User manual for Plant ESdb

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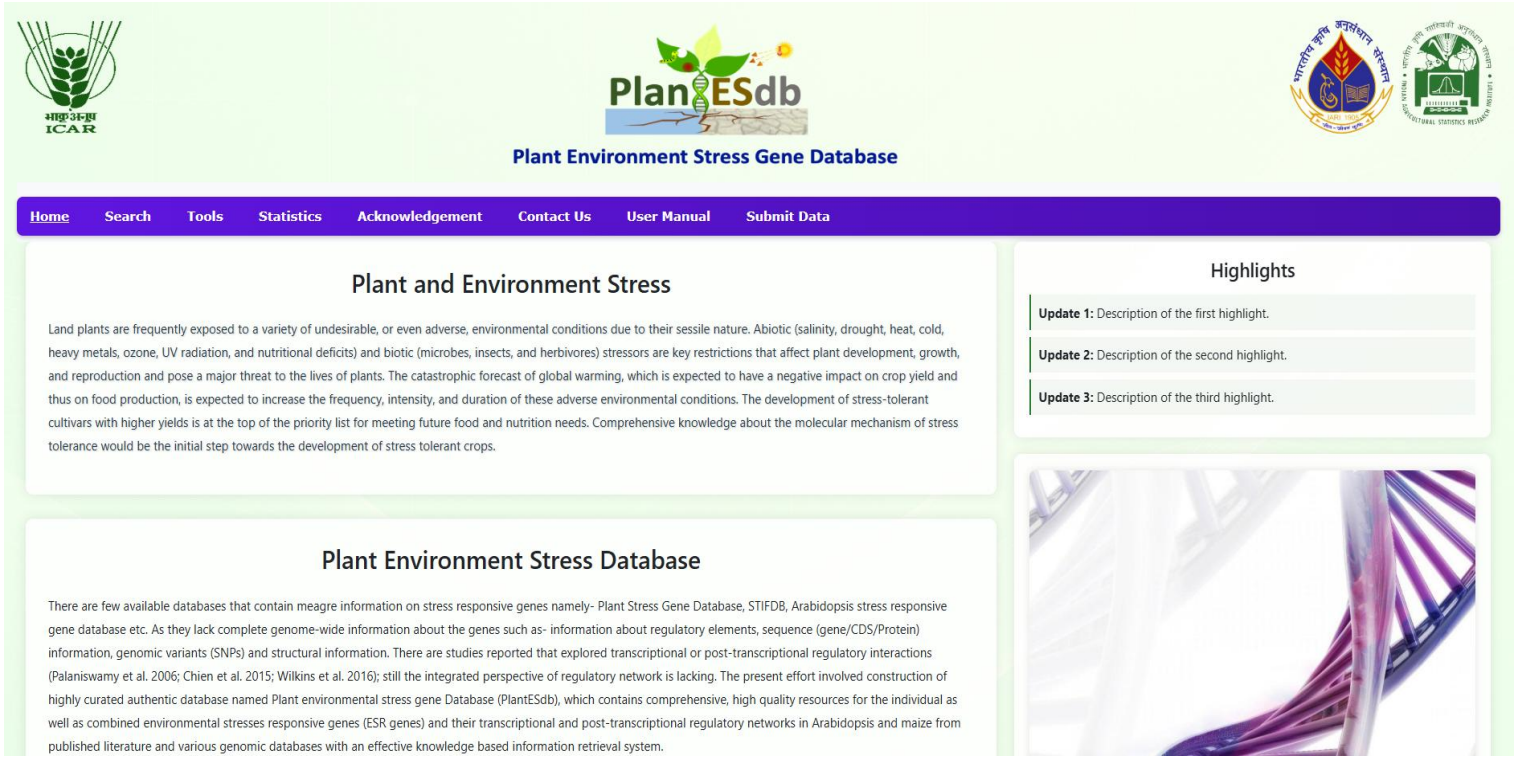
User manual for Plant ESdb

Home page
With
navbar



Keyword Search And Pubmed Search with Ids

PlantESdb

Plant Environment Stress Gene Database

Home | Search | Tools | Statistics | Acknowledgement | Contact Us | User Manual | Submit Data

- Keyboard search
- Pubmed search

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 Database

There are few available databases that contain meagre information on stress responsive genes namely- Plant Stress Gene Database, STIFDB, Arabidopsis stress responsive gene database etc. As they lack complete genome-wide information about the genes such as- information about regulatory elements, sequence (gene/CDS/Protein) information, genomic variants (SNPs) and structural information. There are studies reported that explored transcriptional or post-transcriptional regulatory interactions (Palaniswamy et al. 2006; Chien et al. 2015; Wilkins et al. 2016); still the integrated perspective of regulatory network is lacking. The present effort involved construction of 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 stresses responsive genes (ESR genes) and their transcriptional and post-transcriptional regulatory networks in Arabidopsis and maize from ...ious genomic databases with an effective knowledge based information retrieval system.

localhost:3000/mg/mg_index.php#

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

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

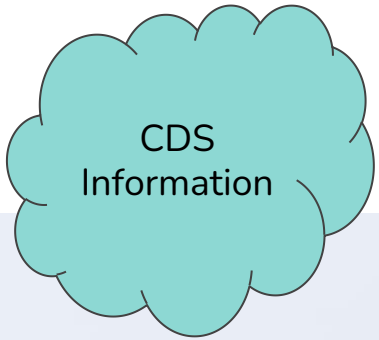
Email: info@iasri.icar.gov.in

Phone: +91-11-2584-xxxx

Official Website

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

After entering the Ids we gets the General Information for Arabidopsis



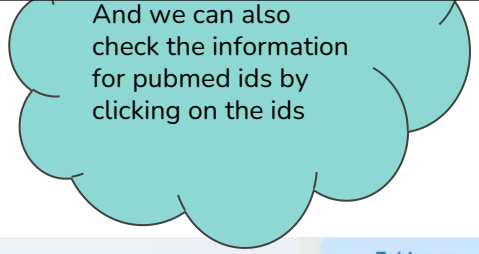
Evidence | Gene | CDS | mRNA | Protein

PPi | Pathway | Domain | Ontology | ExternalLink

Orthologs | Regulatory Network

Information of Gene ID: AT1G01310

Items	Information
CDS id	AT1G01310
Sequence	>AT1G01310 ATGGAGCTTCGTAAACGGAAAATACGAGCTCCATTACATATCTTCGTCGGCATAACGTTCTTCCTCCTTCAGCTTTGGTC GGGAACGGCCCAAATTAACCATGAAGACTCTTCCACAAAACCCTCCGTTAAAAACTCTCCGTCAGCGACGAGTACTCGGC TTCTGTTGTCACCACCTTCGTTCACCGGAAACCGATTCTCGTTCAGGTTCAGGTGGAGGAGAATACGACGTCGTAACAGA GTCAACAGAGCGAGCAGAGAGTTTTTAATCGCACATAACCTCGTAAGAGCGCGCGTGGGAGAACCACCGTTTCAATGGGA CGGAAGATTAGCGGCGTACGCGCGCACGTGGGCGAATCAGCGCGTGGGTGATTGTAGGCTTGTTCACTCTAACGGGCCGT ATGGAGAAAACATATTTTGGGCCGGAAAGAATAACTGGAGCCCCAGAGATATTGTTAATGTGTGGGCCGATGAGGATAAA TTCTACGACGTGAAAGGTAACACGTGTGAGCCGCAACACATGTGTGGGCACTACACGCAGATCGTGTGGAGAGATAGTAC CAAGGTCGGATGCGCAAGTGTGGATTGTTCGAACGGCGGCGTTTATGCGATTTGTGTTTATAACCCACCGGGAAATTACG AAGGTGAAAATCCGTTTGGAAGTTATGATGATCAGATTGGTCTTGCCCGGGATGATCCACCGGCGGTGATCGGAGGAATG GCTTGA



Evidence | Gene | CDS | mRNA | Protein

PPi | Pathway | Domain | Ontology | ExternalLink

Orthologs | Regulatory Network

51 Eviden 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.

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https://translate.google.com/?sl=hi&tl=en&text=kya kar rahe ho&op=translate

NIH National Library of Medicine
National Center for Biotechnology Information

Log in

PubMed®

Search

Advanced User Guide

Save Email Send to 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 PMCID: PMC4763085 DOI: 10.3389/fpls.2016.00180

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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

Gene Information

Information of Gene ID:AT1G01310

Result:

Items	Infromation
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

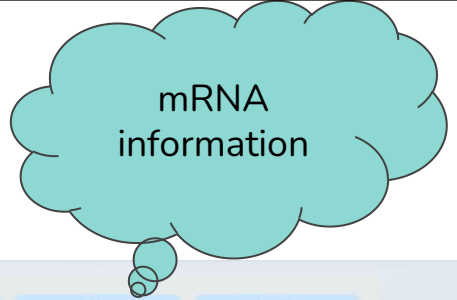
Evidence | Gene | CDS | mRNA | Protein

PPi | Pathway | Domain | Ontology | ExternalLink

Orthologs | Regulatory Network

Information of Gene ID:AT1G01310

Items	Infromation
Protein id	AT1G01310.1
Transcript id	AT1G01310.1
Xref id	A0A178WB87
Database name	Uniprot/SPTREMBL
Protein Sequence	>AT1G01310.1 MELRKRKIRAPLHIFVGITFFLLGLWSGTAQINHEDSSTKPSVKNSPSATSTRLLLSPPSFTGNRFS FRWRRIRRRNRVNRASREFLIAHNLVRARVGEPPFQWDGRLAAYARTWANQRVGDCRLVHSNGF ENIFWAGKNNWSPRDVNVVWADEDKFYDVKGNTCEPQHMCGHYTQIVWRDSTKVGCASVDCSN VYAICVYNPPGNYEGENPFGSYDDQIGLARDDPPAVIGGMA



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

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

vidence | Gene | CDS | mRNA | Protein

PPi | Pathway | Domain | Ontology | ExternalLink

Orthologs | Regulatory Network

Information of Gene ID:AT1G01310

Click here fot String Data

Items	Infromation
Protein id	AT1G01310

Location

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

Contact

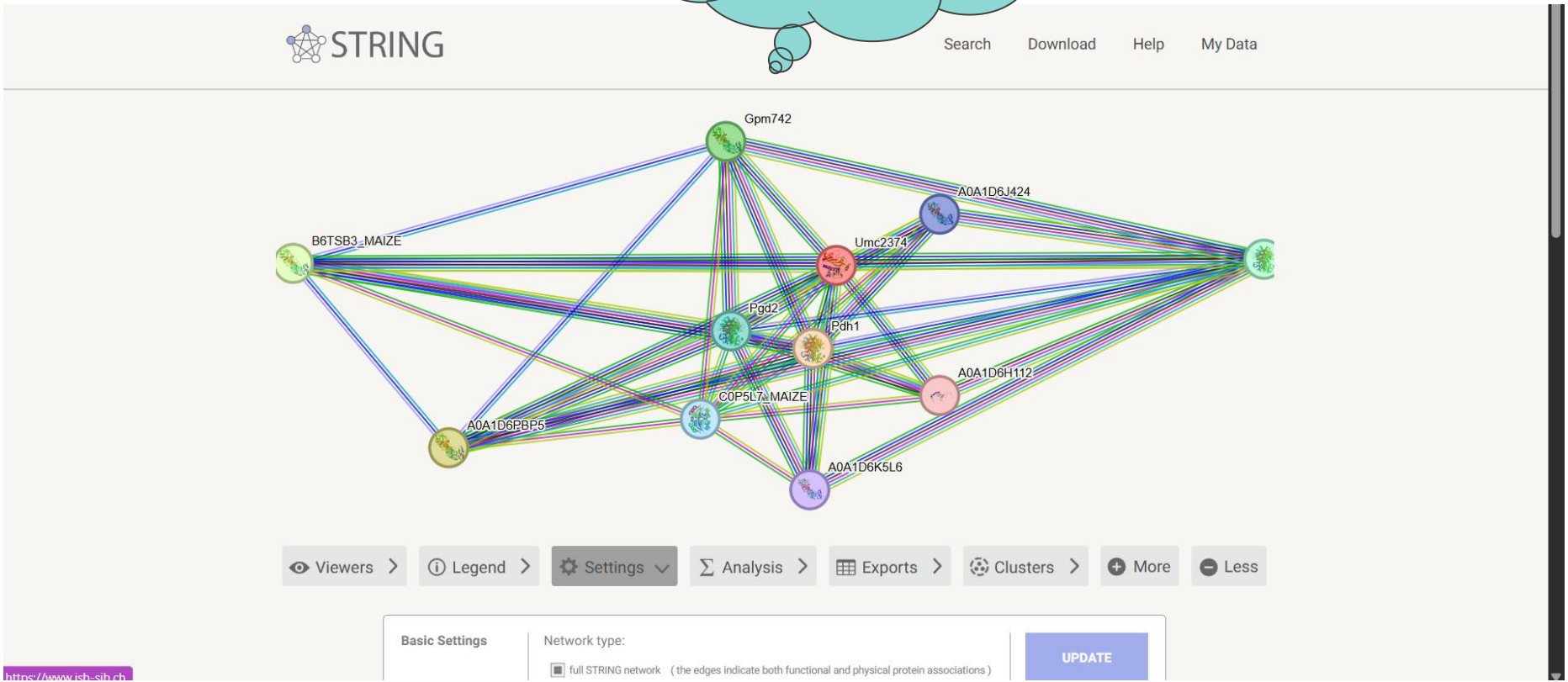
Email: info@iasri.icar.gov.in

Phone: +91-11-2584-xxxx

Official Website

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

STRING Network



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 | C | mRNA | Protein

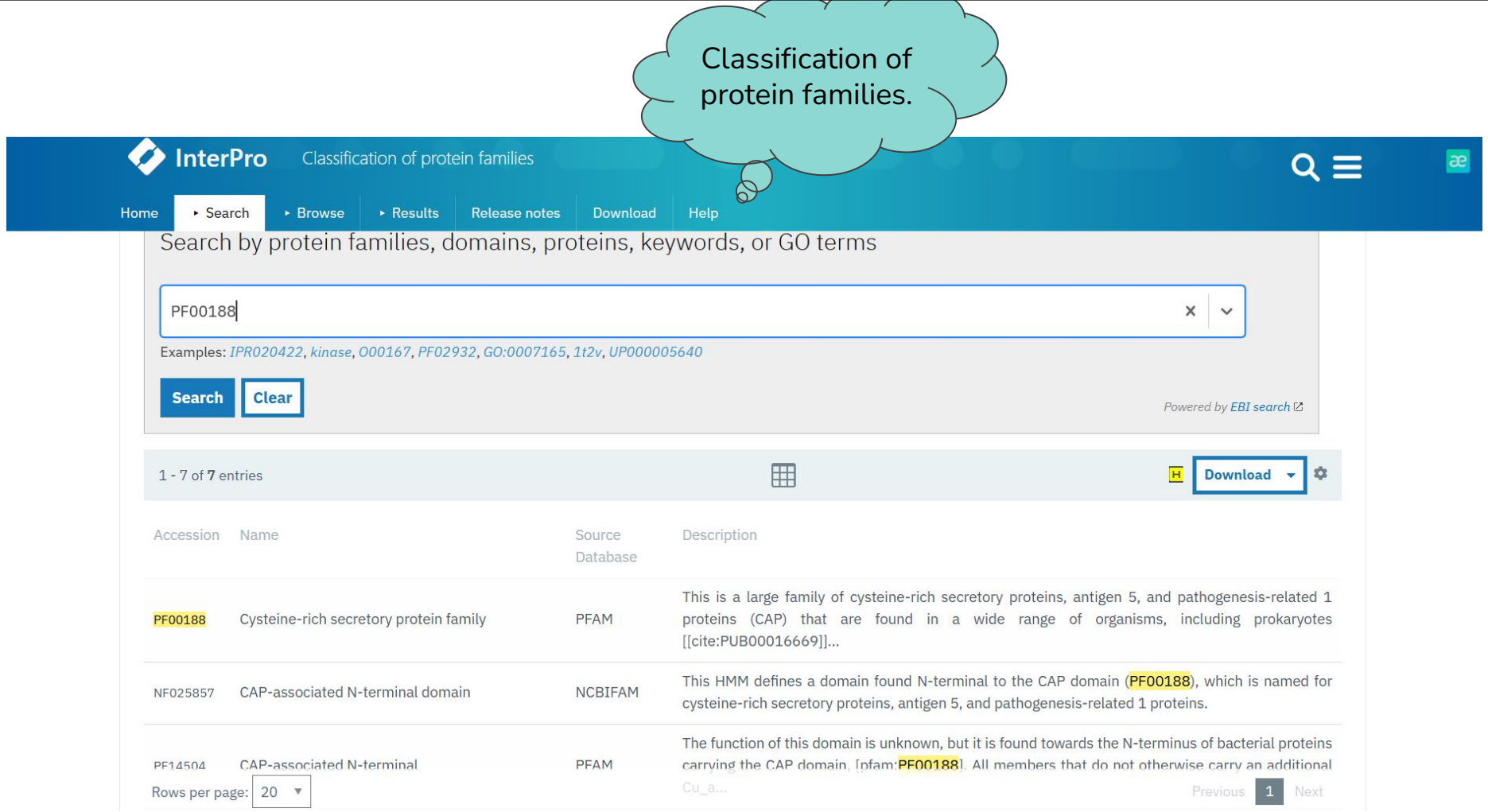
PPi | Pathway | Domain | Ontology | ExternalLink

Orthologs | Regulatory Network

Information of Gene ID:AT1G01310

Result:

Items	Infromation
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
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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

Ontology Information.

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.

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

PlantESdb

Plant Environment Stress Gene Database

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- 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

BLAST Search Tool Against Plant ESdb

Select program

Program:

BlastP

Select Database

Database:

Arabidopsis cds

Enter or upload seq

Enter Sequence (FASTA format):

Upload Sequence File (FASTA format):

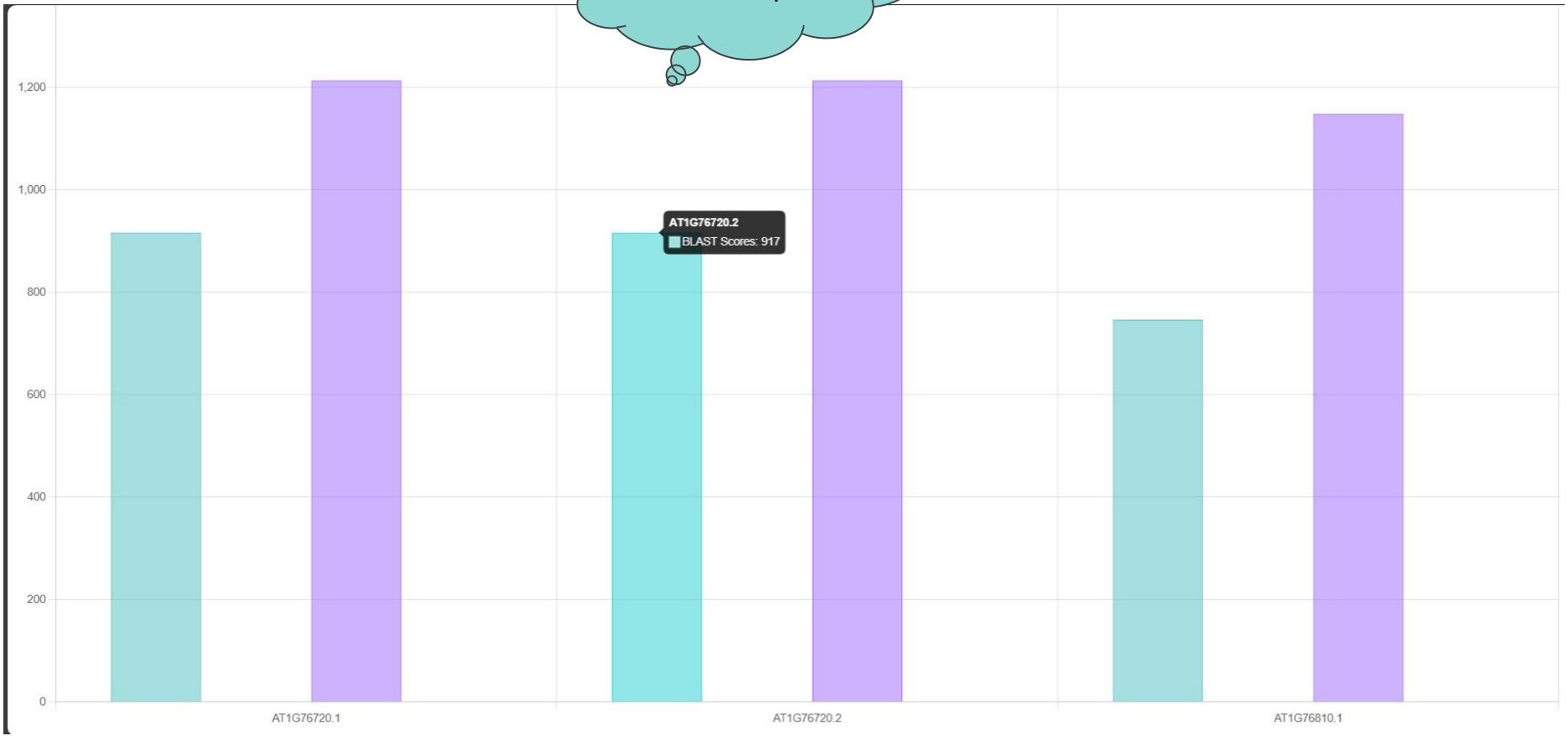
Choose File No file chosen

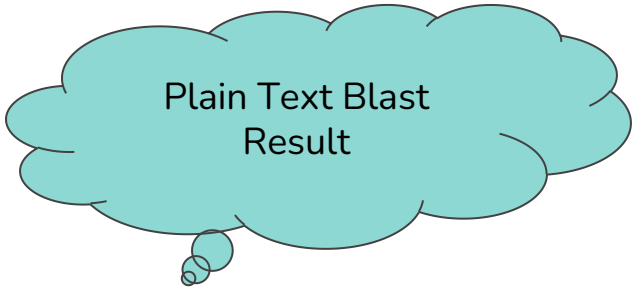
Output Format:

Graphical

Run BLAST

Graphical
Blast output





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

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Regulatory Network Page

PlanESdb

Plant Environment Stress Gene Database

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Cytoscape.js Database

Search Gene Data

Enter Gene IDs to search for related miRNA data.

Select Table:

Arabidopsis

Arabidopsis

Maize

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

h Layout: Force-Directed | Generate Regulatory Network | Calculate Degree Centrality | Export Graph as JSON

Node Connection Table

Degree Centrality Values

Copy | CSV | Excel

Search:

Then click on generate Regulatory Network

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

We can calculate Degree Centrality by click here.

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:

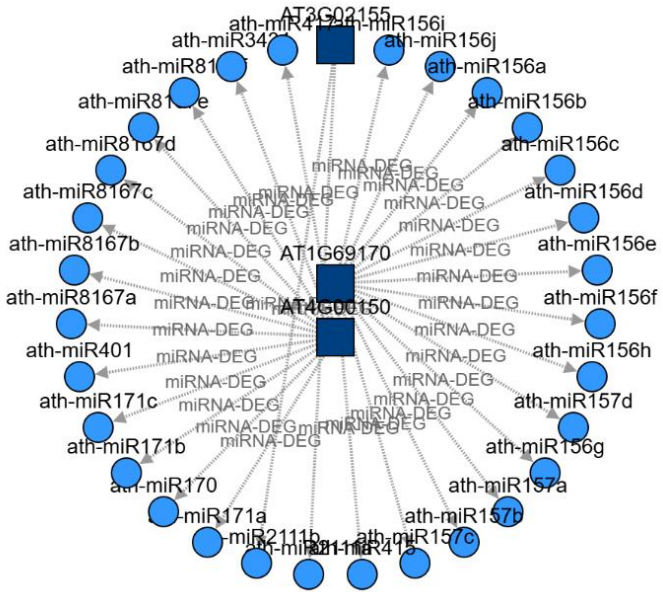
Select Graph Layout: Concentric

Generate Regulatory Network

Calculate Degree Centrality

Export Graph as JSON

Download Graph as Image



User can
Submit data

PlanESdb

Plant Environment Stress Gene Database

Home | Search | Tools | Statistics | Acknowledgement | Contact Us | User Manual | Submit Data

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

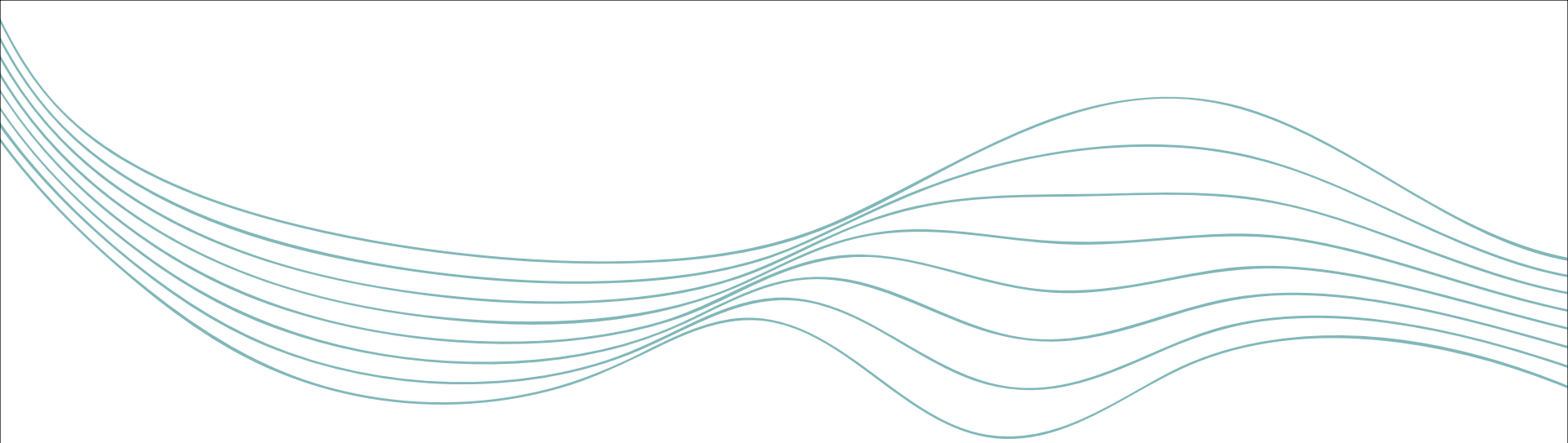
Indian Agricultural Statistics Research Institute
Library Avenue, Pusa,

Contact

Email: info@iasri.icar.gov.in

Official Website

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



THANKS

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