

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.




TinoTranscriptDB
Tinospora cordifolia Transcripts & SSR Database


About
Database
Tutorial
Download
Feedback
Links
Team
Contact Us

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 marker 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.





TinoTranscriptDB
Tinospora cordifolia Transcripts & SSR Database



[About](#)
[Database](#)
[Tutorial](#)
[Download](#)
[Feedback](#)
[Links](#)
[Team](#)
[Contact Us](#)

SSRs Information Perfect SSR Search

Get TF Categories SSR Generation

Get GO Categories


Annotation Search


Tinospora cordifolia (Willd.) Miq. (Giles) plant is well known for its anti-spasmodic, anti-inflammatory, antipyretic, and analgesic properties. It is a shrub with large, glabrous, deciduous structure belongs to the Menispermaceae family. The present database 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 incorporating 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 as understanding functional diversity of allelic variants, if any. Moreover, it is equally useful for the generation of high density marker based genetic maps for gene/QTL discovery, phylogenetic studies and comparative genomics.

SSRs Information:


Perfect SSR Search:

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





TinoTranscriptDB
Tinospora cordifolia Transcripts & SSR Database



[About](#)
[Database](#)
[Tutorial](#)
[Download](#)
[Feedback](#)
[Links](#)
[Team](#)
[Contact Us](#)

Search by SSRs Type

Type of SSRs Select Search Reset eg. Di to Hexa

Search by Custom Motif Sequence

Type of Motif Sequence Select Search Reset eg. AAT, TGA

Search by Motif Length & Repeat Type

Motif length and Repeat type SSR Type Motif Repeat Search Reset eg. 3 & 5

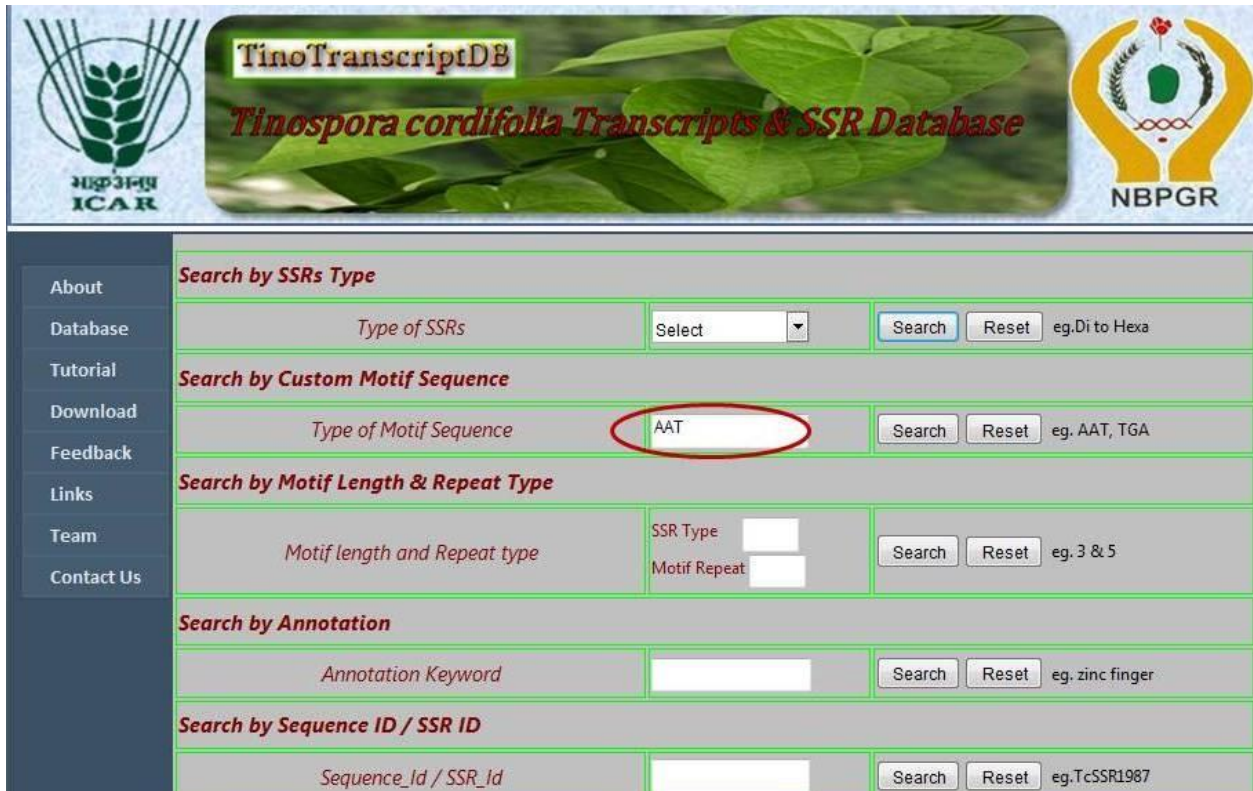
Search by Annotation

Annotation Keyword Search Reset eg. zinc finger

Search by Sequence ID / SSR ID

Sequence_Id / SSR_Id Search Reset eg. TcSSR1987

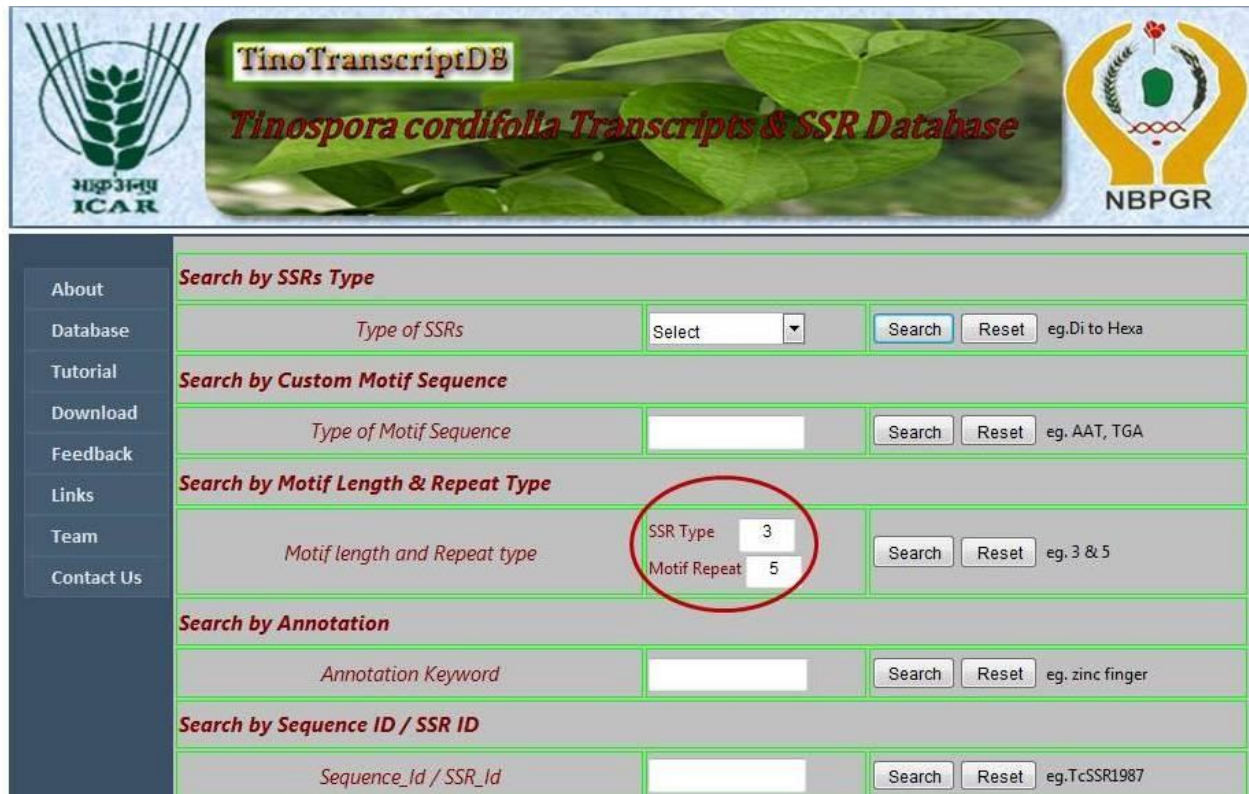
*User can search the database using search criteria "Search by Custom Motif Sequence"



The screenshot shows the TinoTranscriptDB website interface. The header includes the ICAR logo on the left, the title "TinoTranscriptDB" and "Tinospora cordifolia Transcripts & SSR Database" in the center, and the NBPGR logo on the right. A left sidebar contains navigation links: About, Database, Tutorial, Download, Feedback, Links, Team, and Contact Us. The main content area features several search sections:

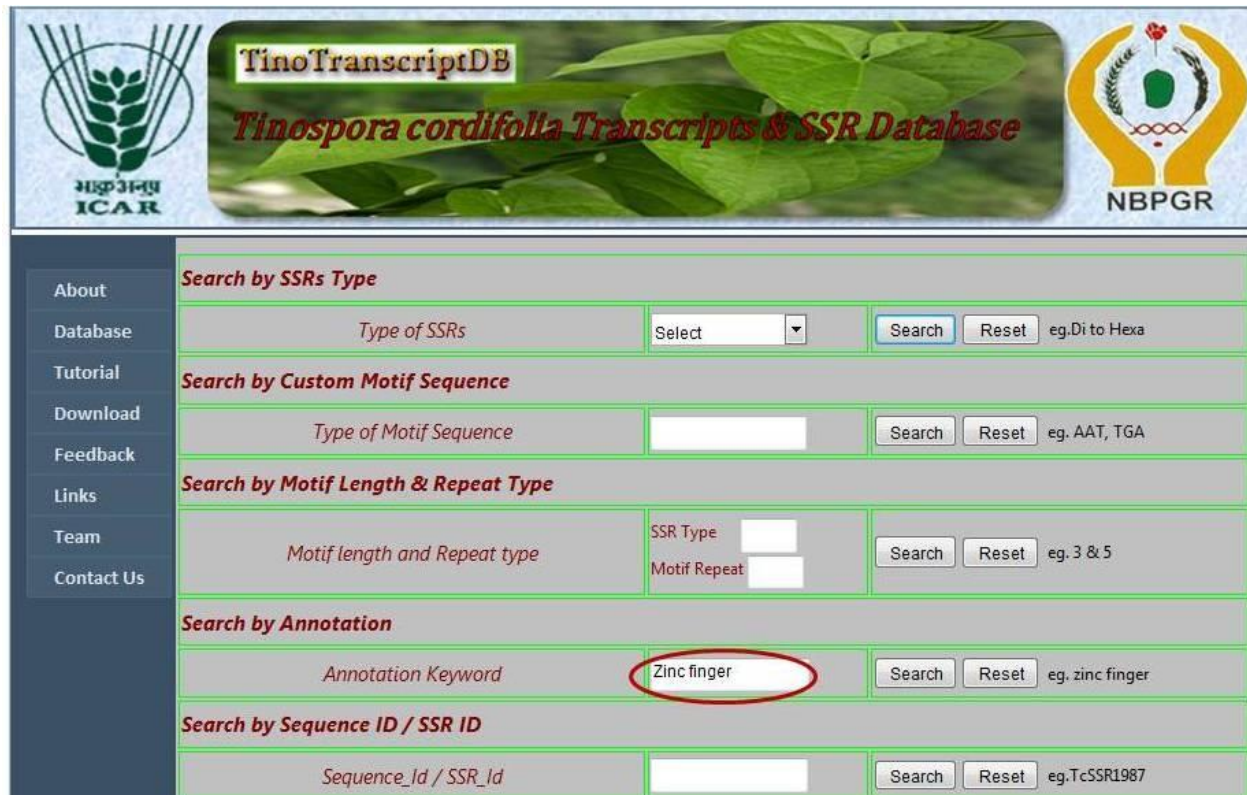
- Search by SSRs Type**: Includes a "Type of SSRs" dropdown menu (set to "Select"), "Search" and "Reset" buttons, and an example "eg. Di to Hexa".
- Search by Custom Motif Sequence**: Includes a "Type of Motif Sequence" dropdown menu (set to "AAT" and circled in red), "Search" and "Reset" buttons, and an example "eg. AAT, TGA".
- Search by Motif Length & Repeat Type**: Includes input fields for "Motif length and Repeat type", "SSR Type", and "Motif Repeat", "Search" and "Reset" buttons, and an example "eg. 3 & 5".
- Search by Annotation**: Includes an "Annotation Keyword" input field, "Search" and "Reset" buttons, and an example "eg. zinc finger".
- Search by Sequence ID / SSR ID**: Includes a "Sequence_Id / SSR_Id" input field, "Search" and "Reset" buttons, and an example "eg. TcSSR1987".

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



This screenshot shows the same TinoTranscriptDB website interface as the previous one, but with the "Search by Motif Length & Repeat Type" section highlighted. In this section, the "SSR Type" input field is set to "3" and the "Motif Repeat" input field is set to "5". These two input fields are circled in red. The other search sections remain unchanged.

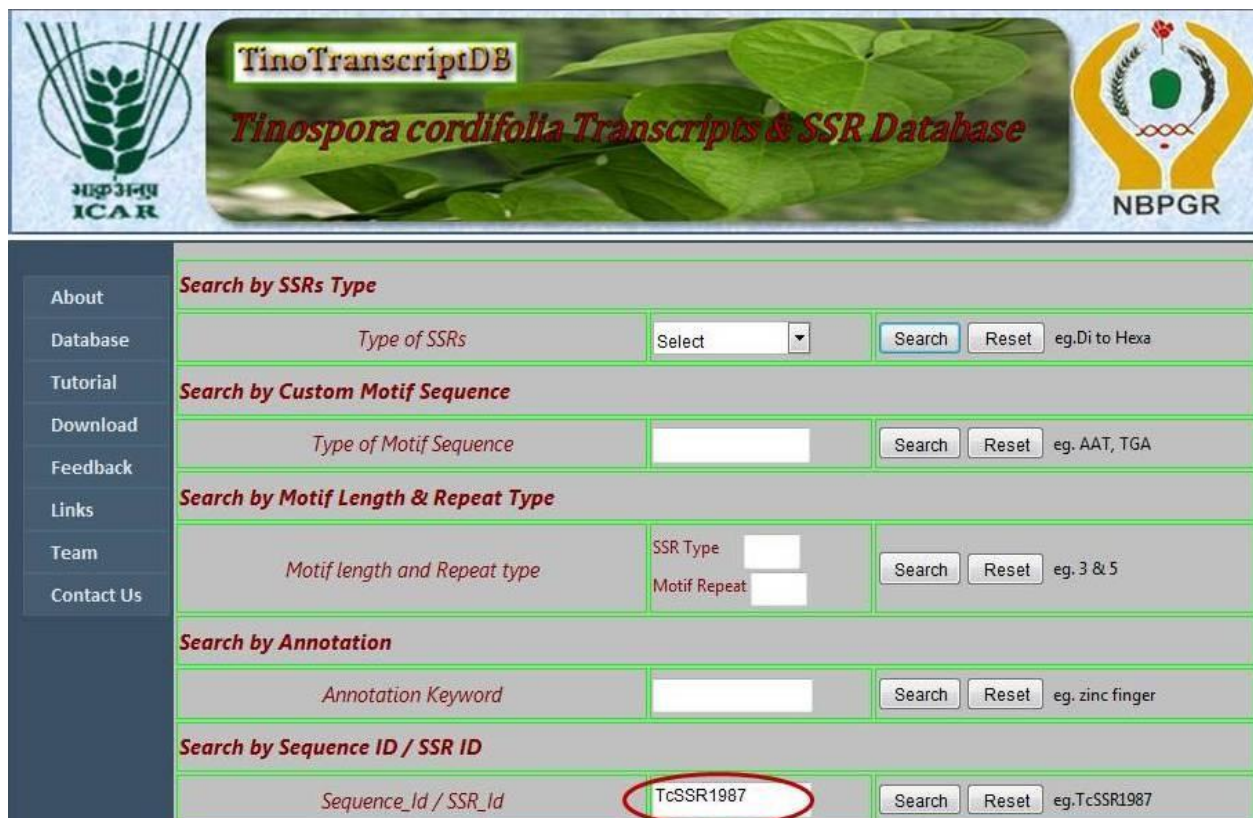
*User can search the database using search criteria "Search by Annotation"



The image shows the TinoTranscriptDB web interface. The header features the ICAR logo on the left, the database title "TinoTranscriptDB Tinospora cordifolia Transcripts & SSR Database" in the center, and the NBPGR logo on the right. A left sidebar contains navigation links: About, Database, Tutorial, Download, Feedback, Links, Team, and Contact Us. The main content area has six search sections, each with a title, input fields, and search buttons. The "Search by Annotation" section is highlighted with a red circle around the "Zinc finger" text in the "Annotation Keyword" field.

Search by SSRs Type		
Type of SSRs	Select	Search Reset eg. Di to Hexa
Search by Custom Motif Sequence		
Type of Motif Sequence		Search Reset eg. AAT, TGA
Search by Motif Length & Repeat Type		
Motif length and Repeat type	SSR Type Motif Repeat	Search Reset eg. 3 & 5
Search by Annotation		
Annotation Keyword	Zinc finger	Search Reset eg. zinc finger
Search by Sequence ID / SSR ID		
Sequence_Id / SSR_Id		Search Reset eg. TcSSR1987



*User can search the database using search criteria "SSR ID"



The image shows the same TinoTranscriptDB web interface as above. In this instance, the "Search by Sequence ID / SSR ID" section is highlighted with a red circle around the "TcSSR1987" text in the "Sequence_Id / SSR_Id" field.

Search by SSRs Type		
Type of SSRs	Select	Search Reset eg. Di to Hexa
Search by Custom Motif Sequence		
Type of Motif Sequence		Search Reset eg. AAT, TGA
Search by Motif Length & Repeat Type		
Motif length and Repeat type	SSR Type Motif Repeat	Search Reset eg. 3 & 5
Search by Annotation		
Annotation Keyword		Search Reset eg. zinc finger
Search by Sequence ID / SSR ID		
Sequence_Id / SSR_Id	TcSSR1987	Search Reset eg. 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.

 TinoTranscriptDB <i>Tinospora cordifolia Transcripts & SSR Database</i> 								
About Database Tutorial Download Feedback Links Team Contact Us	SSR Type and Repeat Search Result :						Go Back	
	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 Details” user can access three pairs of SSR specific primers which can be used for the PCR amplification and marker development.

TinoTranscriptDB

Tinospora cordifolia Transcripts & SSR Database

About
Database
Tutorial
Download
Feedback
Links
Team
Contact Us

Primer pair-1

Forward Primer	GGGTTTCTTTGCAATTACT
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	GGGTTTCTTTGCAATTACT
Length (bp)	21
Tm0C	55.24
GC%	33.33
Reverse Primer	ACTACAACAATGGGTGAAAA
Length (bp)	21
Tm0C	54.75
GC%	33.33
Product Size (bp)	236

Primer pair-3


Forward Primer	TTTCTTTGCAATTACTGGAG
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"





TinoTranscriptDB
Tinospora cordifolia Transcripts & SSR Database




[About](#)
[Database](#)
[Tutorial](#)
[Download](#)
[Feedback](#)
[Links](#)
[Team](#)
[Contact Us](#)


TcSSR015 Annotation Details

[Go to Back](#)


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	NolPR YozE SAM-like superfamily
Sequence	
<div style="border: 1px solid #ccc; padding: 5px;"> >Tcordifolia_859 CGAGAAGGGCTTAGCTGAAACATGCTAGGTGTGCTTGATGAGCTTTGTGACTGTGAAGAGGGTA GGGGAAGGCGCGGGACATCCATTGGCCATACCAAGTGTTGTGAAGAAGCTTCATAGAGTGTCA </div>	

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





TinoTranscriptDB
Tinospora cordifolia Transcripts & SSR Database



[About](#)
[Database](#)
[Tutorial](#)
[Download](#)
[Feedback](#)
[Links](#)
[Team](#)
[Contact Us](#)

Tinospora cordifolia Analysis Summary

Raw Data:
 A total of 43,090 denovo assembled transcripts were generated by assembling all the publicly 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.

The screenshot displays the TinoTranscriptDB website interface. The header includes the ICAR logo, the site title "TinoTranscriptDB Tinospora cordifolia Transcripts & SSR Database", and the NBPGR logo. A sidebar on the left contains navigation links: About, Database, Tutorial, Download, Feedback, Links, Team, and Contact Us. The main content area is titled "Category wise Transcription Factor related Transcripts of Tinospora cordifolia" and lists various TF categories with their transcript counts and "Get Sequence" buttons. A Firefox download dialog is open, showing the file "B3.fasta" (97.1 KB) being downloaded from "http://localhost:14867". The dialog asks "What should Firefox do with this file?" with options to "Open with Blast2GO_Launcher (default)", "Save File" (selected), or "Do this automatically for files like this from now on.".

Category wise Transcription Factor related Transcripts of Tinospora cordifolia			
AP2 (22)	Get Sequence	ARF (70)	Get Sequence
B3 (124)	Get Sequence	BBR-BPC (27)	Get Sequence
bHLH (448)	Get Sequence	ARR-B (14)	Get Sequence
C3H (174)	Get Sequence	BES1 (34)	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

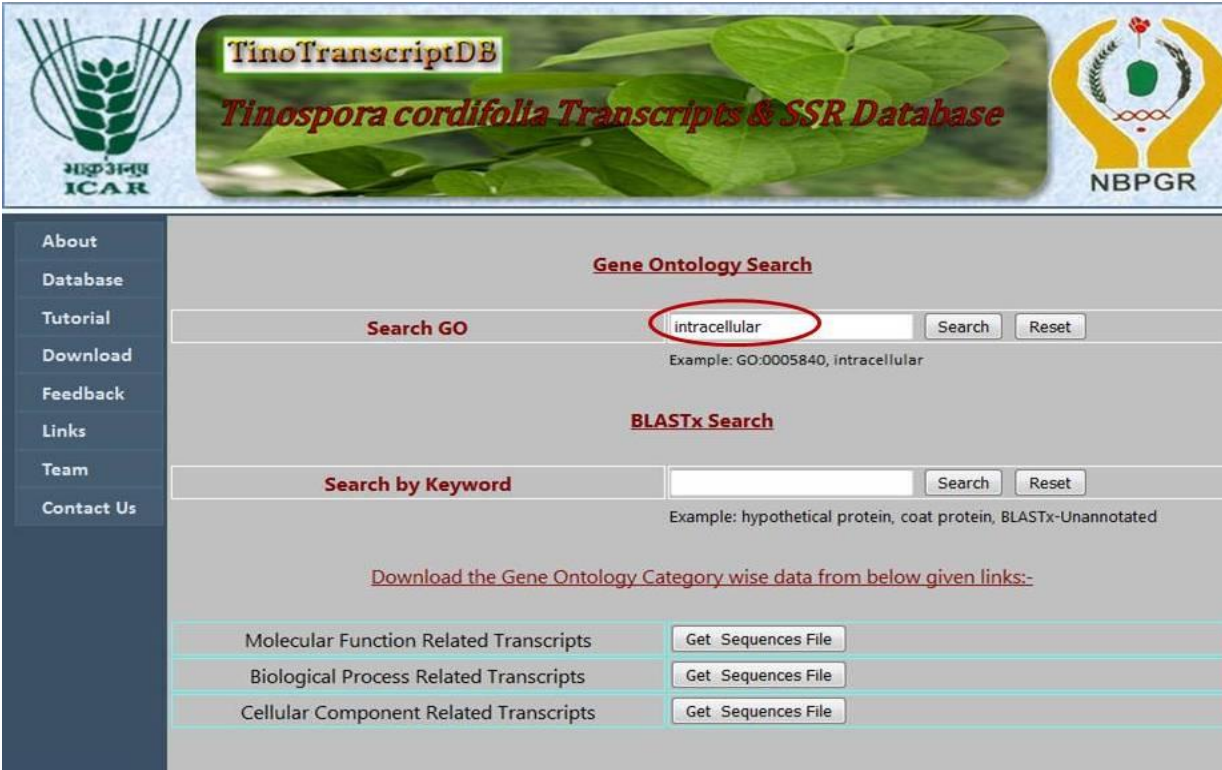
Get GO Categories: From this page user can get detailed sequence informations for all three GO categories.

The screenshot displays the TinoTranscriptDB website interface for Cellular Component Related Categories. The header and sidebar are identical to the previous screenshot. The main content area is titled "Cellular Component Related Categories" and lists various cellular components with their GO IDs and "Get Sequence" buttons. A Firefox download dialog is open, showing the file "Chloroplast.fasta" (264 KB) being downloaded from "http://localhost:14867". The dialog asks "What should Firefox do with this file?" with options to "Open with Blast2GO_Launcher (default)", "Save File" (selected), or "Do this automatically for files like this from now on.".

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			
Biological Process			
Abscisic acid	GO:0009738	Autophagy	GO:0006914

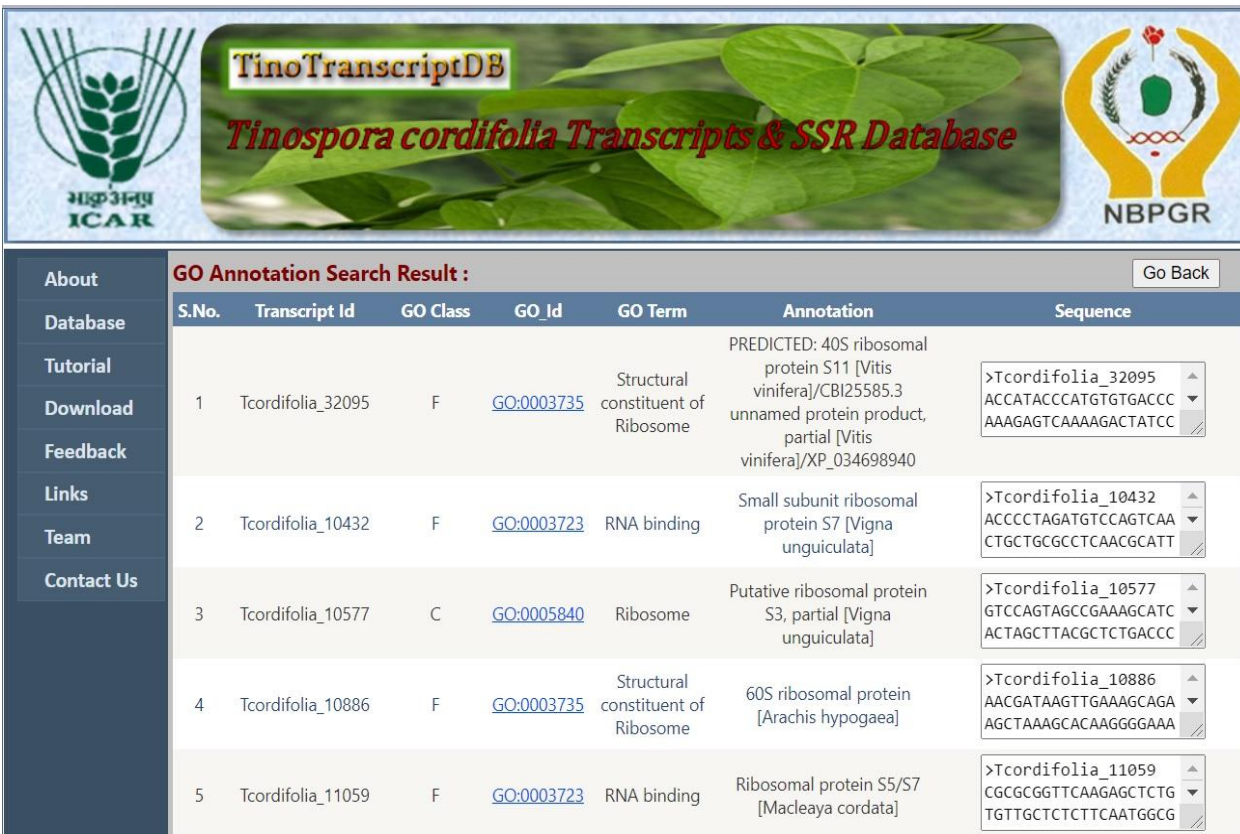
Annotation Search:

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



The image shows the TinoTranscriptDB website interface. At the top, there is a header with the ICAR logo on the left, the database title "TinoTranscriptDB Tinospora cordifolia Transcripts & SSR Database" in the center, and the NBPGR logo on the right. Below the header is a sidebar with navigation links: About, Database, Tutorial, Download, Feedback, Links, Team, and Contact Us. The main content area is titled "Gene Ontology Search". It features a "Search GO" section with a text input field containing "intracellular", a "Search" button, and a "Reset" button. Below this is an example: "Example: GO:0005840, intracellular". There is also a "BLASTx Search" section with a "Search by Keyword" text input field, a "Search" button, and a "Reset" button. Below this is an example: "Example: hypothetical protein, coat protein, BLASTx-Unannotated". At the bottom, there is a section titled "Download the Gene Ontology Category wise data from below given links:-". It contains three rows, each with a category name and a "Get Sequences File" button: "Molecular Function Related Transcripts", "Biological Process Related Transcripts", and "Cellular Component Related Transcripts".

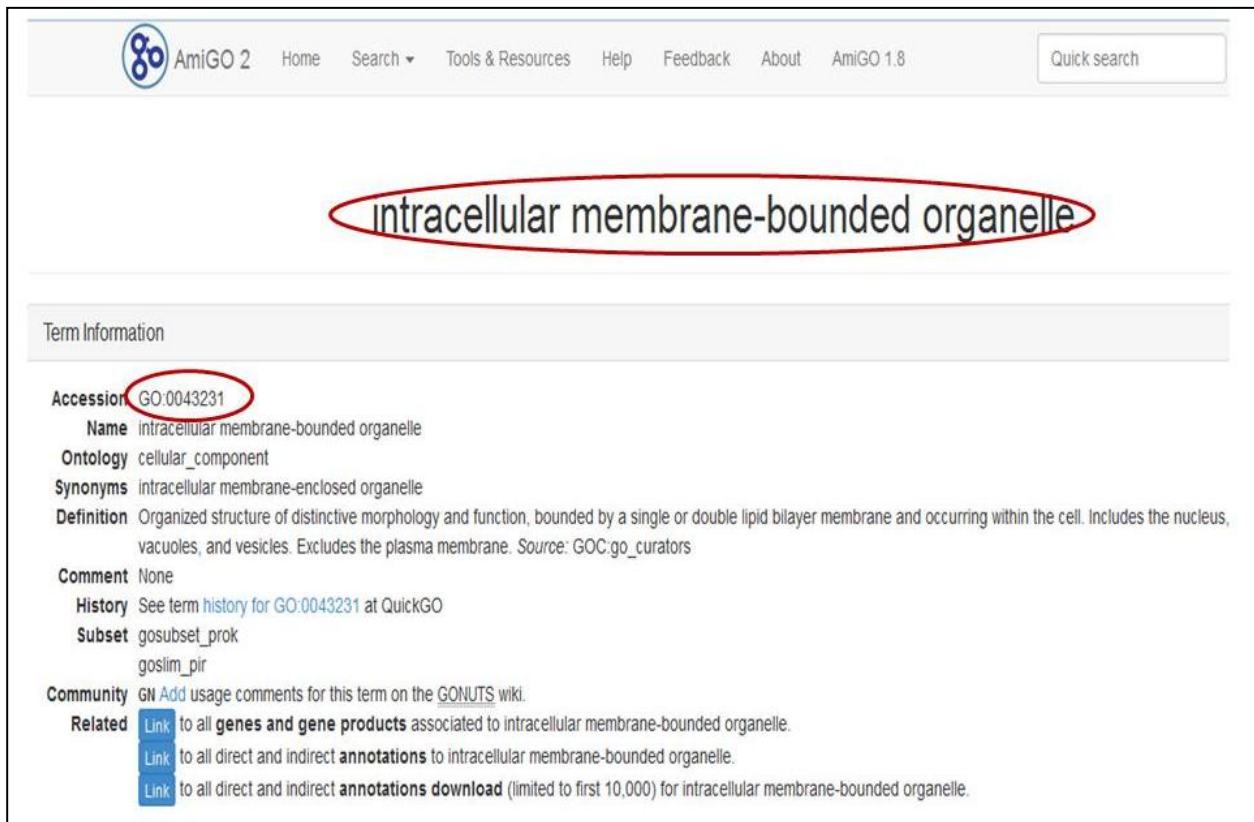
This is the Gene Ontology Search Result page



The image shows the TinoTranscriptDB website interface. At the top, there is a header with the ICAR logo on the left, the database title "TinoTranscriptDB Tinospora cordifolia Transcripts & SSR Database" in the center, and the NBPGR logo on the right. Below the header is a sidebar with navigation links: About, Database, Tutorial, Download, Feedback, Links, Team, and Contact Us. The main content area is titled "GO Annotation Search Result :". It features a "Go Back" button in the top right corner. Below the title is a table with 7 columns: S.No., Transcript Id, GO Class, GO_Id, GO Term, Annotation, and Sequence. The table contains 5 rows of data. Each row has a "GO_Id" link and a "Sequence" box with a "Get Sequences File" button.

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]/CB125585.3 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 AGCTAAAGCACAAAGGGGAAA
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.



AmiGO 2 Home Search Tools & Resources Help Feedback About AmiGO 1.8 Quick search

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

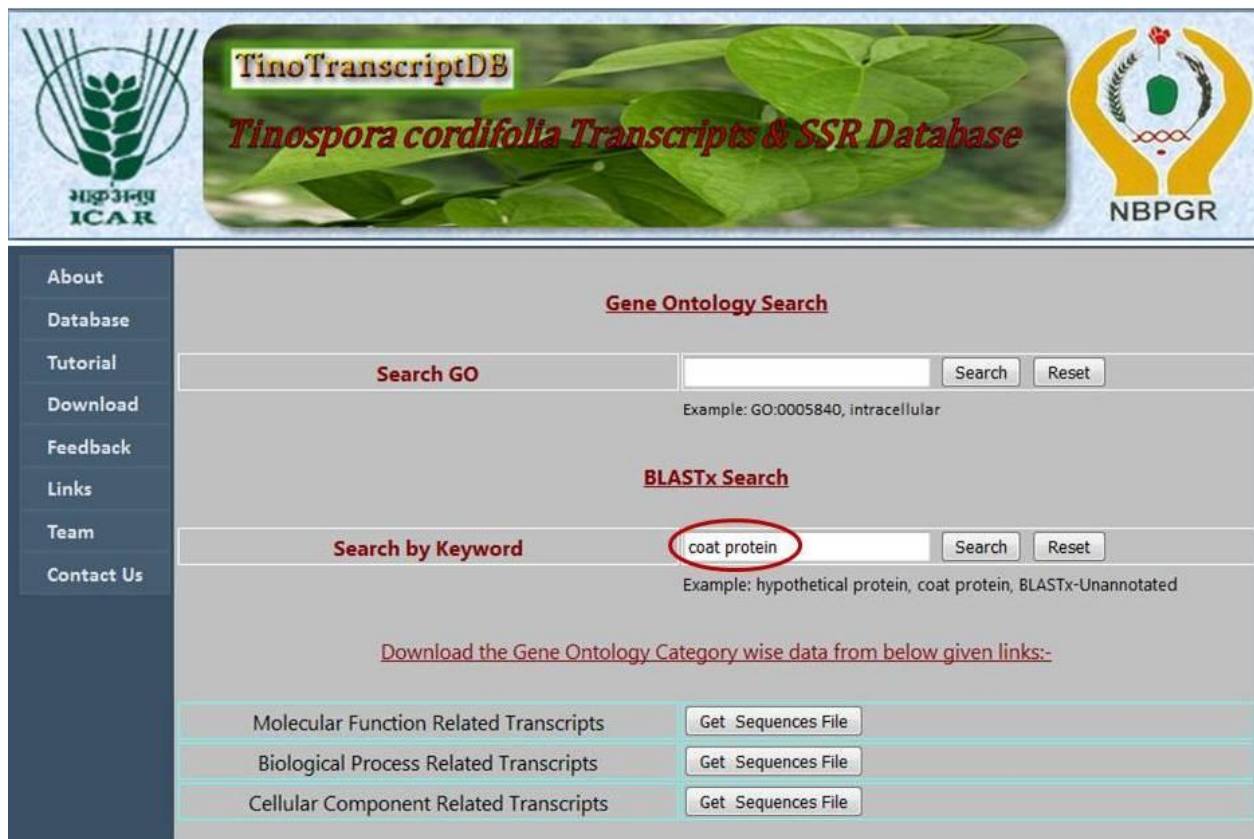
History See term history for GO:0043231 at QuickGO

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"



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Tinospora cordifolia Transcripts & SSR Database

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Gene Ontology Search

Search GO Search Reset

Example: GO:0005840, intracellular

BLASTx Search


Search by Keyword Search Reset

Example: hypothetical protein, coat protein, BLASTx-Unannotated

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

Molecular Function Related Transcripts	Get Sequences File
Biological Process Related Transcripts	Get Sequences File
Cellular Component Related Transcripts	Get Sequences File

This is the BLASTx Search Result page




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Tinospora cordifolia Transcripts & SSR Database

ICAR NBPGR

BLASTx Annotation Search Result : Go Back

S.No.	Transcript Id	Accession	BLASTx Annotation	Sequence
1	Tcordifolia_37876	AEM23894	Coat protein [Nerine virus X]	>Tcordifolia_37876 GTAGTGTGGAGAATGTAAC ACCCCAACCCCGTATCTTT
2	Tcordifolia_38020	YP_446996	Coat protein [Nerine virus X]/YP_446996	>Tcordifolia_38020 CAGAACTGGGTTCTGGACAG GCGTGCGGAAGCTTTAACCA
3	Tcordifolia_38284	YP_010087748	Coat protein [Euonymus yellow mottle associated virus]/QCY52828	>Tcordifolia_38284 TGCTACACGACGCGGACGT 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 GGGAGTGGGAGATGAAGGA
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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TinoTranscriptDB

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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.



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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



भारतीय
ICAR



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Tinospora cordifolia Transcripts & SSR Database



NBPGR

	Download Data	
About Database Tutorial Download Feedback Links Team Contact Us	<u>Perfect SSRs</u>	
	Tinospora_Di-nucleotide	Data
	Tinospora_Tri-nucleotide	Download
	Tinospora_Tetra-nucleotide	Download
	Tinospora_Penta-nucleotide	Download
	Tinospora_Hexa-nucleotide	Download
	Tinospora_All	Download
	<u>Imperfect SSRs</u>	
	I-SSRs	Download
	<u>Compound SSRs</u>	
	C-SSRs	Download
	<u>Annotation Data</u>	
	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
