	SCP

Classification of protein families.



InterPro

Classification of protein families



Home

Search

Browse

Results

Release notes

Download

Help

Search by protein families, domains, proteins, keywords, or GO terms

PF00188



Examples: *IPR020422*, *kinase*, *O00167*, *PF02932*, *GO:0007165*, *1t2v*, *UP000005640*

Search

Clear

Powered by [EBI search](#)

1 - 7 of 7 entries



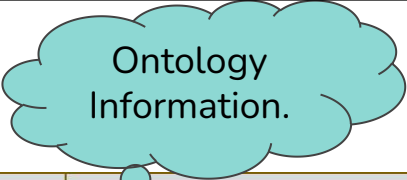
Download



Accession	Name	Source Database	Description
PF00188	Cysteine-rich secretory protein family	PFAM	This is a large family of cysteine-rich secretory proteins, antigen 5, and pathogenesis-related 1 proteins (CAP) that are found in a wide range of organisms, including prokaryotes [cite:PUB00016669] ...
NF025857	CAP-associated N-terminal domain	NCBIFAM	This HMM defines a domain found N-terminal to the CAP domain (PF00188), which is named for cysteine-rich secretory proteins, antigen 5, and pathogenesis-related 1 proteins.
PF14504	CAP-associated N-terminal	PFAM	The function of this domain is unknown, but it is found towards the N-terminus of bacterial proteins carrying the CAP domain, [pfam:PF00188] . All members that do not otherwise carry an additional Cu_a...

Rows per page: 20

Previous 1 Next



AT1G01310	839333	Na	1	120154	121130	+	CAP (Cysteine-rich secretory proteins Antigen 5 and Pathogenesis-related 1 protein) superfamily protein; (source:Araport11)	protein_coding	Na	Na
-----------	--------	----	---	--------	--------	---	---	----------------	----	----

Evidence

Gene

CDS

mRNA

Protein

PPI

Pathway

Domain

Ontology

ExternalLink

Orthologs

[Regulatory Network](#)

Information for Gene ID: AT1G01310

Gene ID	AT1G01310
GO Term	biological_process_unknown
GO ID	GO:0008150
Category	B
GO Slim	unknown biological processes
Evidence Code	ND

Orthologues Information.



Arabidopsis thaliana (TAIR10)

Location: 1:120,154-121,130

Gene: AT1G01310

Transcript: AT1G01310.201

Gene-based displays

- Summary
 - Splice variants
 - Transcript comparison
 - Gene alleles
- Sequence
 - Secondary Structure
 - Gene families
 - Literature
- Plant Compara
 - Genomic alignments
 - Gene tree
 - Gene gain/loss tree
 - Orthologues
 - Paralogues
- Pan-taxonomic Compara
 - Gene Tree
 - Orthologues
- Ontologies
 - GO: Anatomical entity
 - Phenotypes
- Genetic Variation
 - Variant table
 - Variant image
 - Structural variants
- Gene expression
- Pathway
- Molecular interactions
- Regulation
- External references
- Supporting evidence
- ID History
 - Gene history

Configure this page

Gene: AT1G01310

Description

CAP (Cysteine-rich secretory proteins, Antigen 5, and Pathosis-related 1 protein) superfamily protein [Source:NCBI gene (formerly Entrezgene);Acc:[839333](#)]

Gene Synonyms

F6F3.11, F6F3_11

Location

[Chromosome 1: 120,154-121,130](#) forward strand.

About this gene

This gene has 1 transcript ([splice variant](#)), [138 orthologues](#) and [19 paralogues](#).

Transcripts

Hide transcript table

Show/hide columns (1 hidden)

Filter

Name	Transcript ID	bp	Protein	Biotype	UniProt	RefSeq	Flags
AT1G01310.201	AT1G01310.1	977	241aa	Protein coding	Q6ID87	-	Ensembl Canonical

Orthologues

Download orthologues

Summary of orthologues of this gene [Hide](#)

Click on 'Show details' to display the orthologues for one or more groups of species. Alternatively, click on 'Configure this page' to choose a custom list of species.

Species set	Show details	With 1:1 orthologues	With 1:many orthologues	With many:many orthologues	Without orthologues
All (174 species)	☒	0	7	44	123
Vertebrates (12 species)	☐	0	0	12	0
Metazoa (24 species)	☐	0	1	23	0
Plants (10 species)	☐	0	2	2	6

For Blast and Regulatory
Network Tool



Plant Environment Stress Gene Database

[Home](#) [Search](#) [Tools](#) [Statistics](#) [Acknowledgement](#) [Contact Us](#) [User Manual](#) [Submit Data](#)

[Blast](#)
[Regulatory
network](#)

Plant and Environment Stress

Land plants are frequently exposed to a variety of undesirable, or even adverse, environmental conditions due to their sessile nature. Abiotic (salinity, drought, heat, cold, heavy metals, ozone, UV radiation, and nutritional deficits) and biotic (microbes, insects, and herbivores) stressors are key restrictions that affect plant development, growth, and reproduction and pose a major threat to the lives of plants. The catastrophic forecast of global warming, which is expected to have a negative impact on crop yield and thus on food production, is expected to increase the frequency, intensity, and duration of these adverse environmental conditions. The development of stress-tolerant cultivars with higher yields is at the top of the priority list for meeting future food and nutrition needs. Comprehensive knowledge about the molecular mechanism of stress tolerance would be the initial step towards the development of stress tolerant crops.

Highlights

Update 1: Description of the first highlight.

Update 2: Description of the second highlight.

Update 3: Description of the third highlight.



Plant Environment Stress Gene Database



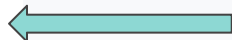
[Home](#) [Search](#) [Tools](#) [Statistics](#) [Acknowledgement](#) [Contact Us](#) [User Manual](#) [Submit Data](#)

BLAST Search Tool Against Plant ESdb

Select
program



Select
Database



Enter or
upload
seq



Program:

BlastN

Database:

Arabidopsis cds

Enter Sequence (FASTA format):

Upload Sequence File (FASTA format):

[Choose File](#) No file chosen

Output Format:

Plain Text

Run BLAST

Plain Text Blast Result

Output:

BLAST RESULT

Copy

CSV

Excel

Search:

Query ID	Subject ID	% Identity	Alignment Length	Mismatches	Gap Opens	Query Start	Query End	Subject Start	Subject End	E-value	Bit Score
AT1G76820.1	AT1G76720.1	90.059	1348	77	15	548	1860	555	1880	0.0	1694
AT1G76820.1	AT1G76720.1	75.843	356	33	20	135	483	1	310	1.74e-29	132
AT1G76820.1	AT1G76720.2	90.059	1348	77	15	548	1860	654	1979	0.0	1694
AT1G76820.1	AT1G76720.2	75.843	356	33	20	135	483	31	340	1.74e-29	132
AT1G76820.1	AT1G76810.1	86.197	1333	117	24	522	1802	718	2035	0.0	1380
AT1G76820.1	AT1G76810.1	80.964	394	38	20	135	502	1	383	2.12e-73	278

Showing 1 to 6 of 6 entries

Previous

1

Next



Regulatory
Network
Page



Plant Environment Stress Gene Database



[Home](#) [Search](#) [Tools](#) [Statistics](#) [Acknowledgement](#) [Contact Us](#) [User Manual](#) [Submit Data](#)

Cytoscape.js Database

Search Gene Data

Enter Gene IDs to search for related miRNA data.

Select Table:

Arabidopsis

Arabidopsis

Maize

v4

Enter Gene IDs (comma or space separated):

e.g. gene1, gene2

Search

After selecting
the table we
just have to
enter ids then
search.

Download as .txt

Layout: Force-Directed

Generate Regulatory Network

Calculate Degree Centrality

Export Graph as JSON

Node Connection Table

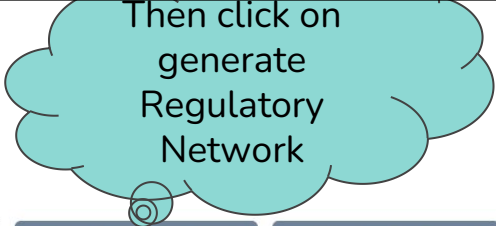
Degree Centrality Values

Copy

CSV

Excel

Search:



Enter Gene IDs to search for related miRNA data.

Select Table:

Arabidopsis

Select Version:

V4

Enter Gene IDs (comma or space separated):

AT1G69170 ,AT3G02155,AT4G00150

Search

Select Node Color:

Yellow

Select Graph Layout:

Force-Directed

Generate Regulatory Network

Calculate Degree Centrality

Export Graph as JSON

Download Graph as Image

Node Connection Table

Degree Centrality Values

Database Table

Copy

CSV

Excel

Search:

GENE ID

MIRNA ID

RELATION

AT1G69170

ath-miR156i

miRNA-DEG

AT1G69170

ath-miR156j

miRNA-DEG

AT1G69170

ath-miR156a

miRNA-DEG

AT1G69170

ath-miR156b

miRNA-DEG

AT1G69170

ath-miR156c

miRNA-DEG

Search Gene Data

Enter Gene IDs to search for related miRNA data.

Select Table:

Arabidopsis

Select Version:

V4

Enter Gene IDs (comma or space separated):

AT1G69170 ,AT3G02155,AT4G00150

Search

Download as .txt

Select Node Color:

Select Graph Layout:

Concentric

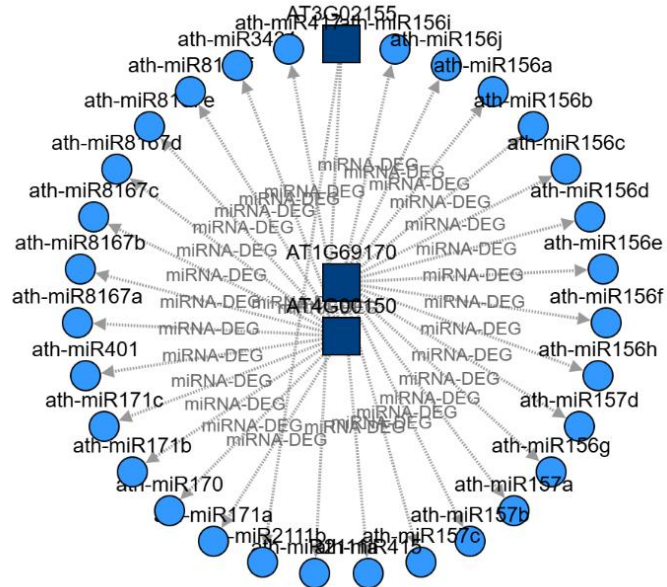
Generate Regulatory Network

Calculate Degree Centrality

Export Graph as JSON

Download Graph as Image

We can calculate Degree Centrality by click here.





Plant Environment Stress Gene Database



User can
Submit data

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Enter Stress Data

Please fill out the form below to submit your data.

Name:

Organization:

Email:

PubMed ID:

Publication Year:

Gene Name:

Comments:

Submit

Location

Indian Agricultural Statistics Research Institute
Library Avenue, Pusa,
New Delhi - 110 012

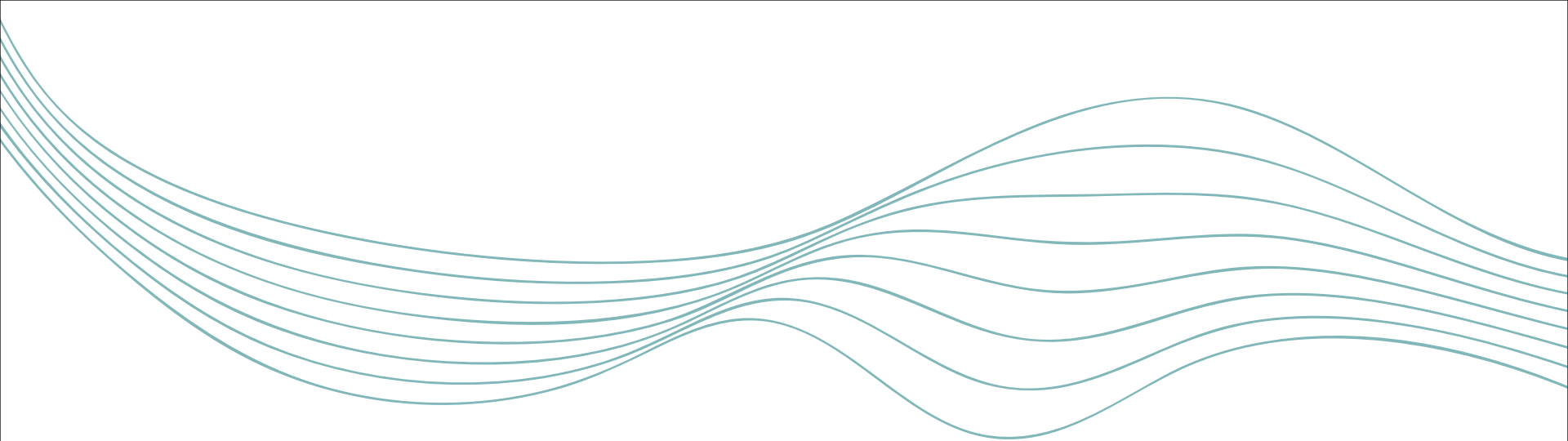
Contact

Email: info@iasri.icar.gov.in

Official Website

<https://iasri.icar.gov.in/>



A series of approximately ten thin, teal-colored wavy lines that originate from the top left corner and flow horizontally across the upper half of the slide, creating a sense of movement and depth.

THANKS

....