TUTORIALS of
ApTransDB

ApTransDB (*Andrographis paniculata* Transcripts & SSR Database) accessible via the web address http://www.nbpgr.ernet.in:8080/Andrographis/ having nine different tabs:

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

Andrographis paniculata is a herb well known in Asia and belongs to the family *Acanthaceae*. It is native to Asia and distributed throughout India, China, Sri Lanka and Taiwan. *Andrographis paniculata* is a potential medicinal plant of immense economic importance. Leaves of *A. paniculata* contains active constitutents like andrographolide, homoandrographolide, andrographestrol and andrographonone. *A. paniculata,* also known as *Kalmegh* in India, is mentioned in ancient Indian medicine (Ayurvedic) literature as a constituent of ayurvedic formulation used for the treatment of liver disorder, and neoplasm. The plant has also hepatoprotective, antioxidant, and hypoglycemic activities and is being used in the management of immune system and neoplastic diseases.

Due to limited information with regard to genomic resources, essential for exploitation of *Andrographis paniculata*, we have generated a database from its entire transcriptome including information relevant to gene sequences and gene-based SSR (EST-SSR) or microsatellite markers. SSR marker is an indespensible tool for molecular mapping, diversity analysis and phylogenetic studies. Moreover, since SSR were designed from transcripts sequences, it is equally useful for comparative genomics including candidate gene determination. Besides molecular markers, the sequences of transcripts will serves as an important resource for the discovery of biosynthetic genes and other regulons associated with its active constituents.

001202

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Database Search: This is the main tab of this database from where user can search predicted perfect SSRs along with 3 primer pairs using different search criteria such as, search by SSRs type, search by SSR motif, search by motif length & repeat type, search by annotation keyword, or search by sequence Id/SSR Id. List of TF categories, annotation of transcripts based on gene ontology (GO) as well as important gene families related to biochemical compounds biosynthesis in *A. paniculata*.

Androg erb well known in Asia and belongs to the family *Acanthaceae*. It is native to Asia and distributed
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importa *lata* contains active constitutents like andrographolide, homoandrographolide, andrographestrol and
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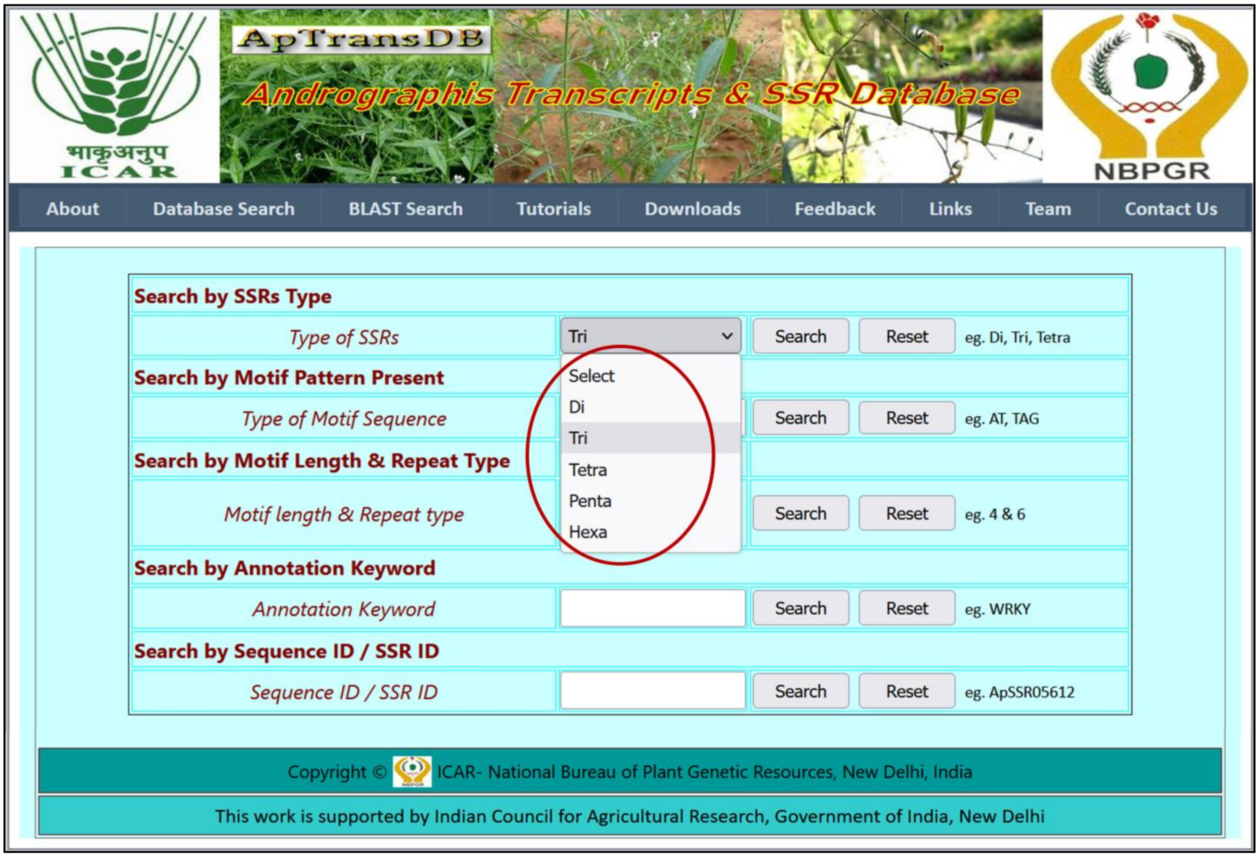
SSRs Information:

Perfect SSR Search:

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



Search by SSRs Type

Type of SSRs: Tri — eg. Di, Tri, Tetra

Search by Motif Pattern Present

Type of Motif Sequence — eg. AT, TAG

Search by Motif Length & Repeat Type

Motif length & Repeat type — eg. 4 & 6

Search by Annotation Keyword

Annotation Keyword — eg. WRKY

Search by Sequence ID / SSR ID

Sequence ID / SSR ID — eg. ApSSR05612

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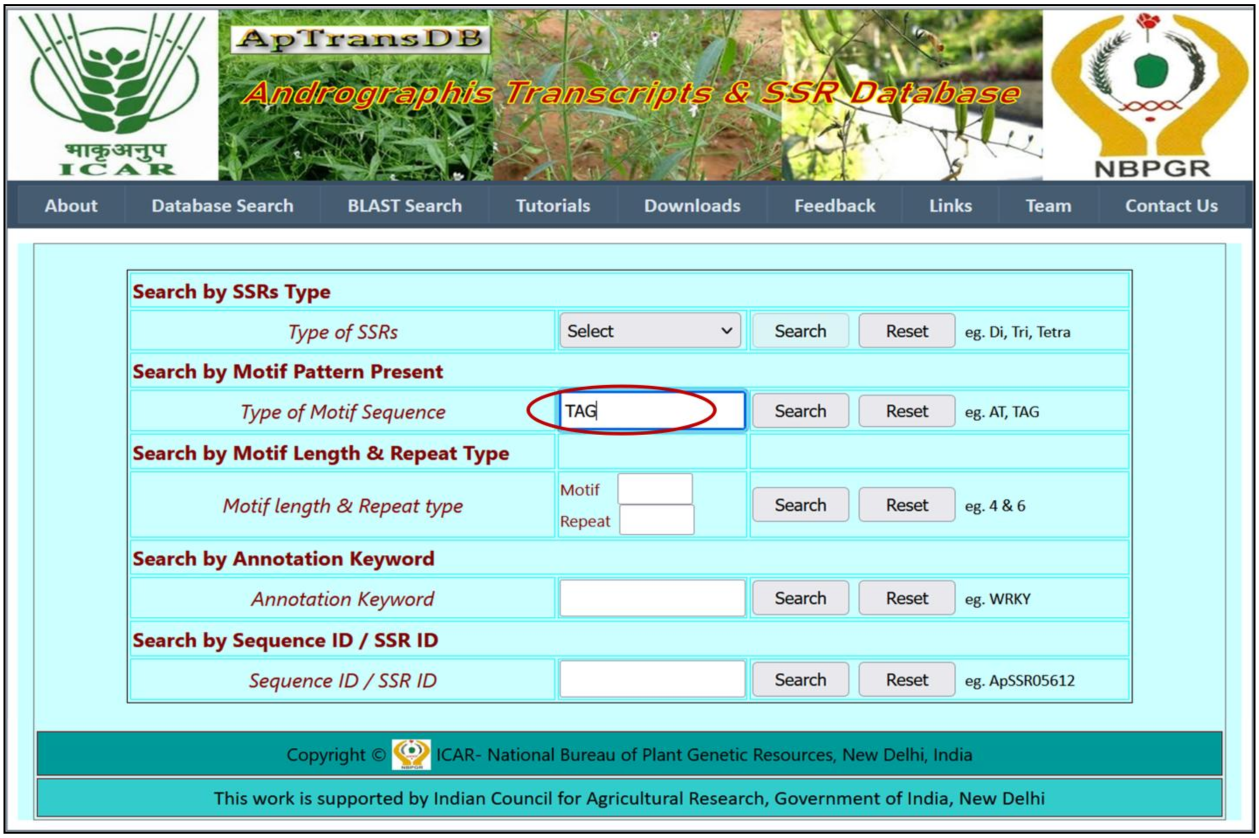
*User can search the database using search criteria “Search by Custom Motif Sequence”



Search by SSRs Type			
Type of SSRs	Select	Search Reset	eg. Di, Tri, Tetra
Search by Motif Pattern Present			
Type of Motif Sequence	TAG	Search Reset	eg. AT, TAG
Search by Motif Length & Repeat Type			
Motif length & Repeat type	Motif Repeat	Search Reset	eg. 4 & 6
Search by Annotation Keyword			
Annotation Keyword		Search Reset	eg. WRKY
Search by Sequence ID / SSR ID			
Sequence ID / SSR ID		Search Reset	eg. ApSSR05612

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

Search by SSRs Type			
Type of SSRs	Select	Search Reset	eg. Di, Tri, Tetra
Search by Motif Pattern Present			
Type of Motif Sequence		Search Reset	eg. AT, TAG
Search by Motif Length & Repeat Type			
Motif length & Repeat type	Motif 4 Repeat 6	Search Reset	eg. 4 & 6
Search by Annotation Keyword			
Annotation Keyword		Search Reset	eg. WRKY
Search by Sequence ID / SSR ID			
Sequence ID / SSR ID		Search Reset	eg. ApSSR05612

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

ApTransDB

Andrographis Transcripts & SSR Database

Search by SSRs Type		
Type of SSRs	Select	eg. Di, Tri, Tetra
Search by Motif Pattern Present		
Type of Motif Sequence		eg. AT, TAG
Search by Motif Length & Repeat Type		
Motif length & Repeat type	Motif Repeat	eg. 4 & 6
Search by Annotation Keyword		
Annotation Keyword	WRKY	eg. WRKY
Search by Sequence ID / SSR ID		
Sequence ID / SSR ID		eg. ApSSR05612

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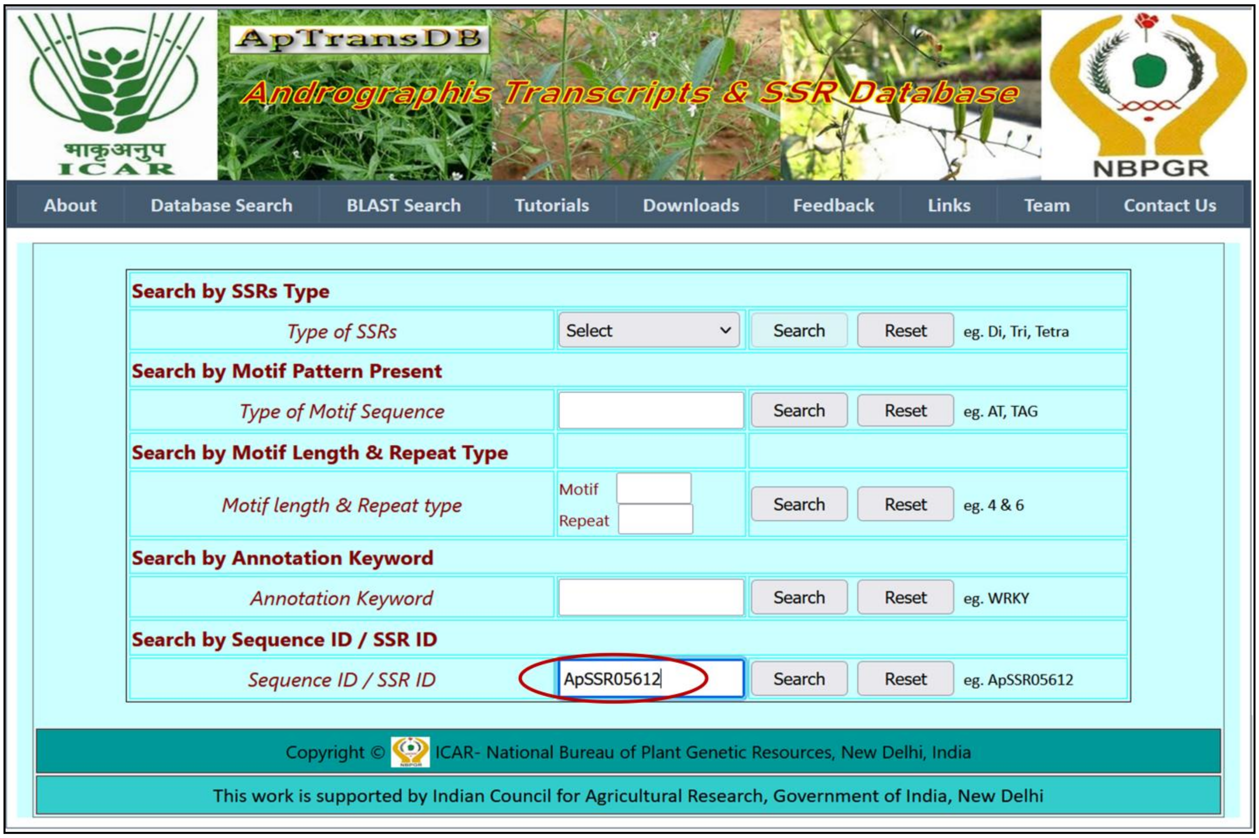
*User can search the database using search criteria “SSR Id”



ApTransDB

Andrographis Transcripts & SSR Database

Search by SSRs Type		
Type of SSRs	Select	eg. Di, Tri, Tetra
Search by Motif Pattern Present		
Type of Motif Sequence		eg. AT, TAG
Search by Motif Length & Repeat Type		
Motif length & Repeat type	Motif Repeat	eg. 4 & 6
Search by Annotation Keyword		
Annotation Keyword		eg. WRKY
Search by Sequence ID / SSR ID		
Sequence ID / SSR ID	ApSSR05612	eg. ApSSR05612

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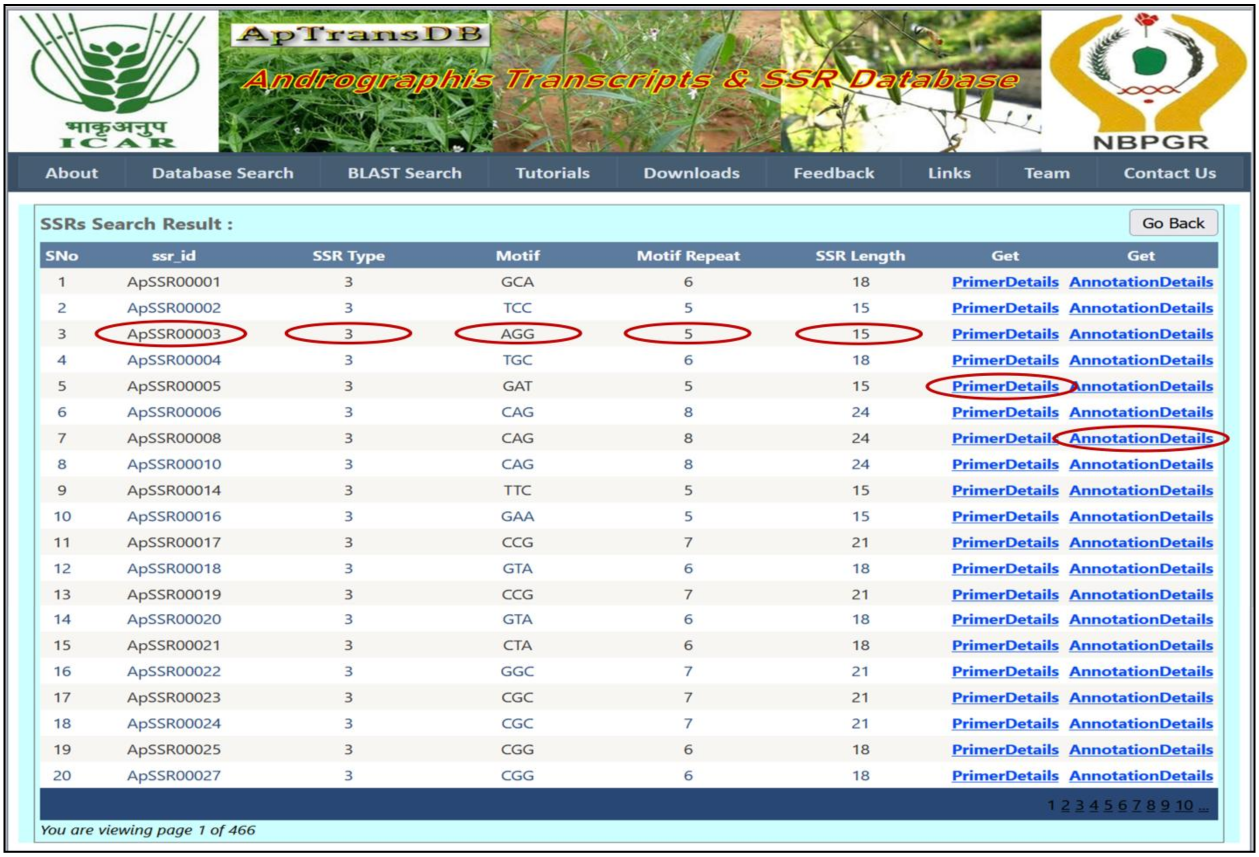
Based on the query search criteria the output is available to the user in real time in terms of 1) Complete SSR details, 2) Best three SSR specific primer pair set along with full primer information and 3) Complete transcript annotation if available.



SSRs Search Result :

SNo	ssr_id	SSR Type	Motif	Motif Repeat	SSR Length	Get	Get
1	ApSSR00001	3	GCA	6	18	PrimerDetails	AnnotationDetails
2	ApSSR00002	3	TCC	5	15	PrimerDetails	AnnotationDetails
3	ApSSR00003	3	AGG	5	15	PrimerDetails	AnnotationDetails
4	ApSSR00004	3	TGC	6	18	PrimerDetails	AnnotationDetails
5	ApSSR00005	3	GAT	5	15	PrimerDetails	AnnotationDetails
6	ApSSR00006	3	CAG	8	24	PrimerDetails	AnnotationDetails
7	ApSSR00008	3	CAG	8	24	PrimerDetails	AnnotationDetails
8	ApSSR00010	3	CAG	8	24	PrimerDetails	AnnotationDetails
9	ApSSR00014	3	TTC	5	15	PrimerDetails	AnnotationDetails
10	ApSSR00016	3	GAA	5	15	PrimerDetails	AnnotationDetails
11	ApSSR00017	3	CCG	7	21	PrimerDetails	AnnotationDetails
12	ApSSR00018	3	GTA	6	18	PrimerDetails	AnnotationDetails
13	ApSSR00019	3	CCG	7	21	PrimerDetails	AnnotationDetails
14	ApSSR00020	3	GTA	6	18	PrimerDetails	AnnotationDetails
15	ApSSR00021	3	CTA	6	18	PrimerDetails	AnnotationDetails
16	ApSSR00022	3	GGC	7	21	PrimerDetails	AnnotationDetails
17	ApSSR00023	3	CGC	7	21	PrimerDetails	AnnotationDetails
18	ApSSR00024	3	CGC	7	21	PrimerDetails	AnnotationDetails
19	ApSSR00025	3	CGG	6	18	PrimerDetails	AnnotationDetails
20	ApSSR00027	3	CGG	6	18	PrimerDetails	AnnotationDetails

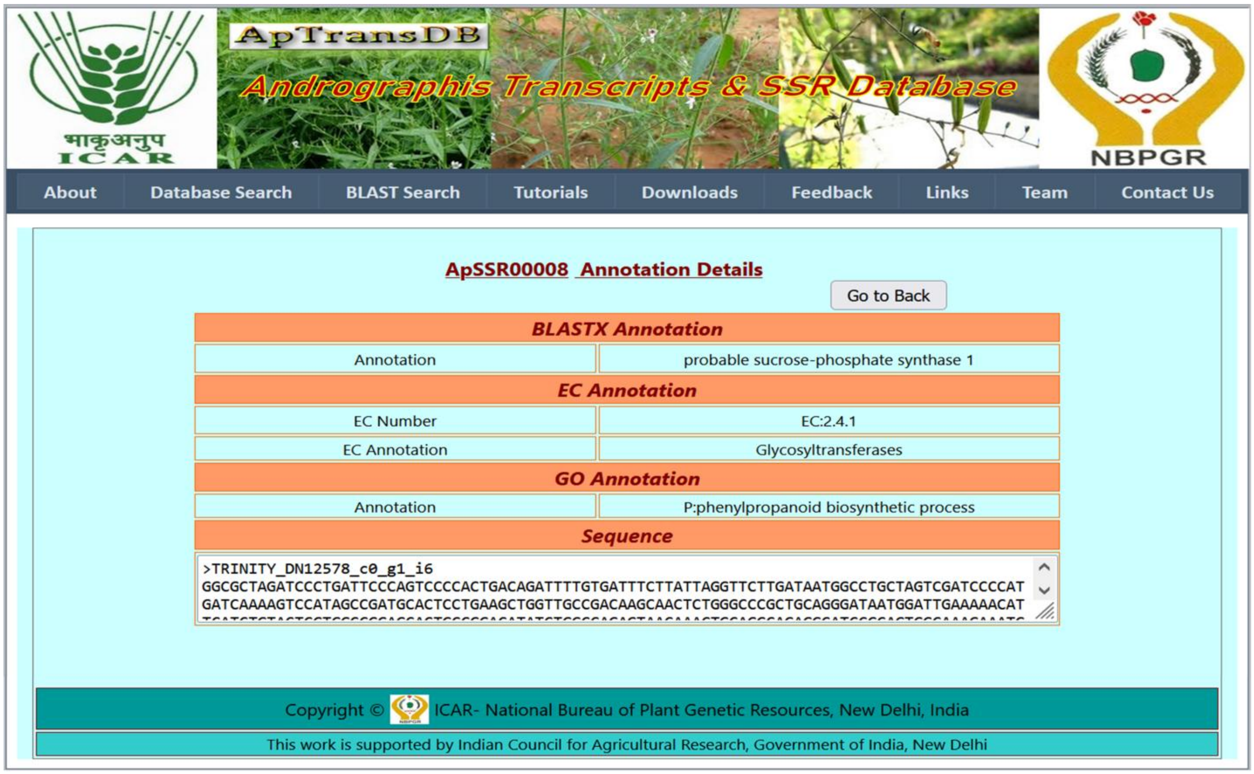
You are viewing page 1 of 466

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

ApSSR00005 Primer pair Details

Primer pair-1	
Forward Primer	AGTTGCACCTTTGAGTTAGAGG
Length (bp)	22
Tm0C	58.26
GC%	45.45
Reverse Primer	CTTGCGTATCTTTCCTTCGGC
Length (bp)	21
Tm0C	59.67
GC%	52.38
Product Size (bp)	201
Primer pair-2	
Forward Primer	AGTTGCACCTTTGAGTTAGAGG
Length (bp)	22
Tm0C	58.26
GC%	45.45
Reverse Primer	GCTTGCGTATCTTTCCTTCGG
Length (bp)	21
Tm0C	59.67
GC%	52.38
Product Size (bp)	202
Primer pair-3	
Forward Primer	AGTTGCACCTTTGAGTTAGAGG
Length (bp)	22
Tm0C	58.26
GC%	45.45
Reverse Primer	TTGCGTATCTTTCCTTCGGC
Length (bp)	20
Tm0C	58.63
GC%	50
Product Size (bp)	200

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



ApSSR00008 Annotation Details

BLASTX Annotation	
Annotation	probable sucrose-phosphate synthase 1
EC Annotation	
EC Number	EC:2.4.1
EC Annotation	Glycosyltransferases
GO Annotation	
Annotation	P:phenylpropanoid biosynthetic process
Sequence	

```
>TRINITY_DN12578_c0_g1_i6
GGCGCTAGATCCCTGATTCCCAGTCCCCACTGACAGATTTTGTGATTTCTTATTAGGTTCTTGATAATGGCCTGCTAGTCGATCCCCAT
GATCAAAAGTCCATAGCCGATGCACTCCTGAAGCTGGTTGCCGACAAGCAACTCTGGGCCCGCTGCAGGGATAATGGATTGAAAAACAT
```

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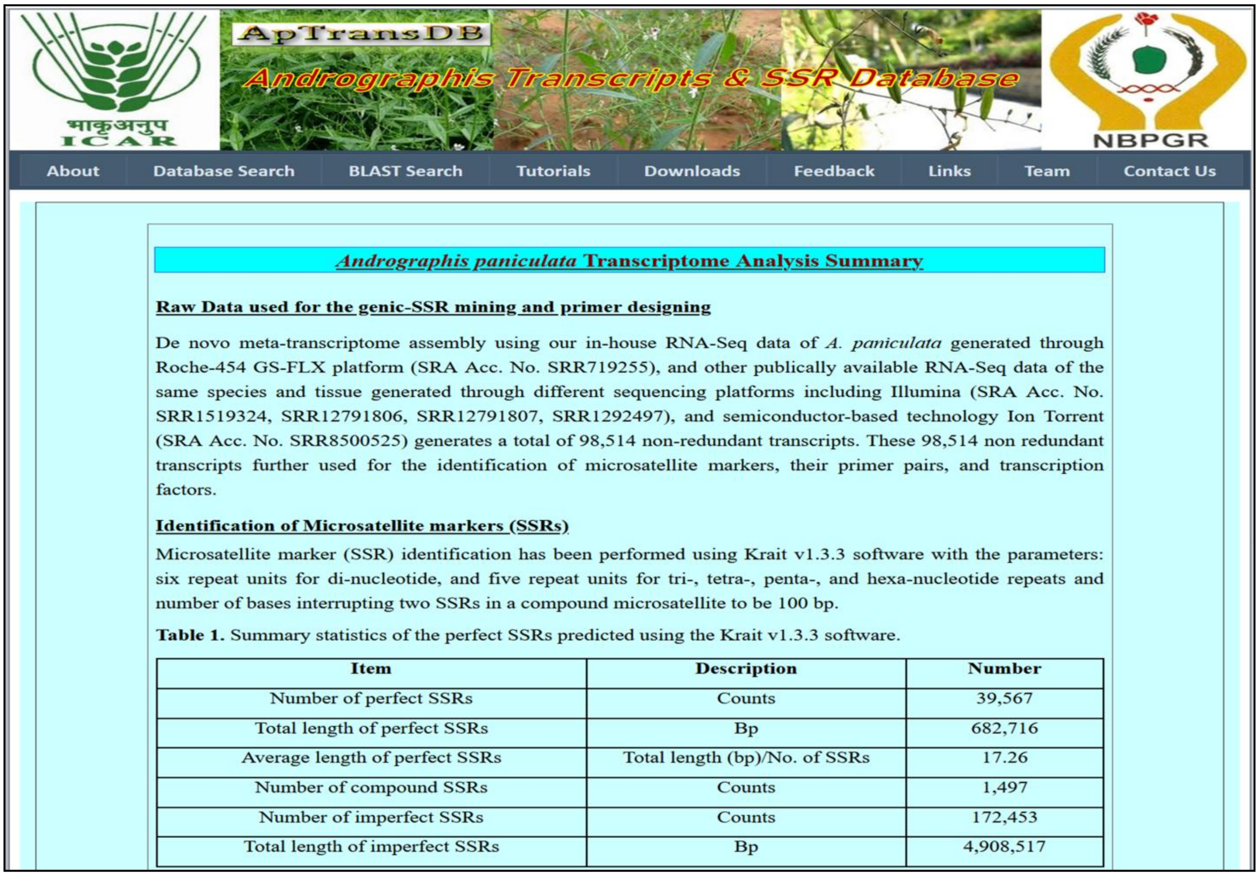
SSR Generation: From this page user can get all information about SSR data generated.



Andrographis paniculata Transcriptome Analysis Summary

Raw Data used for the genic-SSR mining and primer designing

De novo meta-transcriptome assembly using our in-house RNA-Seq data of *A. paniculata* generated through Roche-454 GS-FLX platform (SRA Acc. No. SRR719255), and other publically available RNA-Seq data of the same species and tissue generated through different sequencing platforms including Illumina (SRA Acc. No. SRR1519324, SRR12791806, SRR12791807, SRR1292497), and semiconductor-based technology Ion Torrent (SRA Acc. No. SRR8500525) generates a total of 98,514 non-redundant transcripts. These 98,514 non redundant transcripts further used for the identification of microsatellite markers, their primer pairs, and transcription factors.

Identification of Microsatellite markers (SSRs)

Microsatellite marker (SSR) identification has been performed using Krait v1.3.3 software with the parameters: six repeat units for di-nucleotide, and five repeat units for tri-, tetra-, penta-, and hexa-nucleotide repeats and number of bases interrupting two SSRs in a compound microsatellite to be 100 bp.

Table 1. Summary statistics of the perfect SSRs predicted using the Krait v1.3.3 software.

Item	Description	Number
Number of perfect SSRs	Counts	39,567
Total length of perfect SSRs	Bp	682,716
Average length of perfect SSRs	Total length (bp)/No. of SSRs	17.26
Number of compound SSRs	Counts	1,497
Number of imperfect SSRs	Counts	172,453
Total length of imperfect SSRs	Bp	4,908,517

Get TF Categories: From this page user can get sequence information for all predicted Transcription Factor categories of *A. paniculata*.

Category wise Transcription Factor related Transcripts of *Andrographis paniculata*

AP2 (166)	Get Sequence	**ARF** (387)	Get Sequence	**ARR-B** (99)	Get Sequence
B3 (778)	Get Sequence				
bHLH (2507)	Get Sequence				
C3H (887)	Get Sequence				
CPP (133)	Get Sequence				
E2F/DP (207)	Get Sequence				
FAR1 (794)	Get Sequence				
GeBP (210)	Get Sequence				
HB-other (408)	Get Sequence				
HRT-like (30)	Get Sequence				
LFY (4)	Get Sequence	**LSD** (59)	Get Sequence	**MIKC_MADS** (371)	Get Sequence
M-type_MADS (587)	Get Sequence	**MYB** (767)	Get Sequence	**MYB-Related** (1631)	Get Sequence
NAC (1723)	Get Sequence	**NF-X1** (68)	Get Sequence	**NF-YA** (232)	Get Sequence
NF-YB (183)	Get Sequence	**NF-YC** (259)	Get Sequence	**Nin-like** (219)	Get Sequence
NZZ/SPL (1)	Get Sequence	**RAV** (43)	Get Sequence	**S1Fa-like** (95)	Get Sequence
SAP (3)	Get Sequence	**SBP** (178)	Get Sequence	**SRS** (73)	Get Sequence
STAT (162)	Get Sequence	**TALE** (207)	Get Sequence	**TCP** (300)	Get Sequence
Trihelix (450)	Get Sequence	**VOZ** (36)	Get Sequence	**Whirly** (28)	Get Sequence
WOX (84)	Get Sequence	**WRKY** (970)	Get Sequence	**YABBY** (145)	Get Sequence
ZF-HD (97)	Get Sequence				

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from: http://localhost:14867

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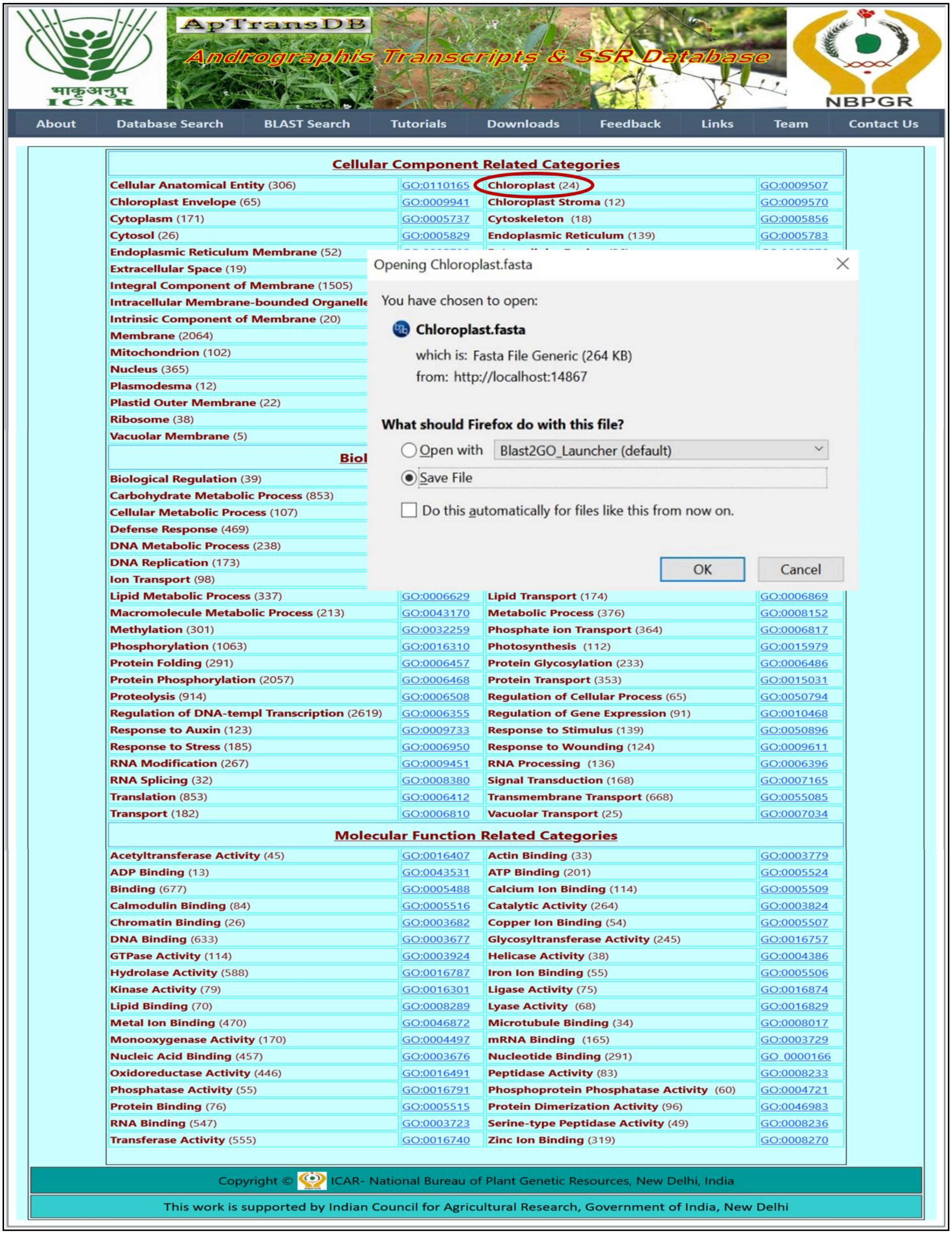
Get GO Categories: From this page user can get sequence information of all the transcripts belongs to major three GO categories: Biological Process, Molecular Function, and Cellular Component.



Cellular Component Related Categories

Cellular Anatomical Entity (306)	GO:0110165	**Chloroplast** (24)	GO:0009507
Chloroplast Envelope (65)	GO:0009941	**Chloroplast Stroma** (12)	GO:0009570
Cytoplasm (171)	GO:0005737	**Cytoskeleton** (18)	GO:0005856
Cytosol (26)	GO:0005829	**Endoplasmic Reticulum** (139)	GO:0005783
Endoplasmic Reticulum Membrane (52)			
Extracellular Space (19)			
Integral Component of Membrane (1505)			
Intracellular Membrane-bounded Organelle			
Intrinsic Component of Membrane (20)			
Membrane (2064)			
Mitochondrion (102)			
Nucleus (365)			
Plasmodesma (12)			
Plastid Outer Membrane (22)			
Ribosome (38)			
Vacuolar Membrane (5)			

Biol

Biological Regulation (39)			
Carbohydrate Metabolic Process (853)			
Cellular Metabolic Process (107)			
Defense Response (469)			
DNA Metabolic Process (238)			
DNA Replication (173)			
Ion Transport (98)			
Lipid Metabolic Process (337)	GO:0006629	**Lipid Transport** (174)	GO:0006869
Macromolecule Metabolic Process (213)	GO:0043170	**Metabolic Process** (376)	GO:0008152
Methylation (301)	GO:0032259	**Phosphate ion Transport** (364)	GO:0006817
Phosphorylation (1063)	GO:0016310	**Photosynthesis** (112)	GO:0015979
Protein Folding (291)	GO:0006457	**Protein Glycosylation** (233)	GO:0006486
Protein Phosphorylation (2057)	GO:0006468	**Protein Transport** (353)	GO:0015031
Proteolysis (914)	GO:0006508	**Regulation of Cellular Process** (65)	GO:0050794
Regulation of DNA-templ Transcription (2619)	GO:0006355	**Regulation of Gene Expression** (91)	GO:0010468
Response to Auxin (123)	GO:0009733	**Response to Stimulus** (139)	GO:0050896
Response to Stress (185)	GO:0006950	**Response to Wounding** (124)	GO:0009611
RNA Modification (267)	GO:0009451	**RNA Processing** (136)	GO:0006396
RNA Splicing (32)	GO:0008380	**Signal Transduction** (168)	GO:0007165
Translation (853)	GO:0006412	**Transmembrane Transport** (668)	GO:0055085
Transport (182)	GO:0006810	**Vacuolar Transport** (25)	GO:0007034

Molecular Function Related Categories

Acetyltransferase Activity (45)	GO:0016407	**Actin Binding** (33)	GO:0003779
ADP Binding (13)	GO:0043531	**ATP Binding** (201)	GO:0005524
Binding (677)	GO:0005488	**Calcium Ion Binding** (114)	GO:0005509
Calmodulin Binding (84)	GO:0005516	**Catalytic Activity** (264)	GO:0003824
Chromatin Binding (26)	GO:0003682	**Copper Ion Binding** (54)	GO:0005507
DNA Binding (633)	GO:0003677	**Glycosyltransferase Activity** (245)	GO:0016757
GTPase Activity (114)	GO:0003924	**Helicase Activity** (38)	GO:0004386
Hydrolase Activity (588)	GO:0016787	**Iron Ion Binding** (55)	GO:0005506
Kinase Activity (79)	GO:0016301	**Ligase Activity** (75)	GO:0016874
Lipid Binding (70)	GO:0008289	**Lyase Activity** (68)	GO:0016829
Metal Ion Binding (470)	GO:0046872	**Microtubule Binding** (34)	GO:0008017
Monooxygenase Activity (170)	GO:0004497	**mRNA Binding** (165)	GO:0003729
Nucleic Acid Binding (457)	GO:0003676	**Nucleotide Binding** (291)	GO_0000166
Oxidoreductase Activity (446)	GO:0016491	**Peptidase Activity** (83)	GO:0008233
Phosphatase Activity (55)	GO:0016791	**Phosphoprotein Phosphatase Activity** (60)	GO:0004721
Protein Binding (76)	GO:0005515	**Protein Dimerization Activity** (96)	GO:0046983
RNA Binding (547)	GO:0003723	**Serine-type Peptidase Activity** (49)	GO:0008236
Transferase Activity (555)	GO:0016740	**Zinc Ion Binding** (319)	GO:0008270

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You have chosen to open:

Chloroplast.fasta

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● Save File
☐ Do this automatically for files like this from now on.

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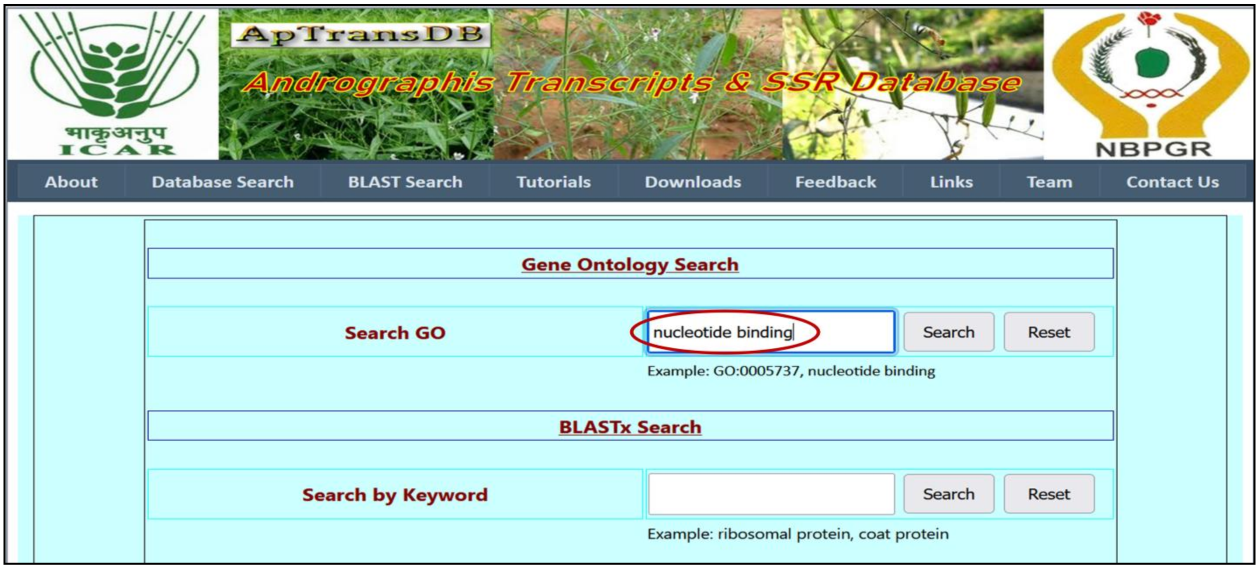
Annotation Search:

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



Gene Ontology Search

Search GO: nucleotide binding

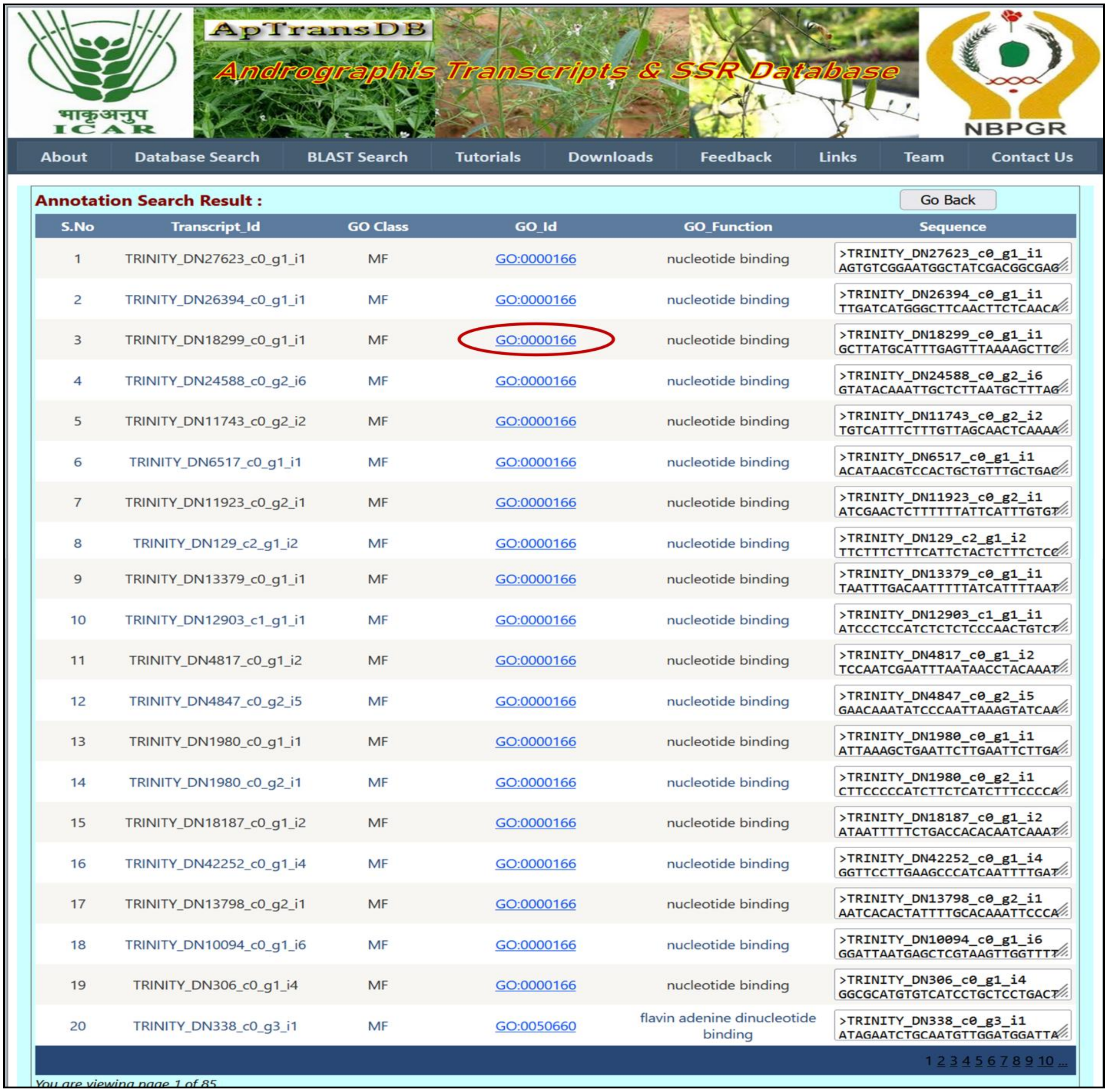
Example: GO:0005737, nucleotide binding

BLASTx Search

Search by Keyword

Example: ribosomal protein, coat protein

This is the Gene Ontology Search Result page.

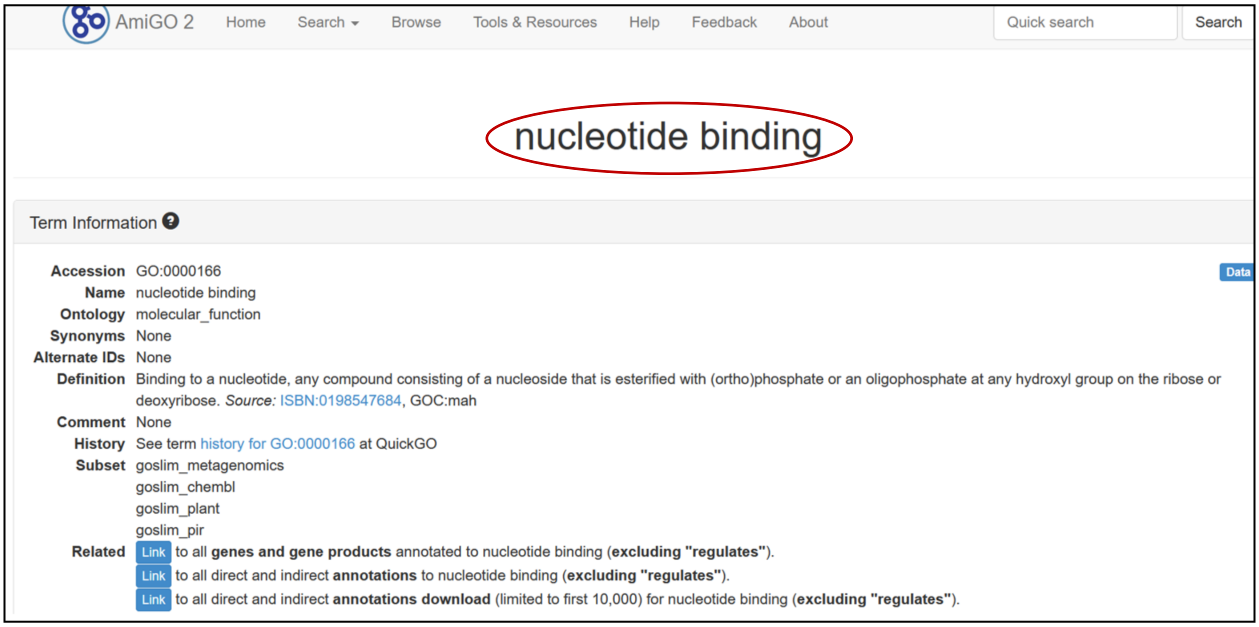


Annotation Search Result :

S.No	Transcript_Id	GO Class	GO_Id	GO_Function	Sequence
1	TRINITY_DN27623_c0_g1_i1	MF	GO:0000166	nucleotide binding	>TRINITY_DN27623_c0_g1_i1 AGTGTCGGAATGGCTATCGACGGCGAG
2	TRINITY_DN26394_c0_g1_i1	MF	GO:0000166	nucleotide binding	>TRINITY_DN26394_c0_g1_i1 TTGATCATGGGCTTCAACTTCTCAACA
3	TRINITY_DN18299_c0_g1_i1	MF	GO:0000166	nucleotide binding	>TRINITY_DN18299_c0_g1_i1 GCTTATGCATTTGAGTTTAAAAGCTTC
4	TRINITY_DN24588_c0_g2_i6	MF	GO:0000166	nucleotide binding	>TRINITY_DN24588_c0_g2_i6 GTATACAAATTGCTCTTAATGCTTTAG
5	TRINITY_DN11743_c0_g2_i2	MF	GO:0000166	nucleotide binding	>TRINITY_DN11743_c0_g2_i2 TGTCATTTCTTTGTTAGCAACTCAAAA
6	TRINITY_DN6517_c0_g1_i1	MF	GO:0000166	nucleotide binding	>TRINITY_DN6517_c0_g1_i1 ACATAACGTCCACTGCTGTTTGCTGAC
7	TRINITY_DN11923_c0_g2_i1	MF	GO:0000166	nucleotide binding	>TRINITY_DN11923_c0_g2_i1 ATCGAACTCTTTTTTATTCATTTGTGT
8	TRINITY_DN129_c2_g1_i2	MF	GO:0000166	nucleotide binding	>TRINITY_DN129_c2_g1_i2 TTCTTTCTTTCATTCTACTCTTTCTCC
9	TRINITY_DN13379_c0_g1_i1	MF	GO:0000166	nucleotide binding	>TRINITY_DN13379_c0_g1_i1 TAATTTGACAATTTTTATCATTTTAAT
10	TRINITY_DN12903_c1_g1_i1	MF	GO:0000166	nucleotide binding	>TRINITY_DN12903_c1_g1_i1 ATCCCTCCATCTCTCTCCCAACTGTCT
11	TRINITY_DN4817_c0_g1_i2	MF	GO:0000166	nucleotide binding	>TRINITY_DN4817_c0_g1_i2 TCCAATCGAATTTAATAACCTACAAAT
12	TRINITY_DN4847_c0_g2_i5	MF	GO:0000166	nucleotide binding	>TRINITY_DN4847_c0_g2_i5 GAACAAATATCCCAATTAAAGTATCAA
13	TRINITY_DN1980_c0_g1_i1	MF	GO:0000166	nucleotide binding	>TRINITY_DN1980_c0_g1_i1 ATTAAAGCTGAATTCTTGAATTCTTGA
14	TRINITY_DN1980_c0_g2_i1	MF	GO:0000166	nucleotide binding	>TRINITY_DN1980_c0_g2_i1 CTTCCCCCATCTTCTCATCTTTCCCCA
15	TRINITY_DN18187_c0_g1_i2	MF	GO:0000166	nucleotide binding	>TRINITY_DN18187_c0_g1_i2 ATAATTTTTCTGACCACACAATCAAAT
16	TRINITY_DN42252_c0_g1_i4	MF	GO:0000166	nucleotide binding	>TRINITY_DN42252_c0_g1_i4 GGTTCCTTGAAGCCCATCAATTTTGAT
17	TRINITY_DN13798_c0_g2_i1	MF	GO:0000166	nucleotide binding	>TRINITY_DN13798_c0_g2_i1 AATCACACTATTTTGCACAAATTCCCA
18	TRINITY_DN10094_c0_g1_i6	MF	GO:0000166	nucleotide binding	>TRINITY_DN10094_c0_g1_i6 GGATTAATGAGCTCGTAAGTTGGTTTT
19	TRINITY_DN306_c0_g1_i4	MF	GO:0000166	nucleotide binding	>TRINITY_DN306_c0_g1_i4 GGCGCATGTGTCATCCTGCTCCTGACT
20	TRINITY_DN338_c0_g3_i1	MF	GO:0050660	flavin adenine dinucleotide binding	>TRINITY_DN338_c0_g3_i1 ATAGAATCTGCAATGTTGGATGGATTA

You are viewing page 1 of 85

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

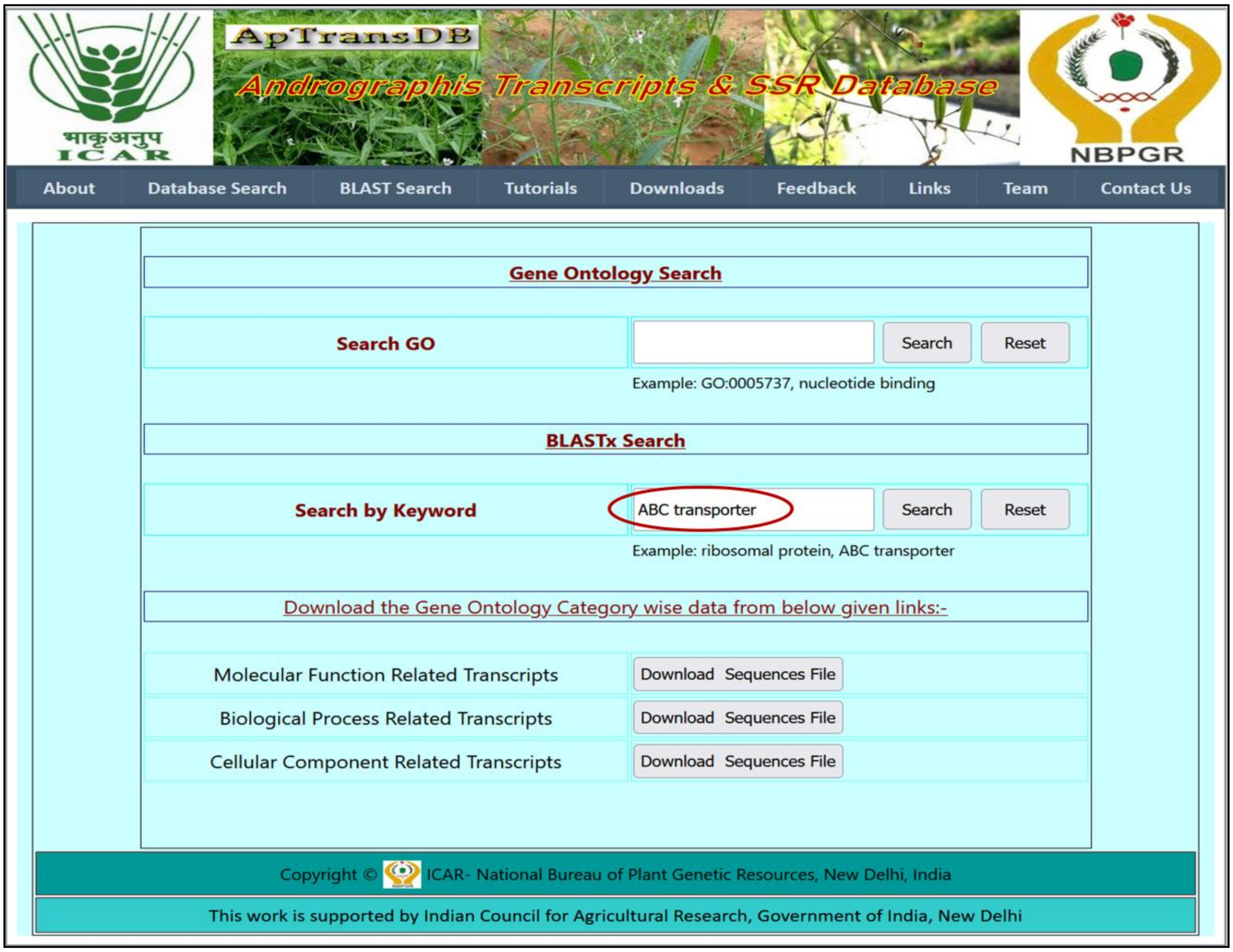


nucleotide binding

Term Information

Accession GO:0000166
Name nucleotide binding
Ontology molecular_function
Synonyms None
Alternate IDs None
Definition Binding to a nucleotide, any compound consisting of a nucleoside that is esterified with (ortho)phosphate or an oligophosphate at any hydroxyl group on the ribose or deoxyribose. *Source:* ISBN:0198547684, GOC:mah
Comment None
History See term history for GO:0000166 at QuickGO
Subset goslim_metagenomics
goslim_chembl
goslim_plant
goslim_pir
Related Link to all **genes and gene products** annotated to nucleotide binding (**excluding "regulates"**).
Link to all direct and indirect **annotations** to nucleotide binding (**excluding "regulates"**).
Link to all direct and indirect **annotations download** (limited to first 10,000) for nucleotide binding (**excluding "regulates"**).

User can search the database using search criteria “BLASTx Search”



Gene Ontology Search

Search GO

Example: GO:0005737, nucleotide binding

BLASTx Search

Search by Keyword ABC transporter

Example: ribosomal protein, ABC transporter

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

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

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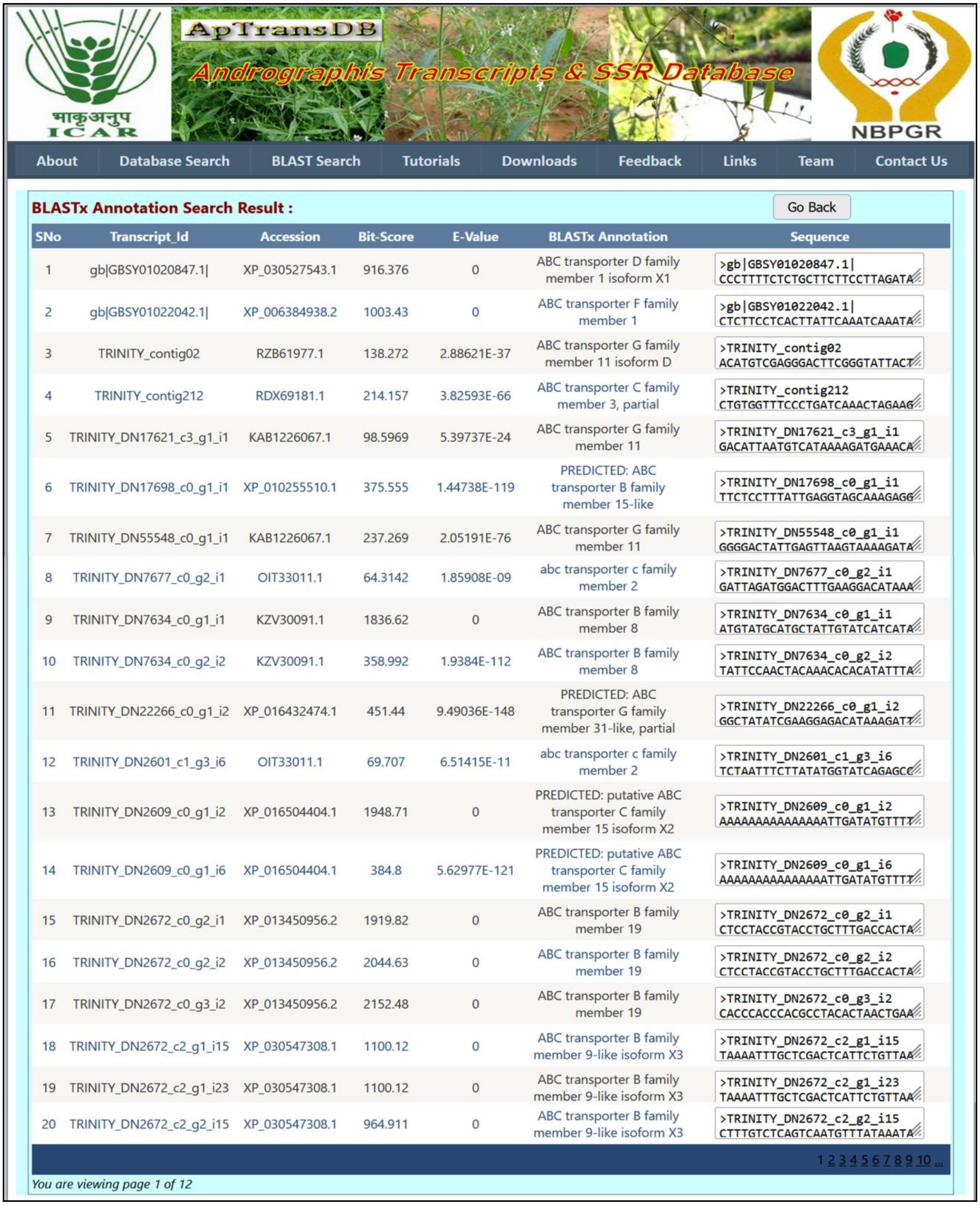
This is the BLASTx Search Result page



BLASTx Annotation Search Result :

SNo	Transcript_Id	Accession	Bit-Score	E-Value	BLASTx Annotation	Sequence
1	gb|GBSY01020847.1|	XP_030527543.1	916.376	0	ABC transporter D family member 1 isoform X1	>gb|GBSY01020847.1| CCCTTTTCTCTGCTTCTTCCTTAGATA
2	gb|GBSY01022042.1|	XP_006384938.2	1003.43	0	ABC transporter F family member 1	>gb|GBSY01022042.1| CTCTTCCTCACTTATTCAAATCAAATA
3	TRINITY_contig02	RZB61977.1	138.272	2.88621E-37	ABC transporter G family member 11 isoform D	>TRINITY_contig02 ACATGTCGAGGGACTTCGGGTATTACT
4	TRINITY_contig212	RDX69181.1	214.157	3.82593E-66	ABC transporter C family member 3, partial	>TRINITY_contig212 CTGTGGTTTCCCTGATCAAACTAGAAG
5	TRINITY_DN17621_c3_g1_i1	KAB1226067.1	98.5969	5.39737E-24	ABC transporter G family member 11	>TRINITY_DN17621_c3_g1_i1 GACATTAATGTCATAAAAGATGAAACA
6	TRINITY_DN17698_c0_g1_i1	XP_010255510.1	375.555	1.44738E-119	PREDICTED: ABC transporter B family member 15-like	>TRINITY_DN17698_c0_g1_i1 TTCTCCTTTATTGAGGTAGCAAAGAGG
7	TRINITY_DN55548_c0_g1_i1	KAB1226067.1	237.269	2.05191E-76	ABC transporter G family member 11	>TRINITY_DN55548_c0_g1_i1 GGGGACTATTGAGTTAAGTAAAAGATA
8	TRINITY_DN7677_c0_g2_i1	OIT33011.1	64.3142	1.85908E-09	abc transporter c family member 2	>TRINITY_DN7677_c0_g2_i1 GATTAGATGGACTTTGAAGGACATAAA
9	TRINITY_DN7634_c0_g1_i1	KZV30091.1	1836.62	0	ABC transporter B family member 8	>TRINITY_DN7634_c0_g1_i1 ATGTATGCATGCTATTGTATCATCATA
10	TRINITY_DN7634_c0_g2_i2	KZV30091.1	358.992	1.9384E-112	ABC transporter B family member 8	>TRINITY_DN7634_c0_g2_i2 TATTCCAACTACAAACACACATATTTA
11	TRINITY_DN22266_c0_g1_i2	XP_016432474.1	451.44	9.49036E-148	PREDICTED: ABC transporter G family member 31-like, partial	>TRINITY_DN22266_c0_g1_i2 GGCTATATCGAAGGAGACATAAAGATT
12	TRINITY_DN2601_c1_g3_i6	OIT33011.1	69.707	6.51415E-11	abc transporter c family member 2	>TRINITY_DN2601_c1_g3_i6 TCTAATTTCTTATATGGTATCAGAGCC
13	TRINITY_DN2609_c0_g1_i2	XP_016504404.1	1948.71	0	PREDICTED: putative ABC transporter C family member 15 isoform X2	>TRINITY_DN2609_c0_g1_i2 AAAAAAAAAAAAAAATTGATATGTTTT
14	TRINITY_DN2609_c0_g1_i6	XP_016504404.1	384.8	5.62977E-121	PREDICTED: putative ABC transporter C family member 15 isoform X2	>TRINITY_DN2609_c0_g1_i6 AAAAAAAAAAAAAAATTGATATGTTTT
15	TRINITY_DN2672_c0_g2_i1	XP_013450956.2	1919.82	0	ABC transporter B family member 19	>TRINITY_DN2672_c0_g2_i1 CTCCTACCGTACCTGCTTTGACCACTA
16	TRINITY_DN2672_c0_g2_i2	XP_013450956.2	2044.63	0	ABC transporter B family member 19	>TRINITY_DN2672_c0_g2_i2 CTCCTACCGTACCTGCTTTGACCACTA
17	TRINITY_DN2672_c0_g3_i2	XP_013450956.2	2152.48	0	ABC transporter B family member 19	>TRINITY_DN2672_c0_g3_i2 CACCCACCCACGCCTACACTAACTGAA
18	TRINITY_DN2672_c2_g1_i15	XP_030547308.1	1100.12	0	ABC transporter B family member 9-like isoform X3	>TRINITY_DN2672_c2_g1_i15 TAAAATTTGCTCGACTCATTCTGTTAA
19	TRINITY_DN2672_c2_g1_i23	XP_030547308.1	1100.12	0	ABC transporter B family member 9-like isoform X3	>TRINITY_DN2672_c2_g1_i23 TAAAATTTGCTCGACTCATTCTGTTAA
20	TRINITY_DN2672_c2_g2_i15	XP_030547308.1	964.911	0	ABC transporter B family member 9-like isoform X3	>TRINITY_DN2672_c2_g2_i15 CTTTGTCTCAGTCAATGTTTATAAATA

1 2 3 4 5 6 7 8 9 10 ...

You are viewing page 1 of 12

Tutorials: From this page user learn how to use this database and how to extract useful information’s from the *Andrographis paniculata* transcripts and SSR database.

TUTORIALS of ApTransDB

ApTransDB (*Andrographis paniculata* Transcripts & SSR Database) accessible via the web address http://www.nbpgr.ernet.in:8080/Andrographis/ having nine different tabs:

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

Andrographis paniculata is a herb well known in Asia and belongs to the family *Acanthaceae*. It is native to Asia and distributed throughout India, China, Sri Lanka and Taiwan. *Andrographis paniculata* is a potential medicinal plant of immense economic

Download: From this page user can download the SSR and annotated transcripts data.

Download Data	
SSR Type	Data
Andrographis_Di-nucleotide	Click here to download
Andrographis_Tri-nucleotide	Click here to download
Andrographis_Tetra-nucleotide	Click here to download
Andrographis_Penta-nucleotide	Click here to download
Andrographis_Hexa-nucleotide	Click here to download
Andrographis_All	Click here to download
Annotation Data	
Andrographis_TF_All	Click here to download
Andrographis_GO_All	Click here to download
Andrographis_BLASTx_All	Click here to download

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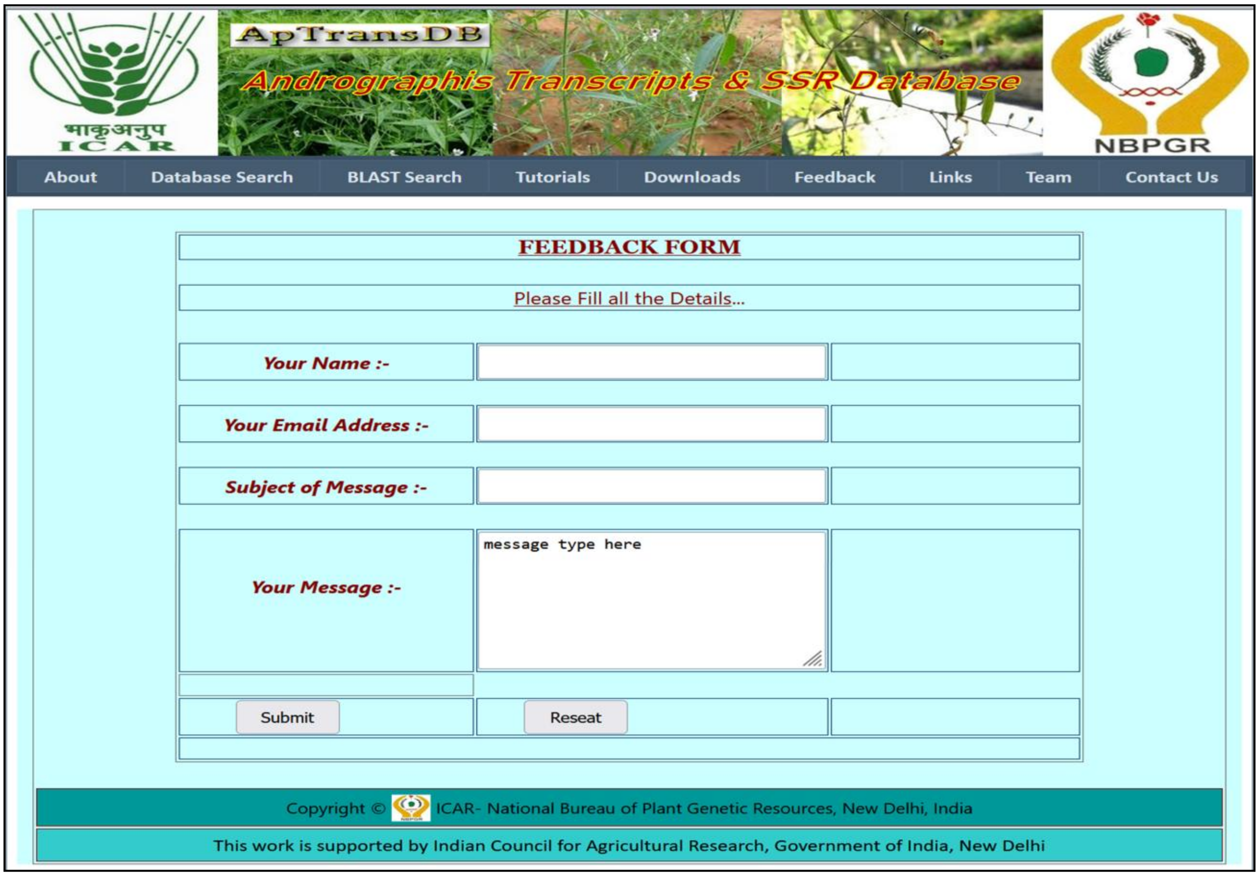
Feedback: User can send their queries or suggestions by filling this feedback form to improve our database.



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Links: Link tab contains useful links related to *Andrographis paniculata* database.

“Team” and **“Contact Us”** tabs having the information about the team members involved in this project