TUTORIALS of TinoTranscriptDB

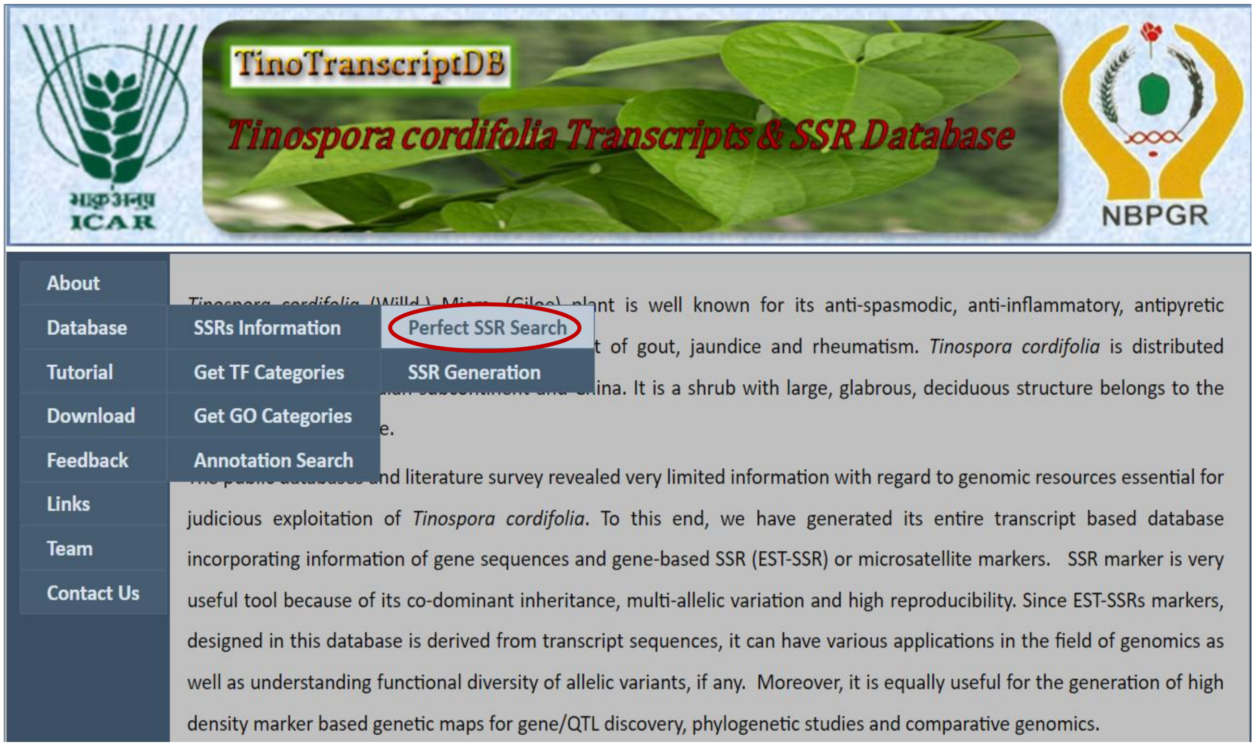
TinoTranscriptDB (*Tinospora cordifolia* Transcripts & SSR Database) http://192.168.1.6/Tinospora/ has Eight different tabs:

About: This page provides basic information about *Tinospora cordifolia*, its medicinal importance and application of transcripts and microsatellite markers.

Tinospora cordifolia (Willd.) Miers. (Giloe) plant is well known for its anti-spasmodic, anti-inflammatory, antipyretic properties and is being used in the treatment of gout, jaundice and rheumatism. *Tinospora cordifolia* is distributed throughout tropical Indian subcontinent and China. It is a shrub with large, glabrous, deciduous structure belongs to the family Menispermaceae.

The public databases and literature survey revealed very limited information with regard to genomic resources essential for judicious exploitation of *Tinospora cordifolia*. To this end, we have generated its entire transcript based database encompassing information of gene sequences and gene-based SSR (EST-SSR) or microsatellite markers. SSR marker is very useful tool because of its co-dominant inheritance, multi-allelic variation and high reproducibility. Since EST-SSRs markers, designed in this database is derived from transcript sequences, it can have various applications in the field of genomics as well such as understanding functional diversity of allelic variants, if any. Moreover, it is equally useful for the generation of high density maker based genetic maps for gene/QTL discovery, phylogenetic studies and comparative genomics.

Database: This is the main tab of the database from where user can mine SSRs along with detailed 3 primer pair informations and the transcripts annotation in term of BLASTx, Gene Ontology (GO), Enzyme commission (EC) information and also get the sequence information for TF and GO Categories.



Tinospora cordifolia (Willd.) Miers (Giloe) plant is well known for its anti-spasmodic, anti-inflammatory, antipyretic … t of gout, jaundice and rheumatism. *Tinospora cordifolia* is distributed … ina. It is a shrub with large, glabrous, deciduous structure belongs to the … e.

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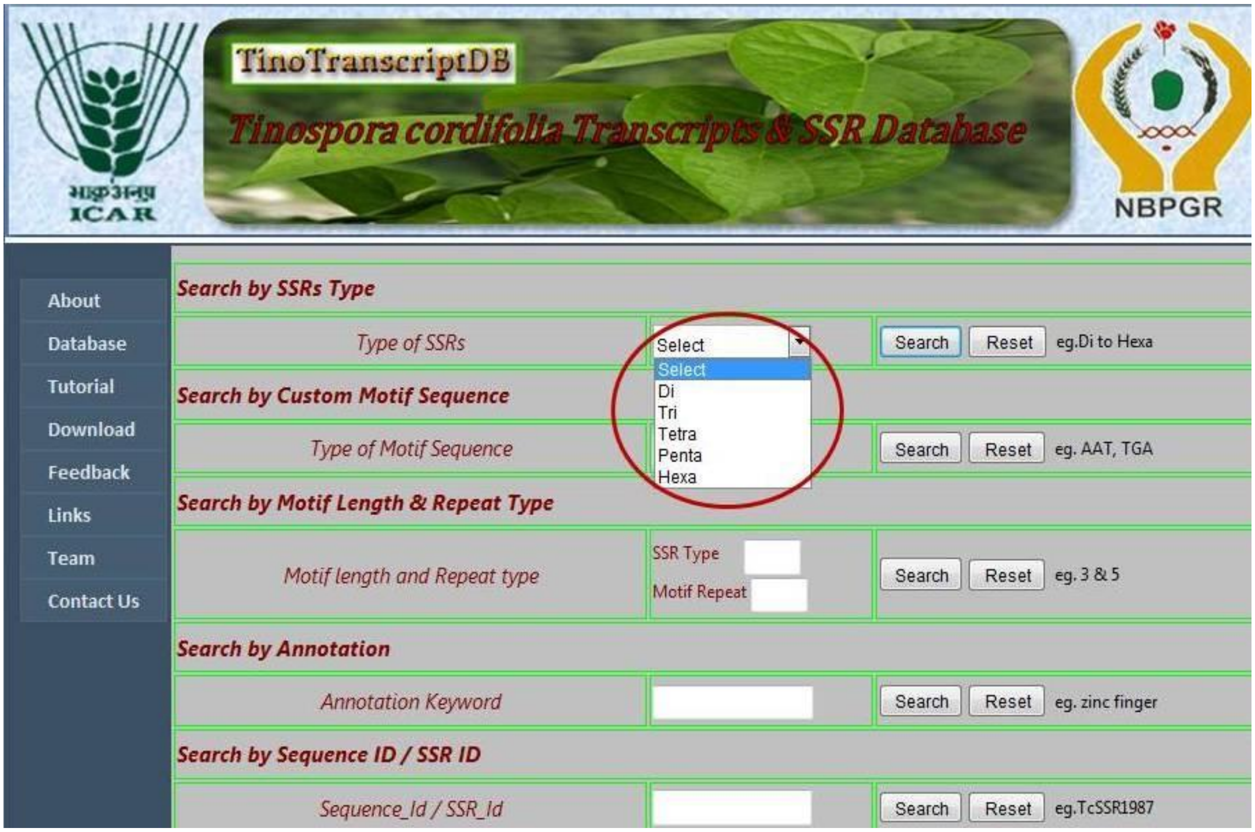
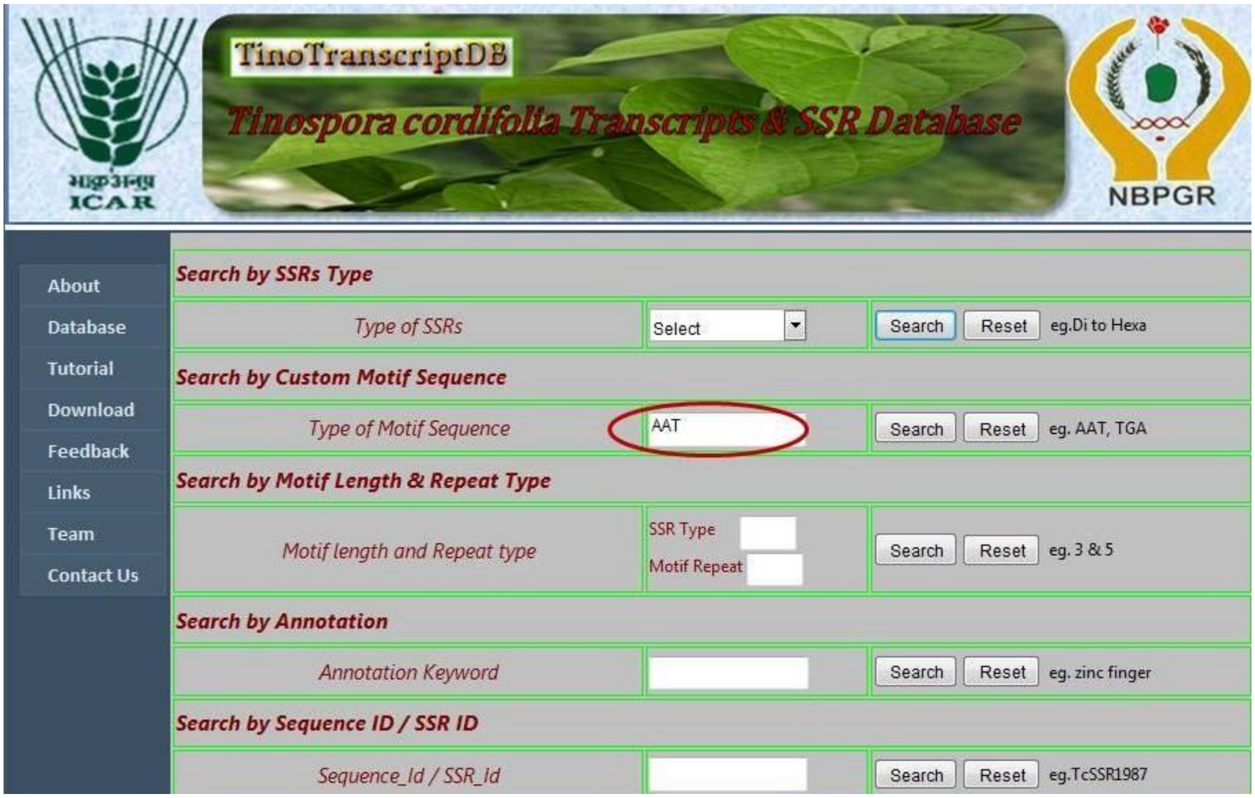
SSRs Information:

Perfect SSR Search:

*User can search the database using search criteria “Search by SSR type”

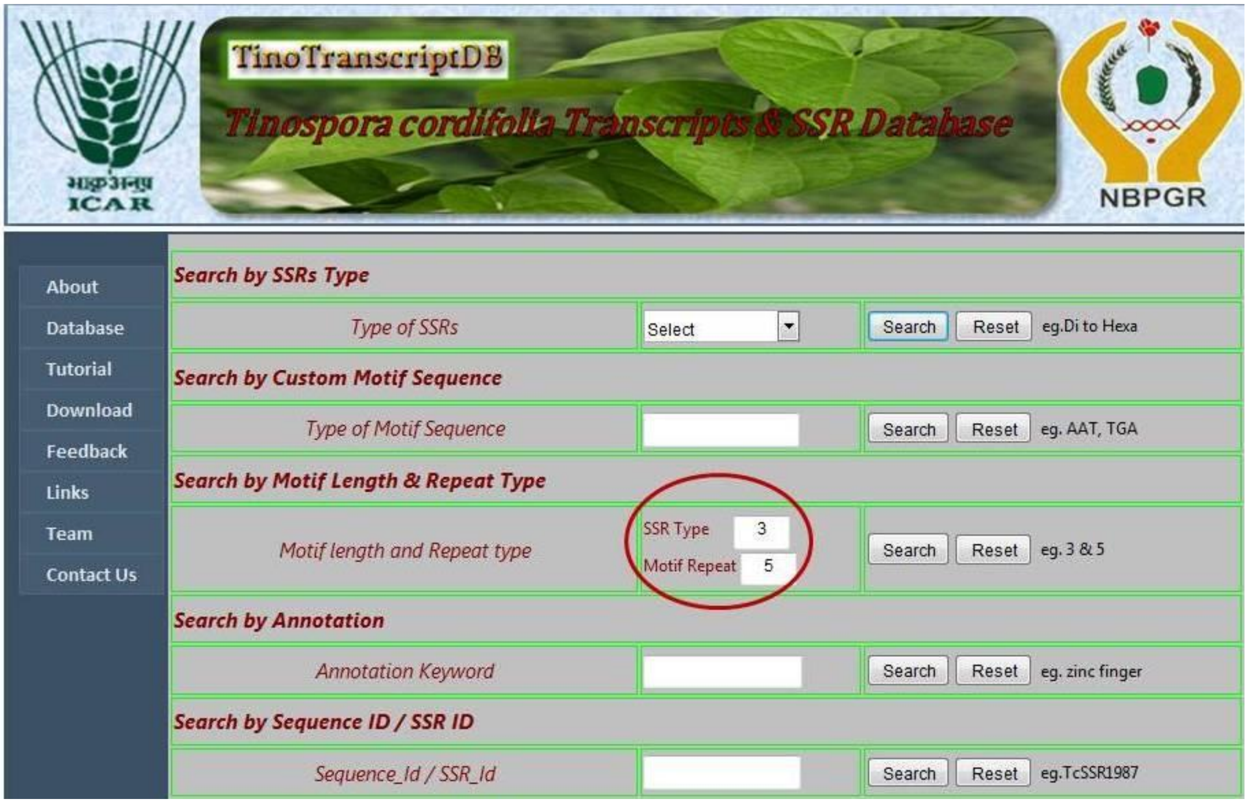


*User can search the database using search criteria “Search by Custom Motif Sequence”



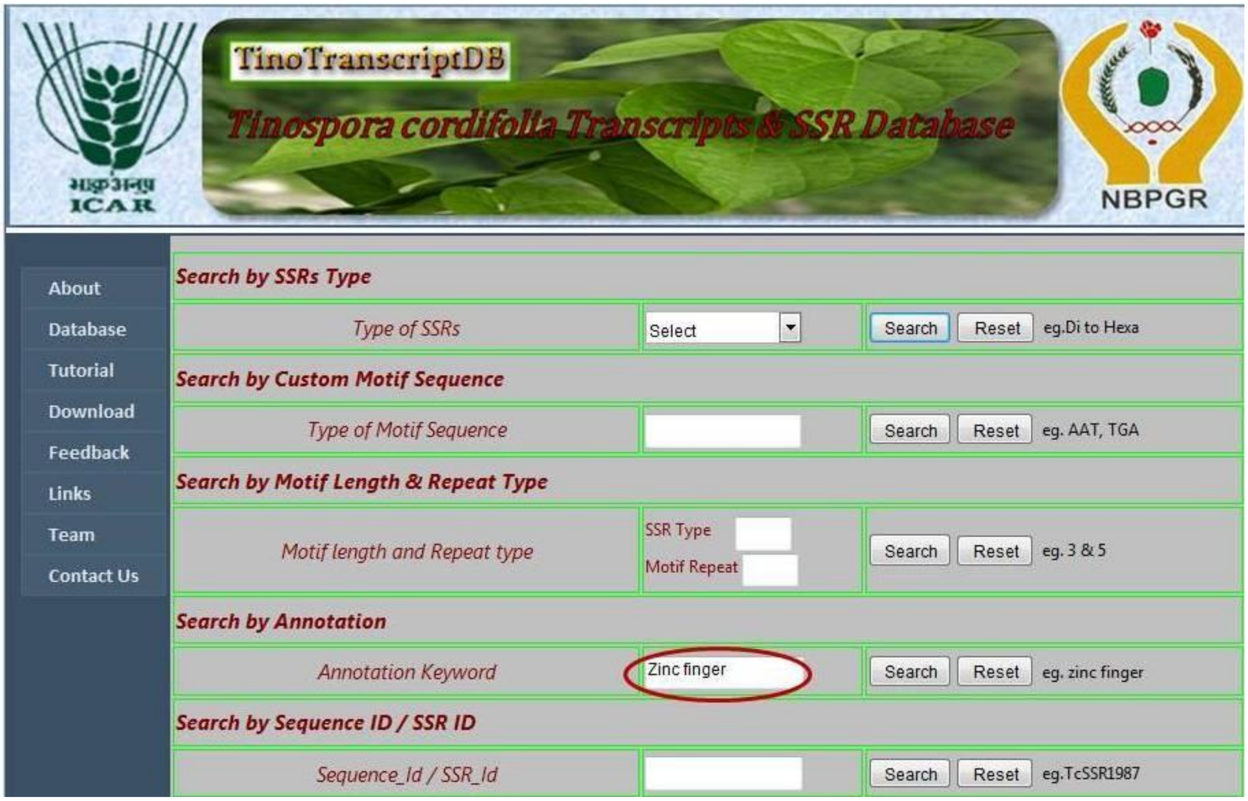
Type of Motif Sequence: AAT

*User can search the database using search criteria “Search by Motif Length and Repeat Type”



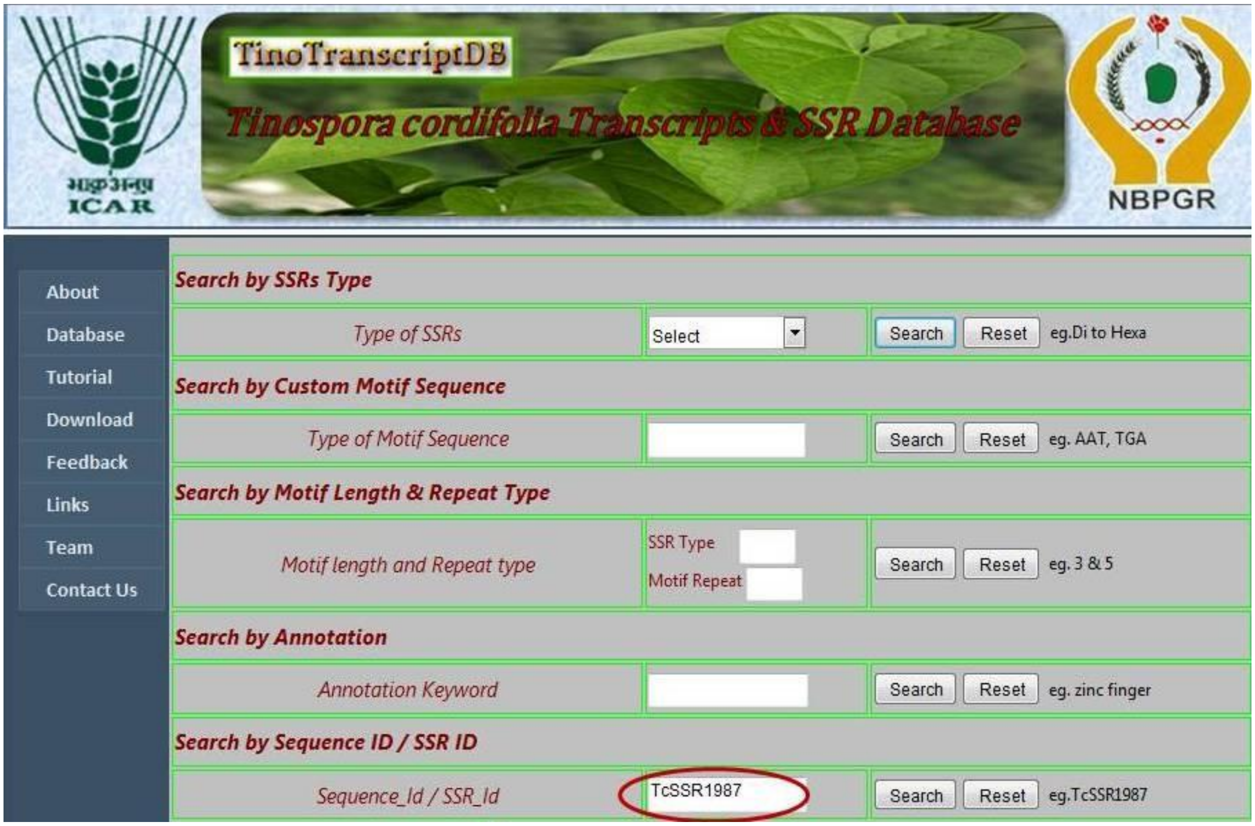
SSR Type: 3
Motif Repeat: 5

*User can search the database using search criteria “Search by Annotation”



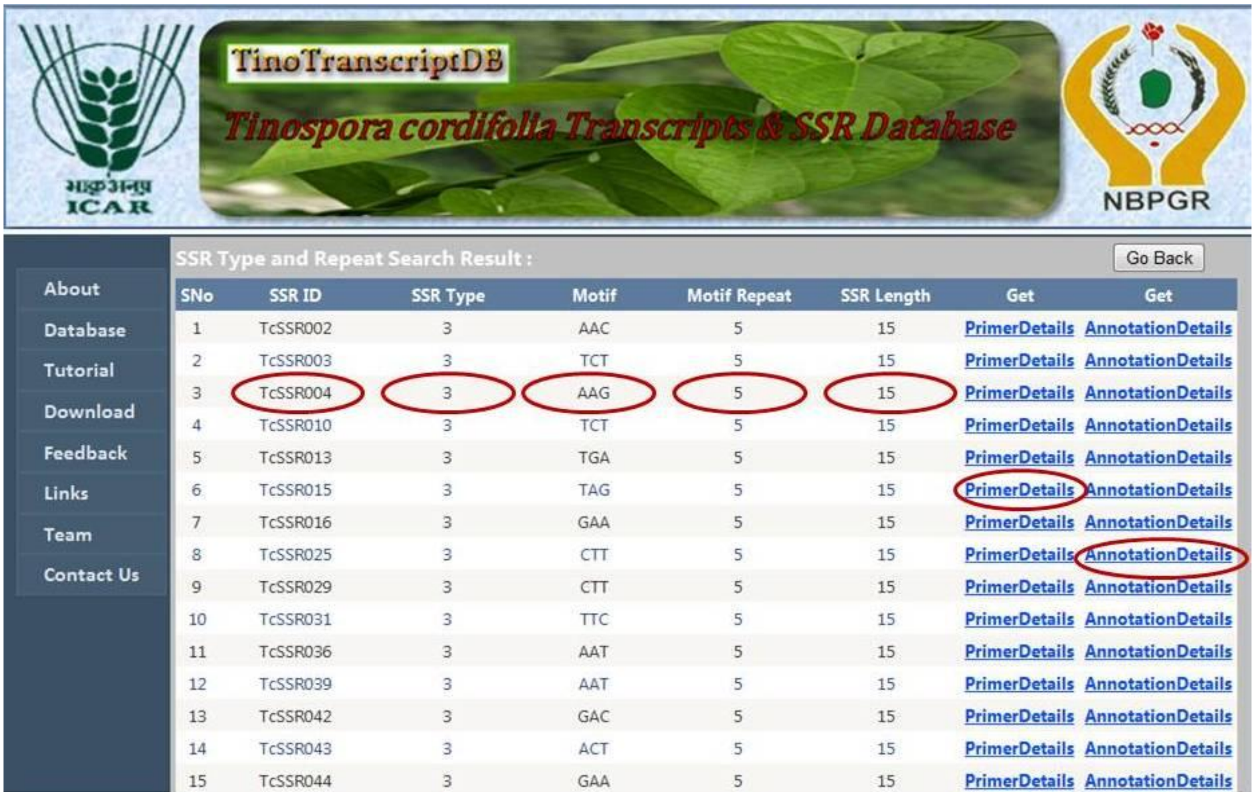
Annotation Keyword: Zinc finger

*User can search the database using search criteria “SSR ID”



Sequence_Id / SSR_Id: TcSSR1987

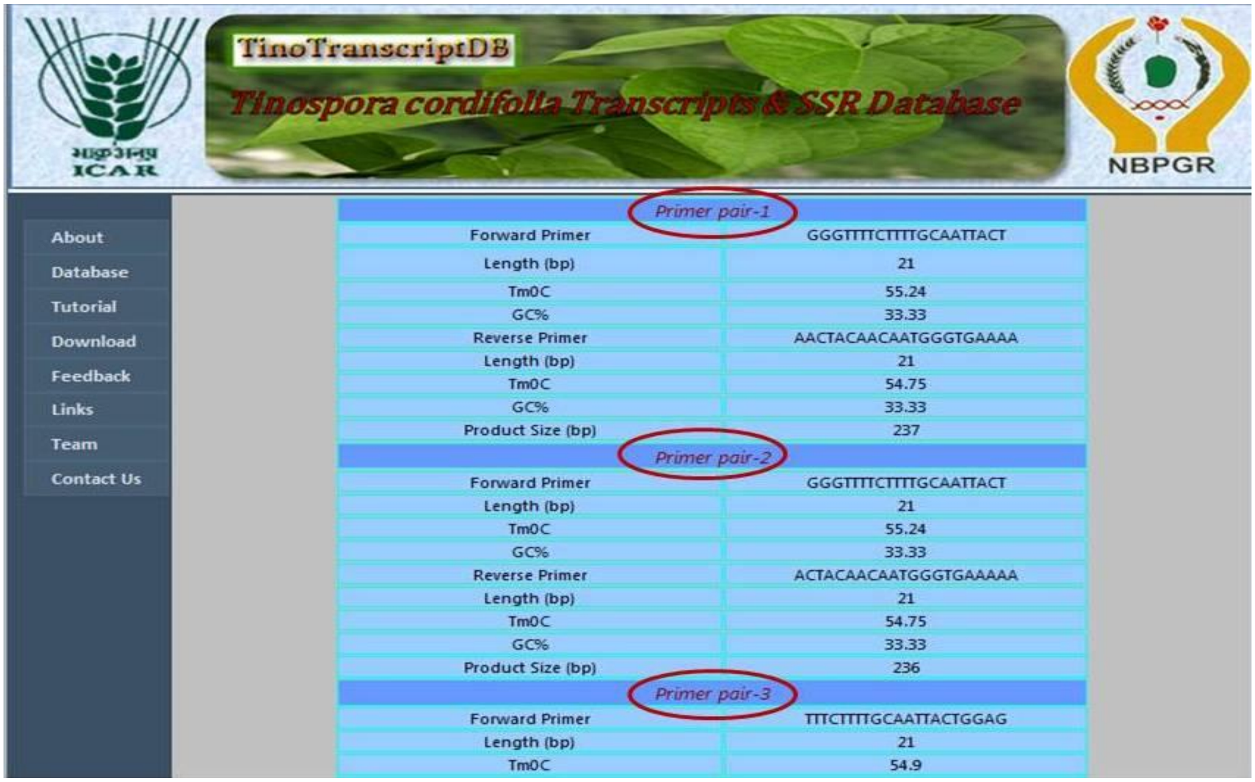
Based on the query search criteria the output is available to the user in real time in terms of 1) Complete SSR details, 2) Best three SSR specific primer pair set along with full primer information and 3) Complete transcript annotation if available.



SSR Type and Repeat Search Result :

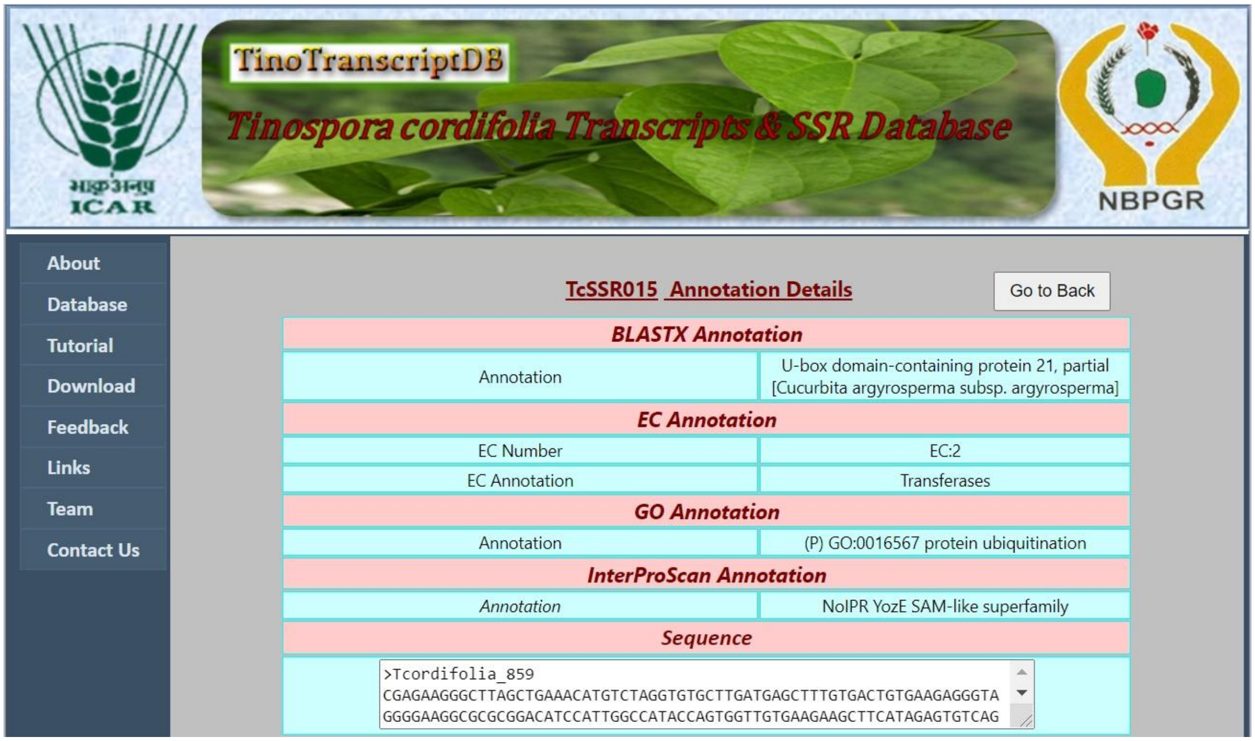
SNo	SSR ID	SSR Type	Motif	Motif Repeat	SSR Length	Get	Get
1	TcSSR002	3	AAC	5	15	PrimerDetails	AnnotationDetails
2	TcSSR003	3	TCT	5	15	PrimerDetails	AnnotationDetails
3	TcSSR004	3	AAG	5	15	PrimerDetails	AnnotationDetails
4	TcSSR010	3	TCT	5	15	PrimerDetails	AnnotationDetails
5	TcSSR013	3	TGA	5	15	PrimerDetails	AnnotationDetails
6	TcSSR015	3	TAG	5	15	PrimerDetails	AnnotationDetails
7	TcSSR016	3	GAA	5	15	PrimerDetails	AnnotationDetails
8	TcSSR025	3	CTT	5	15	PrimerDetails	AnnotationDetails
9	TcSSR029	3	CTT	5	15	PrimerDetails	AnnotationDetails
10	TcSSR031	3	TTC	5	15	PrimerDetails	AnnotationDetails
11	TcSSR036	3	AAT	5	15	PrimerDetails	AnnotationDetails
12	TcSSR039	3	AAT	5	15	PrimerDetails	AnnotationDetails
13	TcSSR042	3	GAC	5	15	PrimerDetails	AnnotationDetails
14	TcSSR043	3	ACT	5	15	PrimerDetails	AnnotationDetails
15	TcSSR044	3	GAA	5	15	PrimerDetails	AnnotationDetails

“Primer Detrails” user can access three pairs of SSR specific primers which can be used for the PCR amplification and marker development.



Primer pair-1	
Forward Primer	GGGTTTTCTTTTGCAATTACT
Length (bp)	21
Tm0C	55.24
GC%	33.33
Reverse Primer	AACTACAACAATGGGTGAAAA
Length (bp)	21
Tm0C	54.75
GC%	33.33
Product Size (bp)	237
Primer pair-2	
Forward Primer	GGGTTTTCTTTTGCAATTACT
Length (bp)	21
Tm0C	55.24
GC%	33.33
Reverse Primer	ACTACAACAATGGGTGAAAAA
Length (bp)	21
Tm0C	54.75
GC%	33.33
Product Size (bp)	236
Primer pair-3	
Forward Primer	TTTCTTTTGCAATTACTGGAG
Length (bp)	21
Tm0C	54.9

Full annotation information is available to the user about the SSR containing transcripts when user click on “Annotation details”

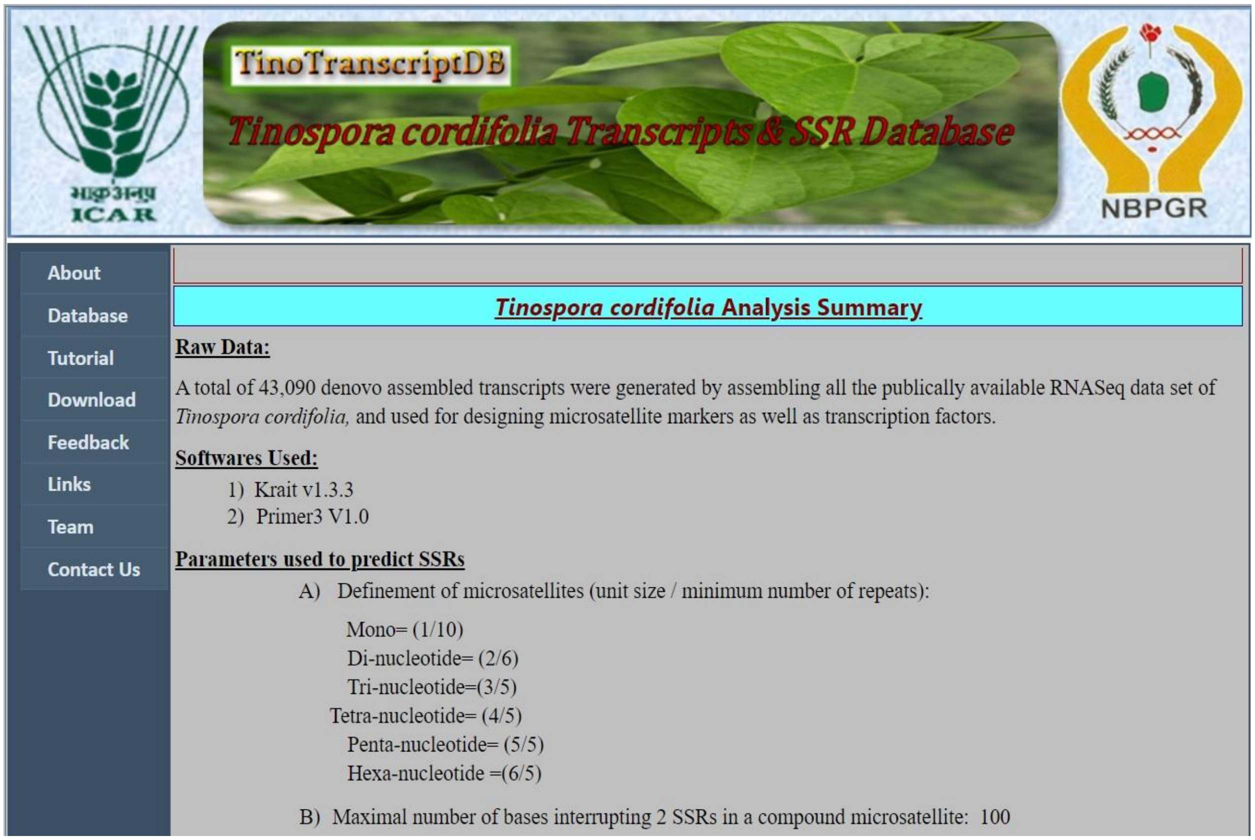


TcSSR015 Annotation Details

BLASTX Annotation	
Annotation	U-box domain-containing protein 21, partial [Cucurbita argyrosperma subsp. argyrosperma]
EC Annotation	
EC Number	EC:2
EC Annotation	Transferases
GO Annotation	
Annotation	(P) GO:0016567 protein ubiquitination
InterProScan Annotation	
Annotation	NoIPR YozE SAM-like superfamily
Sequence	

```
>Tcordifolia_859
CGAGAAGGGCTTAGCTGAAACATGTCTAGGTGTGCTTGATGAGCTTTGTGACTGTGAAGAGGGTA
GGGGAAGGCGCGCGGACATCCATTGGCCATACCAGTGGTTGTGAAGAAGCTTCATAGAGTGTCAG
```

SSR Generation: From this page user can get all information about SSR data generated.



***Tinospora cordifolia* Analysis Summary**

Raw Data:

A total of 43,090 denovo assembled transcripts were generated by assembling all the publically available RNASeq data set of *Tinospora cordifolia,* and used for designing microsatellite markers as well as transcription factors.

Softwares Used:

1) Krait v1.3.3
2) Primer3 V1.0

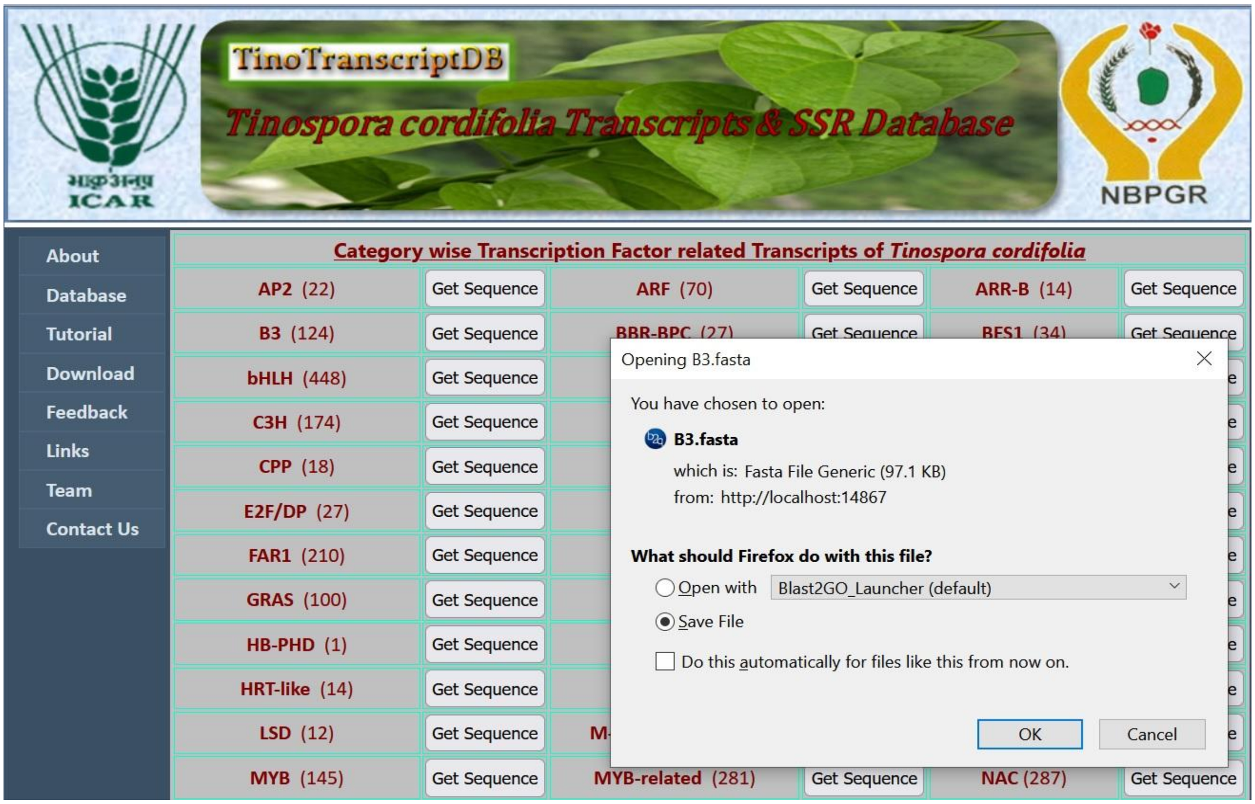
Parameters used to predict SSRs

A) Definement of microsatellites (unit size / minimum number of repeats):

Mono= (1/10)
Di-nucleotide= (2/6)
Tri-nucleotide=(3/5)
Tetra-nucleotide= (4/5)
Penta-nucleotide= (5/5)
Hexa-nucleotide =(6/5)

B) Maximal number of bases interrupting 2 SSRs in a compound microsatellite: 100

Get TF Categories: From this page user can get sequence informations for all predicted Transcription Factor categories.



Category wise Transcription Factor related Transcripts of *Tinospora cordifolia*

AP2 (22)	Get Sequence	ARF (70)	Get Sequence	ARR-B (14)	Get Sequence
B3 (124)	Get Sequence	BBR-BPC (27)	Get Sequence	BES1 (34)	Get Sequence
bHLH (448)	Get Sequence				
C3H (174)	Get Sequence				
CPP (18)	Get Sequence				
E2F/DP (27)	Get Sequence				
FAR1 (210)	Get Sequence				
GRAS (100)	Get Sequence				
HB-PHD (1)	Get Sequence				
HRT-like (14)	Get Sequence				
LSD (12)	Get Sequence				
MYB (145)	Get Sequence	MYB-related (281)	Get Sequence	NAC (287)	Get Sequence

Opening B3.fasta

You have chosen to open:

B3.fasta

which is: Fasta File Generic (97.1 KB)

from: http://localhost:14867

What should Firefox do with this file?

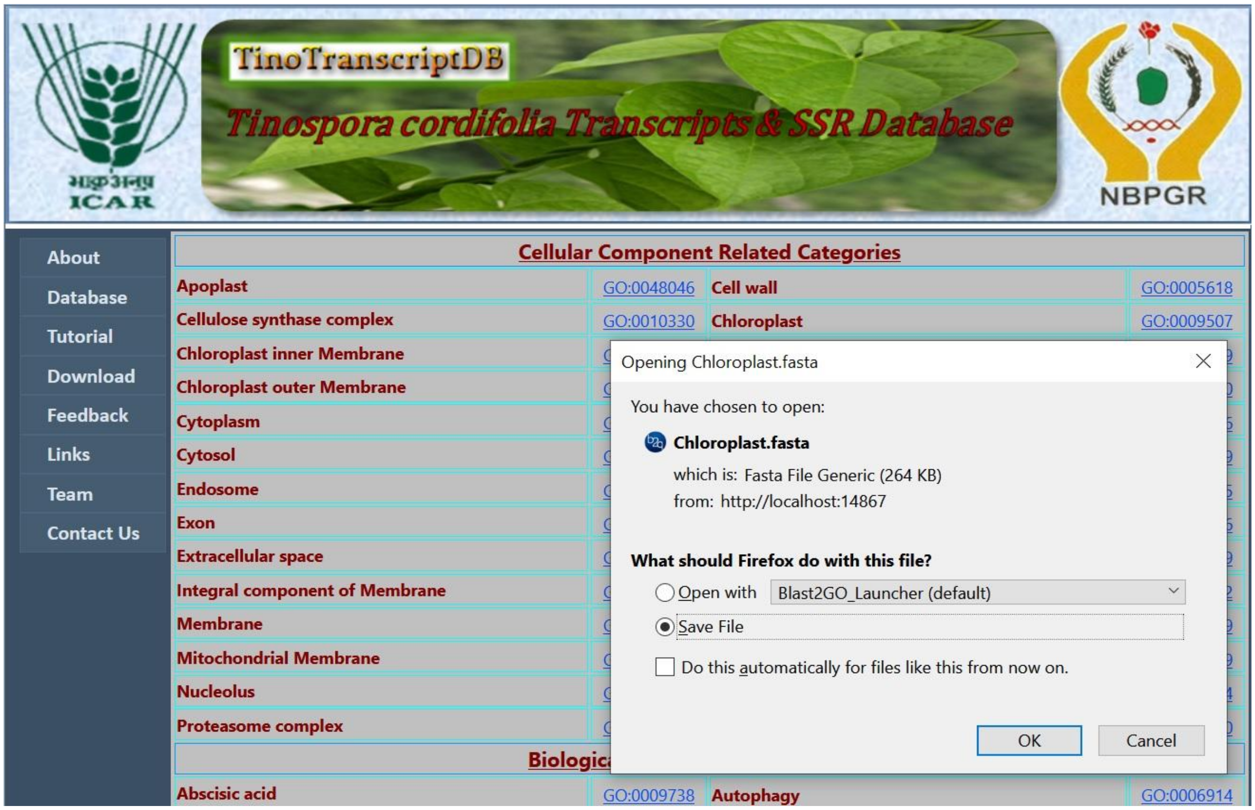
○ Open with Blast2GO_Launcher (default)

● Save File

☐ Do this automatically for files like this from now on.

OK Cancel

Get GO Categories: From this page user can get detailed sequence informations for all three GO categories.



Cellular Component Related Categories

Apoplast	GO:0048046	Cell wall	GO:0005618
Cellulose synthase complex	GO:0010330	Chloroplast	GO:0009507
Chloroplast inner Membrane			
Chloroplast outer Membrane			
Cytoplasm			
Cytosol			
Endosome			
Exon			
Extracellular space			
Integral component of Membrane			
Membrane			
Mitochondrial Membrane			
Nucleolus			
Proteasome complex			

Biologic

Abscisic acid	GO:0009738	Autophagy	GO:0006914

Opening Chloroplast.fasta

You have chosen to open:

Chloroplast.fasta

which is: Fasta File Generic (264 KB)

from: http://localhost:14867

What should Firefox do with this file?

○ Open with Blast2GO_Launcher (default)

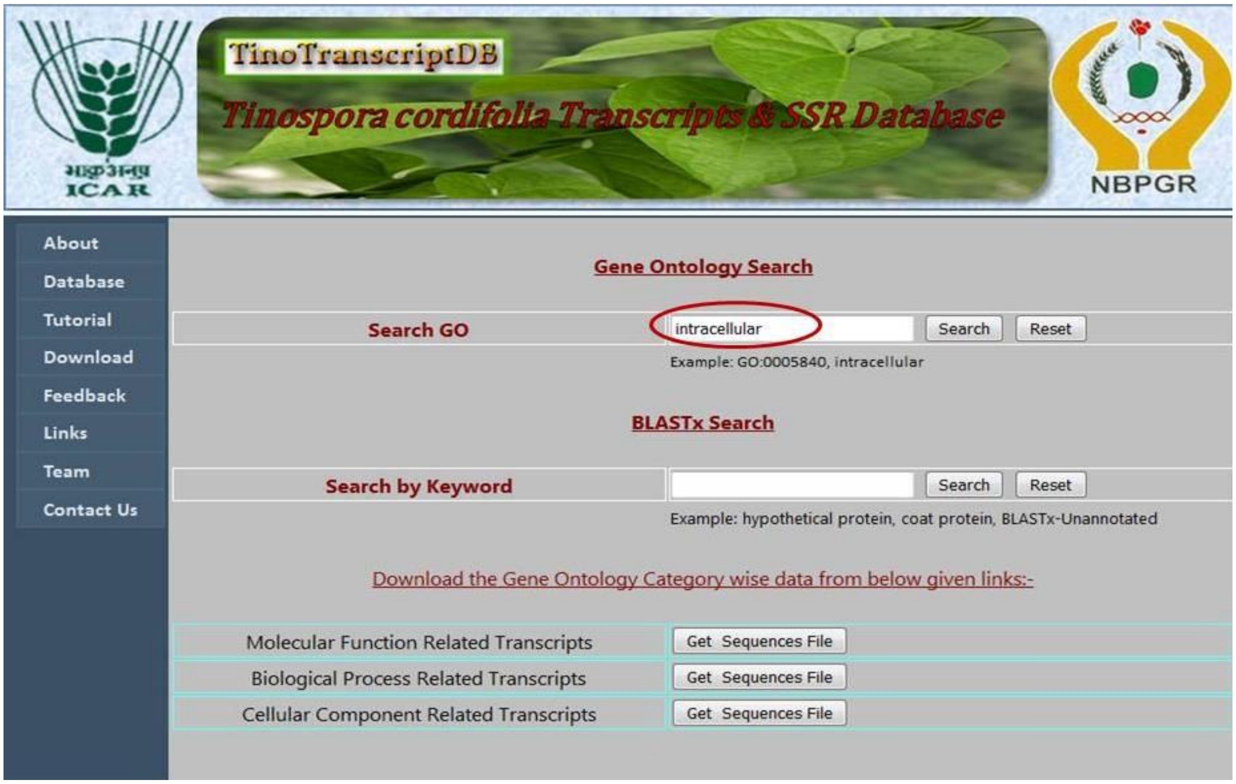
● Save File

☐ Do this automatically for files like this from now on.

OK Cancel

Annotation Search:

*User can search the database using search criteria “GO Search”



Gene Ontology Search

Search GO: intracellular

Example: GO:0005840, intracellular

BLASTx Search

Search by Keyword

Example: hypothetical protein, coat protein, BLASTx-Unannotated

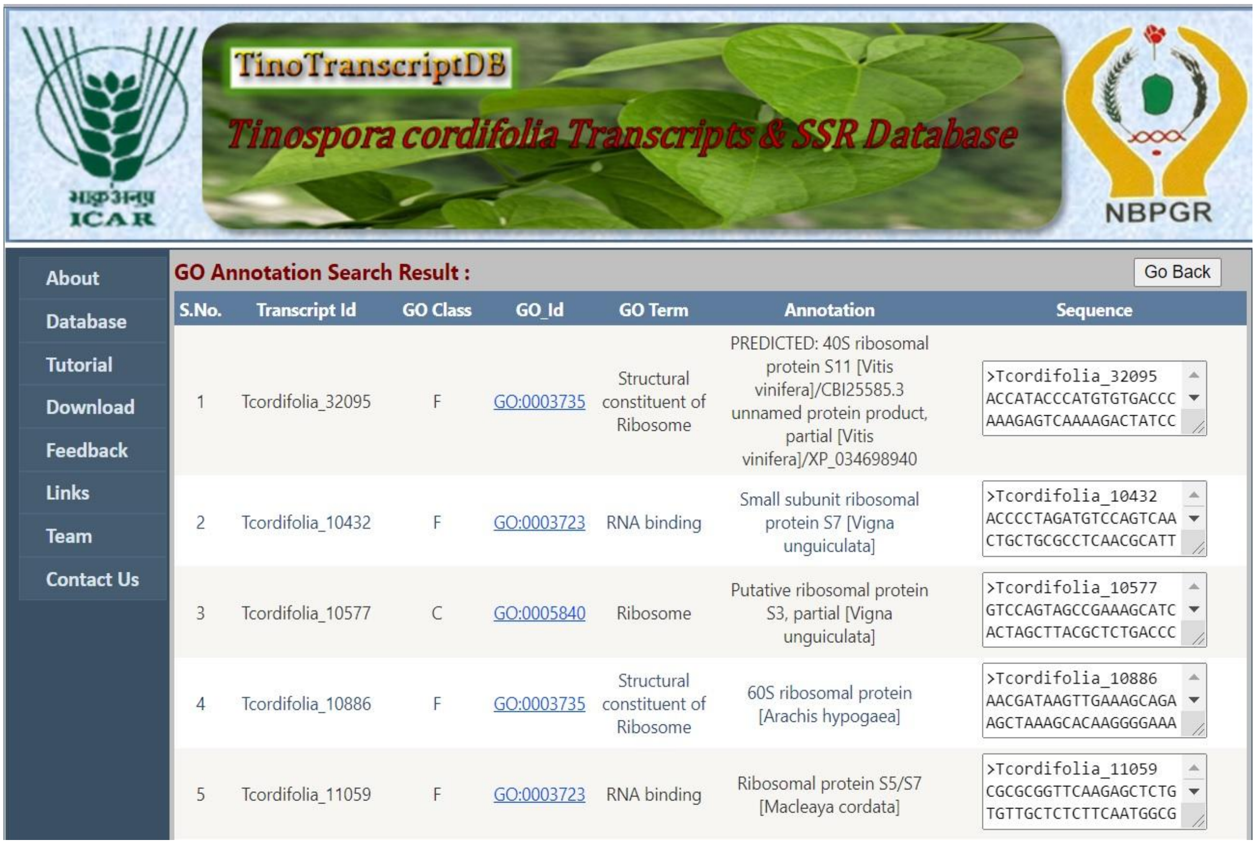
Download the Gene Ontology Category wise data from below given links:-

Molecular Function Related Transcripts

Biological Process Related Transcripts

Cellular Component Related Transcripts

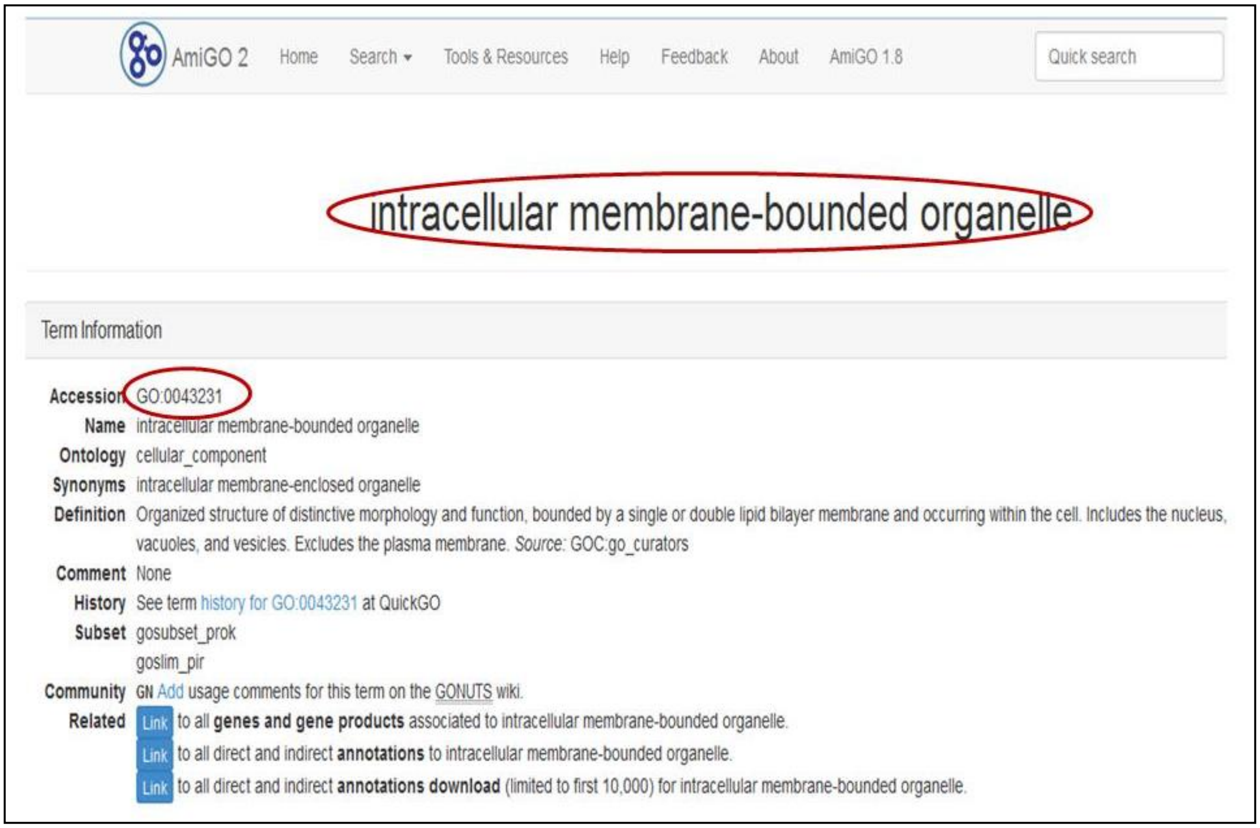
This is the Gene Ontology Search Result page



GO Annotation Search Result :

S.No.	Transcript Id	GO Class	GO_Id	GO Term	Annotation	Sequence
1	Tcordifolia_32095	F	GO:0003735	Structural constituent of Ribosome	PREDICTED: 40S ribosomal protein S11 [Vitis vinifera]/CBI25585.3 unnamed protein product, partial [Vitis vinifera]/XP_034698940	>Tcordifolia_32095 ACCATACCCATGTGTGACCC AAAGAGTCAAAAGACTATCC
2	Tcordifolia_10432	F	GO:0003723	RNA binding	Small subunit ribosomal protein S7 [Vigna unguiculata]	>Tcordifolia_10432 ACCCCTAGATGTCCAGTCAA CTGCTGCGCCTCAACGCATT
3	Tcordifolia_10577	C	GO:0005840	Ribosome	Putative ribosomal protein S3, partial [Vigna unguiculata]	>Tcordifolia_10577 GTCCAGTAGCCGAAAGCATC ACTAGCTTACGCTCTGACCC
4	Tcordifolia_10886	F	GO:0003735	Structural constituent of Ribosome	60S ribosomal protein [Arachis hypogaea]	>Tcordifolia_10886 AACGATAAGTTGAAAGCAGA AGCTAAAGCACAAGGGGAAA
5	Tcordifolia_11059	F	GO:0003723	RNA binding	Ribosomal protein S5/S7 [Macleaya cordata]	>Tcordifolia_11059 CGCGCGGTTCAAGAGCTCTG TGTTGCTCTCTTCAATGGCG

Here go id is linked to http://amigo.geneontology.org/ that gives detailed information about gene ontology type.

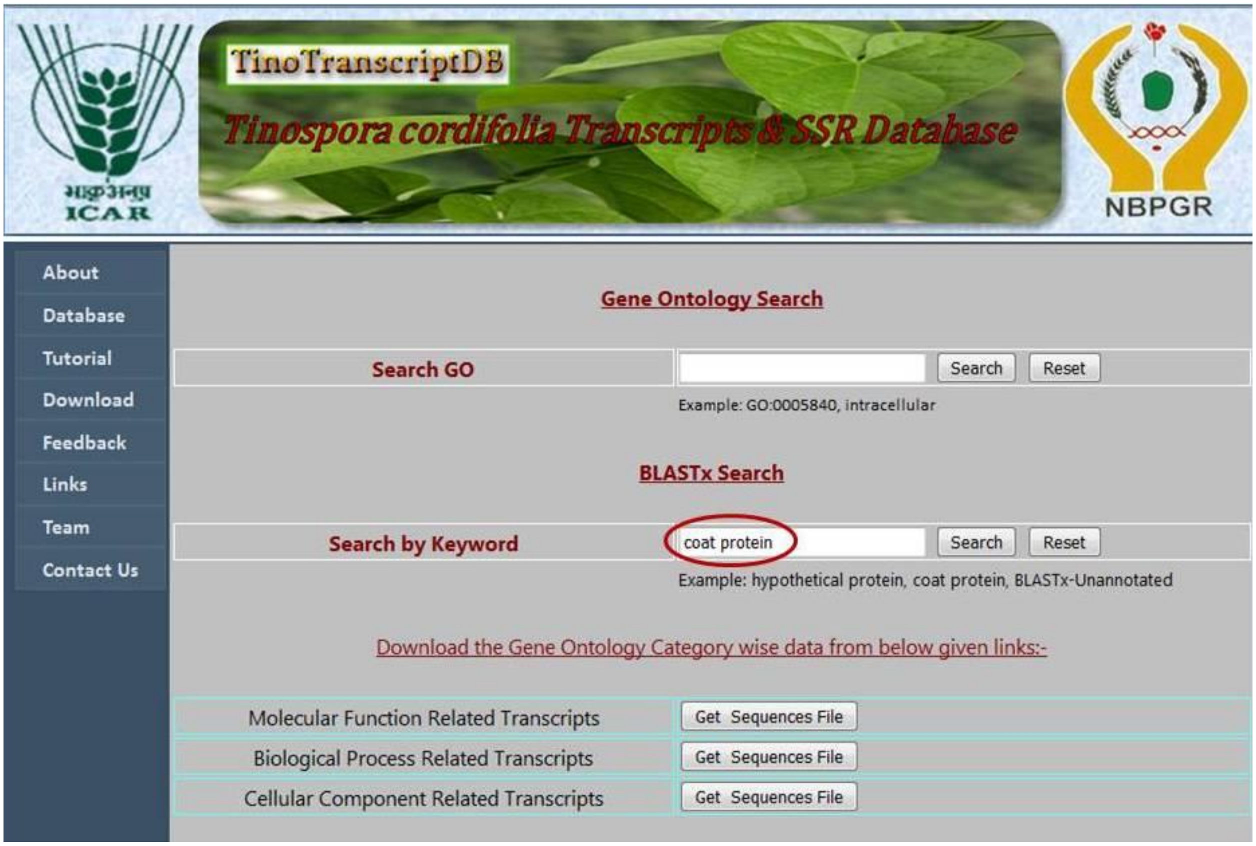


intracellular membrane-bounded organelle

Term Information

Accession GO:0043231
Name intracellular membrane-bounded organelle
Ontology cellular_component
Synonyms intracellular membrane-enclosed organelle
Definition Organized structure of distinctive morphology and function, bounded by a single or double lipid bilayer membrane and occurring within the cell. Includes the nucleus, vacuoles, and vesicles. Excludes the plasma membrane. *Source:* GOC:go_curators
Comment None
History See term history for GO:0043231 at QuickGO
Subset gosubset_prok
goslim_pir
Community GN Add usage comments for this term on the GONUTS wiki.
Related Link to all **genes and gene products** associated to intracellular membrane-bounded organelle.
Link to all direct and indirect **annotations** to intracellular membrane-bounded organelle.
Link to all direct and indirect **annotations download** (limited to first 10,000) for intracellular membrane-bounded organelle.

User can search the database using search criteria "BLASTx Search"



Gene Ontology Search

Search GO

Example: GO:0005840, intracellular

BLASTx Search

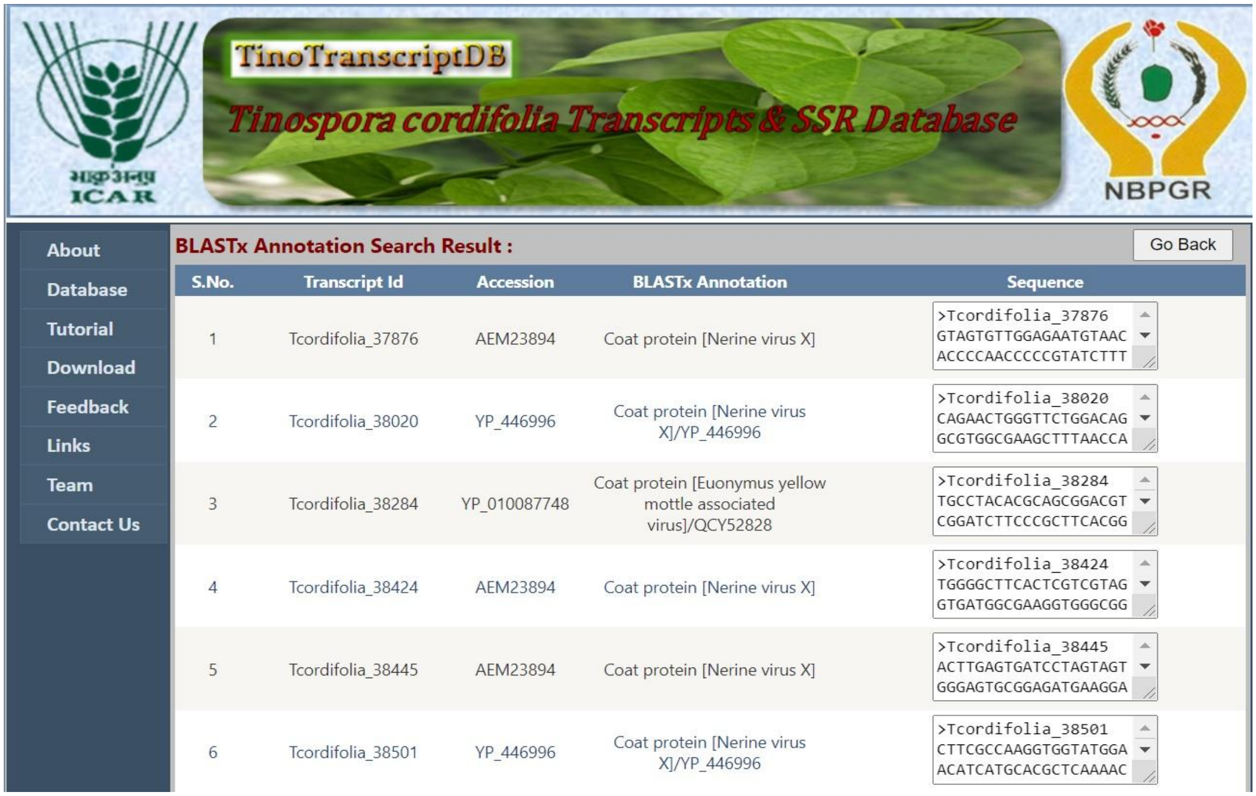
Search by Keyword: coat protein

Example: hypothetical protein, coat protein, BLASTx-Unannotated

Download the Gene Ontology Category wise data from below given links:-

Molecular Function Related Transcripts
Biological Process Related Transcripts
Cellular Component Related Transcripts

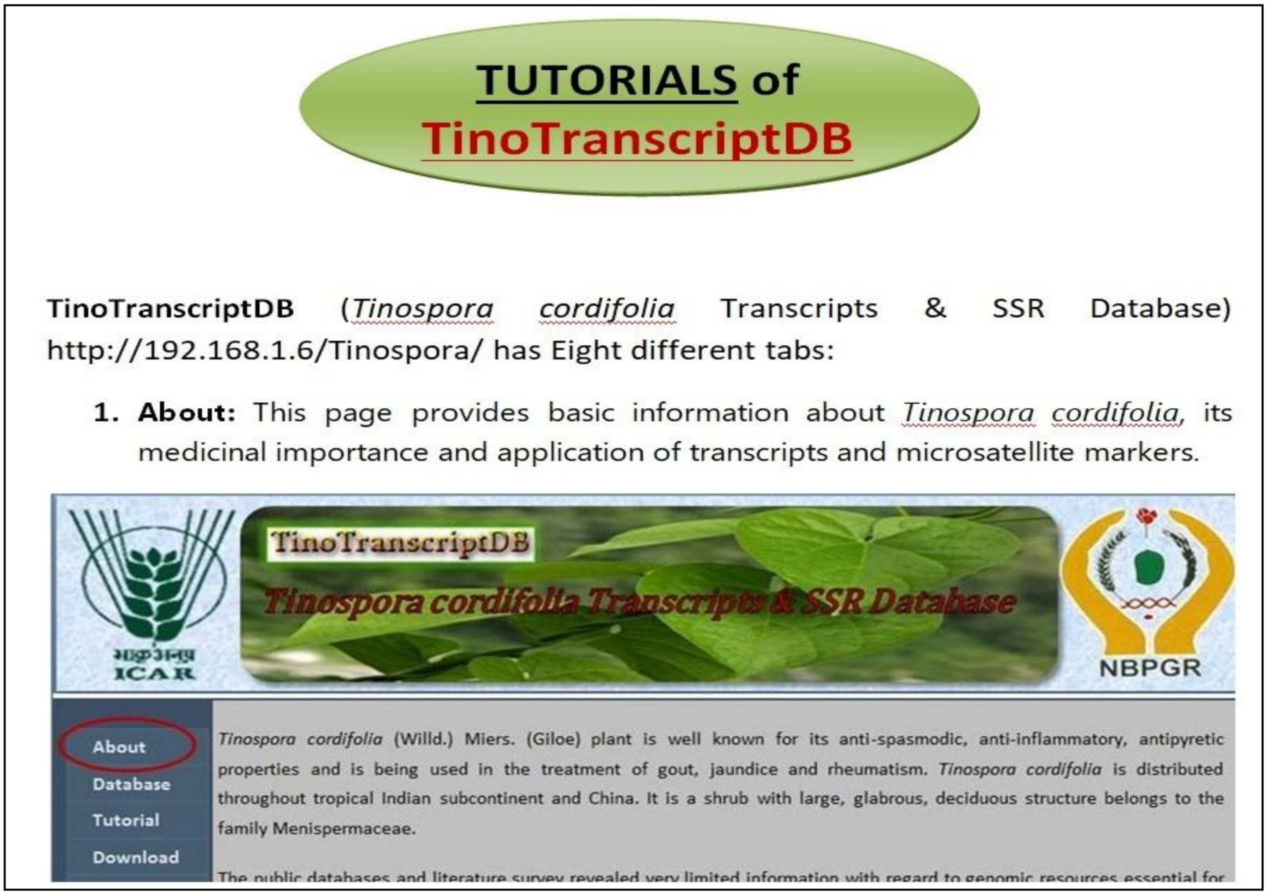
This is the BLASTx Search Result page



BLASTx Annotation Search Result :

S.No.	Transcript Id	Accession	BLASTx Annotation	Sequence
1	Tcordifolia_37876	AEM23894	Coat protein [Nerine virus X]	>Tcordifolia_37876 GTAGTGTTGGAGAATGTAAC ACCCCAACCCCCGTATCTTT
2	Tcordifolia_38020	YP_446996	Coat protein [Nerine virus X]/YP_446996	>Tcordifolia_38020 CAGAACTGGGTTCTGGACAG GCGTGGCGAAGCTTTAACCA
3	Tcordifolia_38284	YP_010087748	Coat protein [Euonymus yellow mottle associated virus]/QCY52828	>Tcordifolia_38284 TGCCTACACGCAGCGGACGT CGGATCTTCCCGCTTCACGG
4	Tcordifolia_38424	AEM23894	Coat protein [Nerine virus X]	>Tcordifolia_38424 TGGGGCTTCACTCGTCGTAG GTGATGGCGAAGGTGGGCGG
5	Tcordifolia_38445	AEM23894	Coat protein [Nerine virus X]	>Tcordifolia_38445 ACTTGAGTGATCCTAGTAGT GGGAGTGCGGAGATGAAGGA
6	Tcordifolia_38501	YP_446996	Coat protein [Nerine virus X]/YP_446996	>Tcordifolia_38501 CTTCGCCAAGGTGGTATGGA ACATCATGCACGCTCAAAAC

Tutorial: From this page user learn how to use this database and how to extract useful information's from the database.



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The public databases and literature survey revealed very limited information with regard to genomic resources essential for

Download: From this page user can download the SSR and Annotation data

Download Data

Perfect SSRs	Data
Tinospora_Di-nucleotide	Download
Tinospora_Tri-nucleotide	Download
Tinospora_Tetra-nucleotide	Download
Tinospora_Penta-nucleotide	Download
Tinospora_Hexa-nucleotide	Download
Tinospora_All	Download
Imperfect SSRs	
I-SSRs	Download
Compound SSRs	
C-SSRs	Download
Annotation Data	
Tinospora_TF_All	Download
Tinospora_GO_All	Download
Tinospora_BLASTx_All	Download

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Feedback: User can send their suggestions to improve the database.

Links: Link tab contains useful links related to *Tinospora cordifolia* database.

"**Team**" and "**Contact Us**" tabs have the information about the team members involved in this project