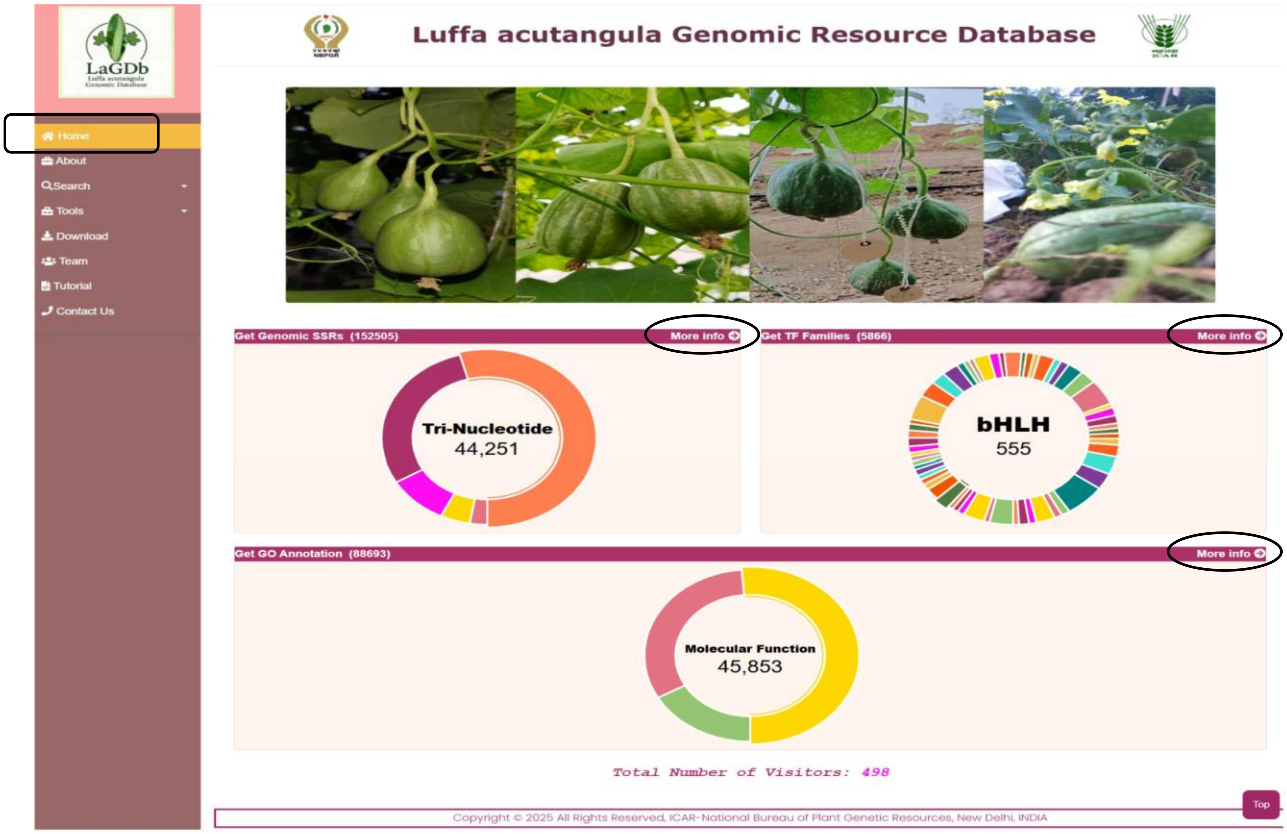
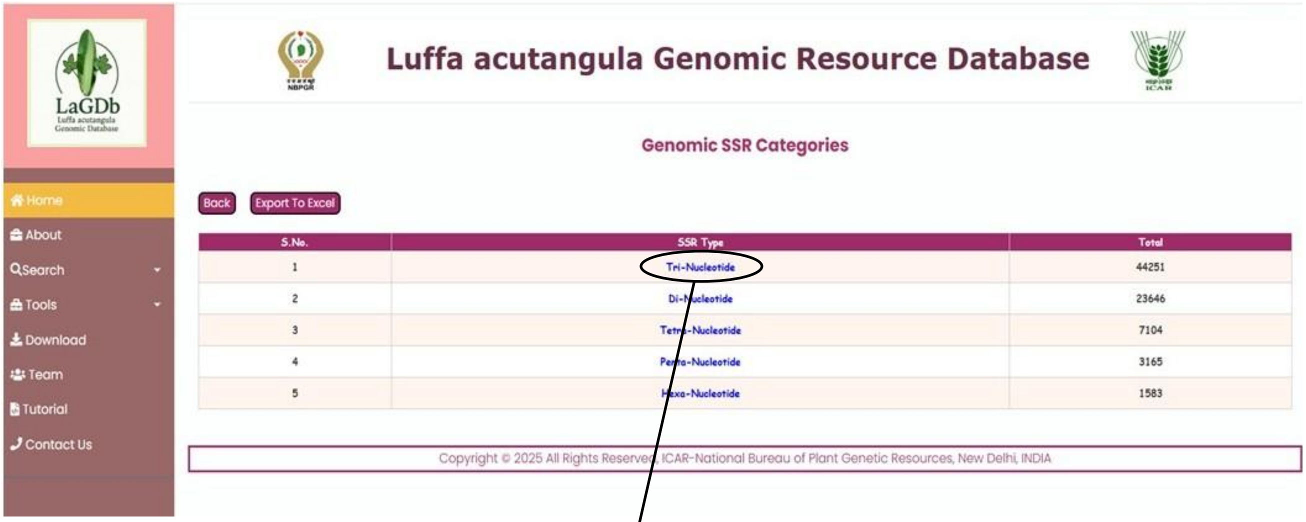
Tutorials of “*Luffa acutangula*” Genomic Resource Database

1. **Home:** The Home page provides an overview of the **Luffa acutangula Genomic Resource Database**. It highlights key features, quick access to tools, visitor count, and statistical summaries of the genomic data resources available.



User can get information about Genomic SSRs, Transcription Factors, and Gene Ontology annotation of the genes predicted in *Luffa acutangula* genome by clicking on the More info tag or circular diagrams of that category.

- By clicking on “More info” tag, under Get Genomic SSRs block, user will get all SSR categories information with the number details.

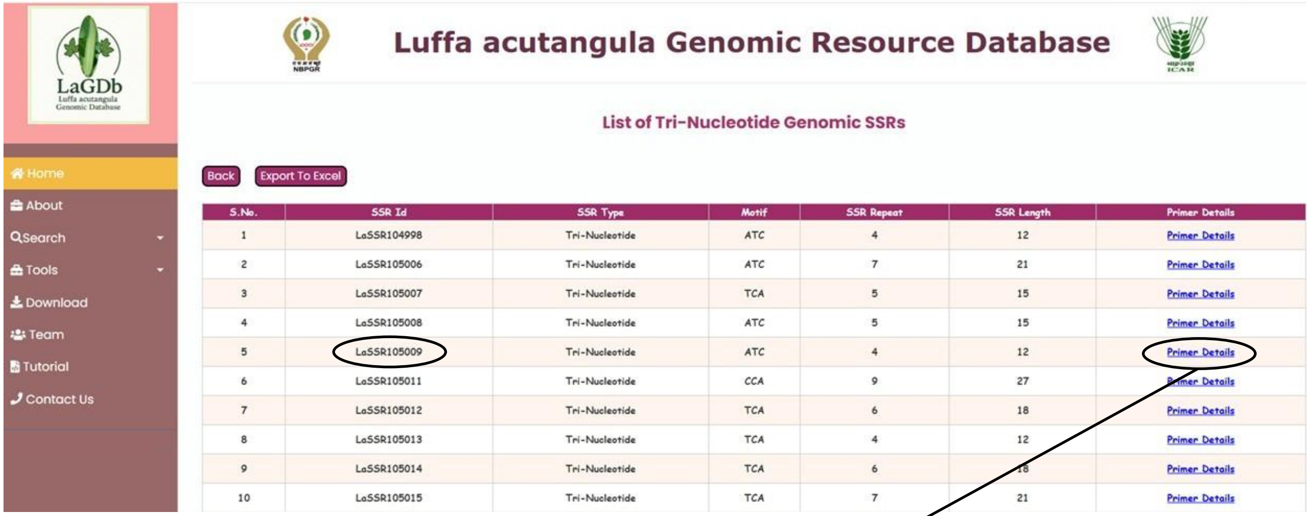


Luffa acutangula Genomic Resource Database

Genomic SSR Categories

S.No.	SSR Type	Total
1	Tri-Nucleotide	44251
2	Di-Nucleotide	23646
3	Tetra-Nucleotide	7104
4	Penta-Nucleotide	3165
5	Hexa-Nucleotide	1583

By clicking on particular category link, user will get list of SSRs predicted in that particular category with the link to get their primers details. User can also get the similar details by clicking on that SSR categories displayed on the circular diagram. eg. Tri-Nucleotide

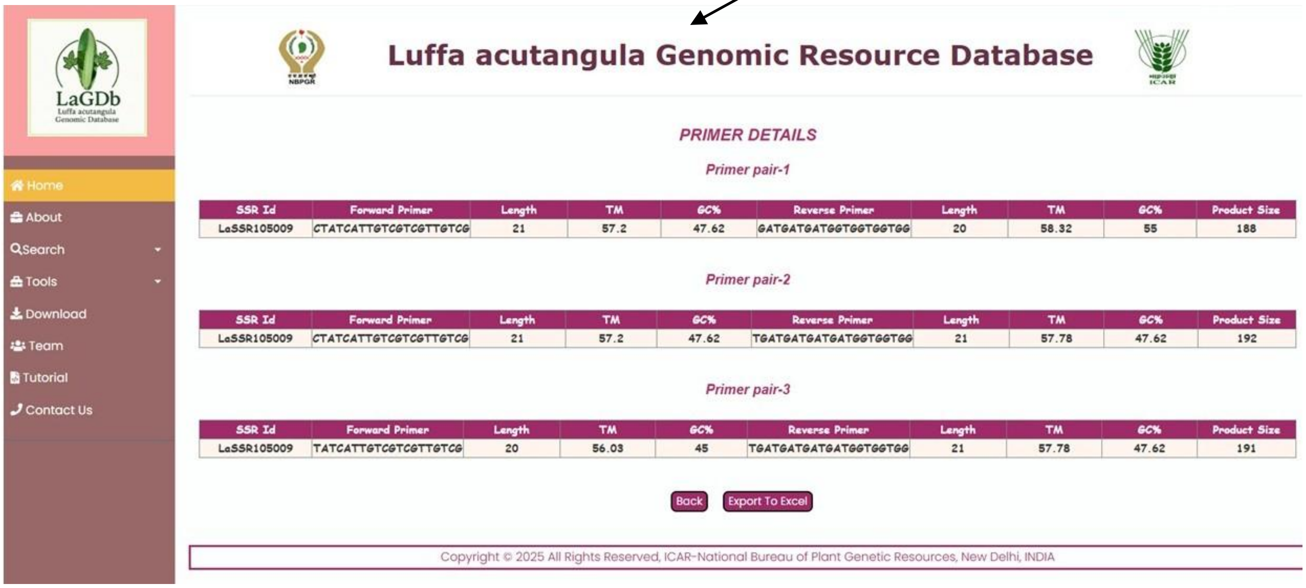


Luffa acutangula Genomic Resource Database

List of Tri-Nucleotide Genomic SSRs

S.No.	SSR Id	SSR Type	Motif	SSR Repeat	SSR Length	Primer Details
1	LaSSR104998	Tri-Nucleotide	ATC	4	12	Primer Details
2	LaSSR105006	Tri-Nucleotide	ATC	7	21	Primer Details
3	LaSSR105007	Tri-Nucleotide	TCA	5	15	Primer Details
4	LaSSR105008	Tri-Nucleotide	ATC	5	15	Primer Details
5	LaSSR105009	Tri-Nucleotide	ATC	4	12	Primer Details
6	LaSSR105011	Tri-Nucleotide	CCA	9	27	Primer Details
7	LaSSR105012	Tri-Nucleotide	TCA	6	18	Primer Details
8	LaSSR105013	Tri-Nucleotide	TCA	4	12	Primer Details
9	LaSSR105014	Tri-Nucleotide	TCA	6	18	Primer Details
10	LaSSR105015	Tri-Nucleotide	TCA	7	21	Primer Details

By clicking on the Primer Details link, it will give three primer pair information of selected genomic SSR.



Luffa acutangula Genomic Resource Database

PRIMER DETAILS

Primer pair-1

SSR Id	Forward Primer	Length	TM	GC%	Reverse Primer	Length	TM	GC%	Product Size
LaSSR105009	CTATCATTGTCGTCGTTGTCG	21	57.2	47.62	GATGATGATGGTGGTGGTGG	20	58.32	55	188

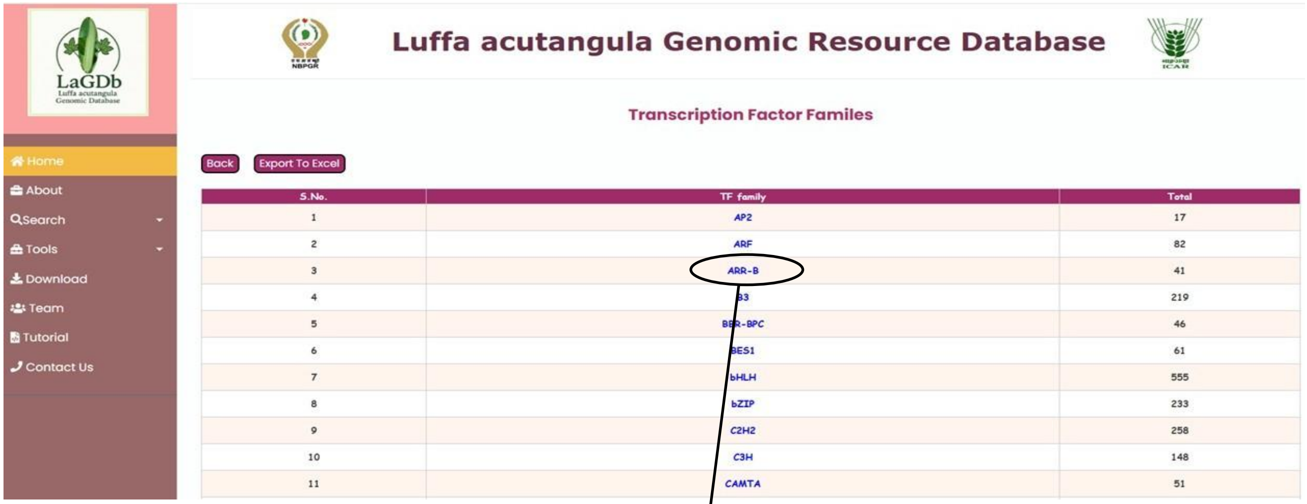
Primer pair-2

SSR Id	Forward Primer	Length	TM	GC%	Reverse Primer	Length	TM	GC%	Product Size
LaSSR105009	CTATCATTGTCGTCGTTGTCG	21	57.2	47.62	TGATGATGATGATGGTGGTGG	21	57.78	47.62	192

Primer pair-3

SSR Id	Forward Primer	Length	TM	GC%	Reverse Primer	Length	TM	GC%	Product Size
LaSSR105009	TATCATTGTCGTCGTTGTCG	20	56.03	45	TGATGATGATGATGGTGGTGG	21	57.78	47.62	191

- By clicking on "More info" tag, under Get TF Families block, user will get all TF categories information with the number details.

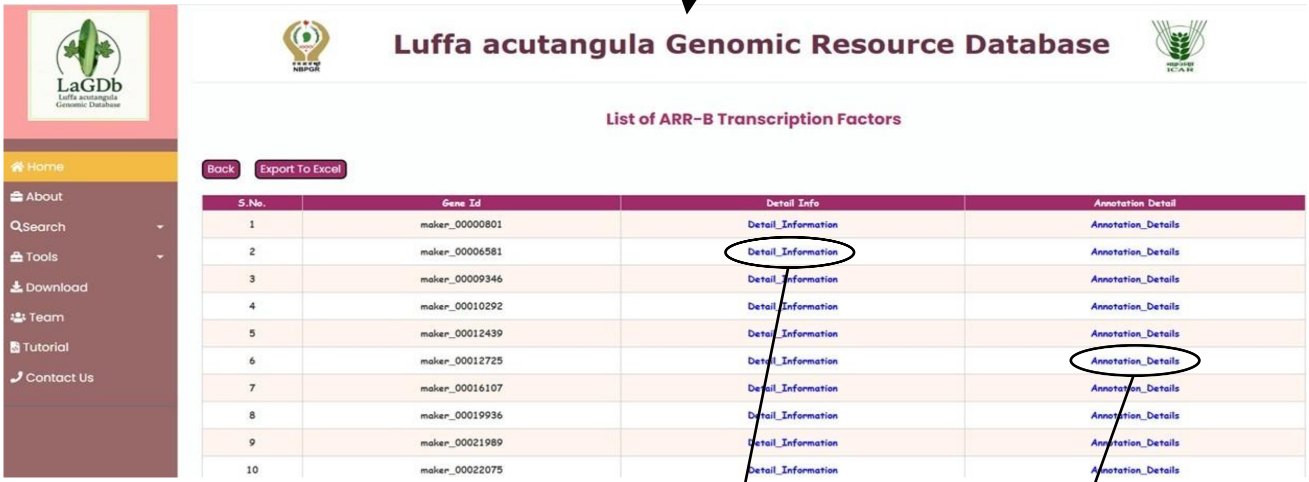


Luffa acutangula Genomic Resource Database

Transcription Factor Familes

S.No.	TF family	Total
1	AP2	17
2	ARF	82
3	ARR-B	41
4	B3	219
5	BBR-BPC	46
6	BES1	61
7	bHLH	555
8	bZIP	233
9	C2H2	258
10	C3H	148
11	CAMTA	51

By clicking on particular category link, user will get list of TFs in that particular category. User can also get the similar details by clicking on that TF category displayed on the circular diagram. eg. ARR-B

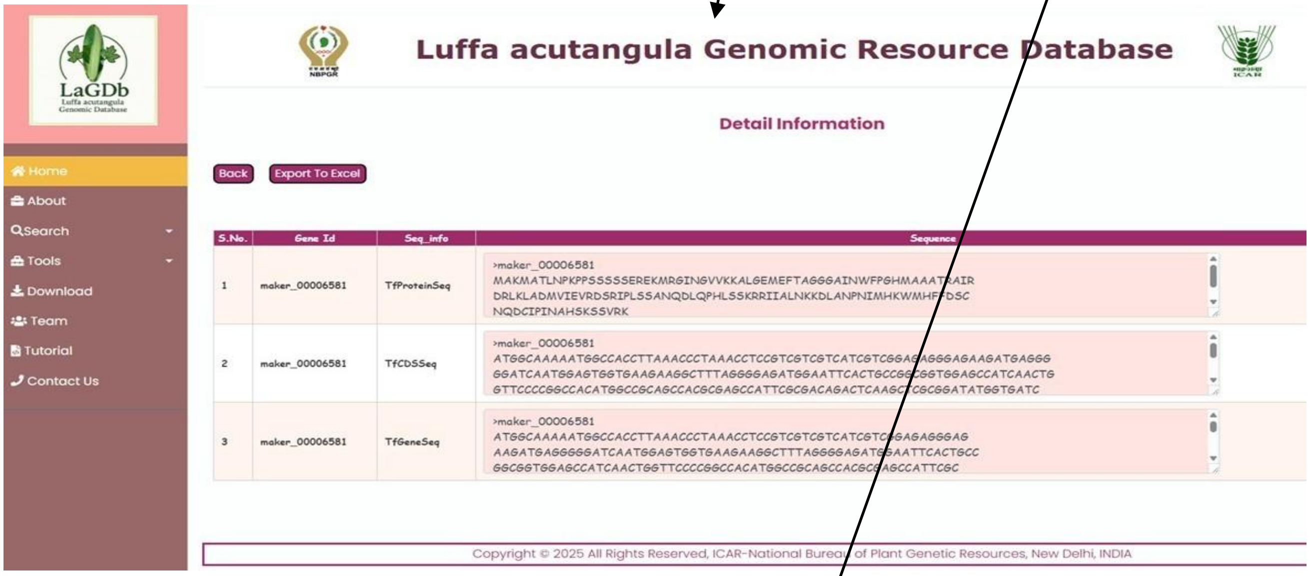


Luffa acutangula Genomic Resource Database

List of ARR-B Transcription Factors

S.No.	Gene Id	Detail Info	Annotation Detail
1	maker_00000801	Detail_Information	Annotation_Details
2	maker_00006581	Detail_Information	Annotation_Details
3	maker_00009346	Detail_Information	Annotation_Details
4	maker_00010292	Detail_Information	Annotation_Details
5	maker_00012439	Detail_Information	Annotation_Details
6	maker_00012725	Detail_Information	Annotation_Details
7	maker_00016107	Detail_Information	Annotation_Details
8	maker_00019936	Detail_Information	Annotation_Details
9	maker_00021989	Detail_Information	Annotation_Details
10	maker_00022075	Detail_Information	Annotation_Details

By clicking on the Detail_Information link, it will give protein, CDS, and gene sequences of selected TF.

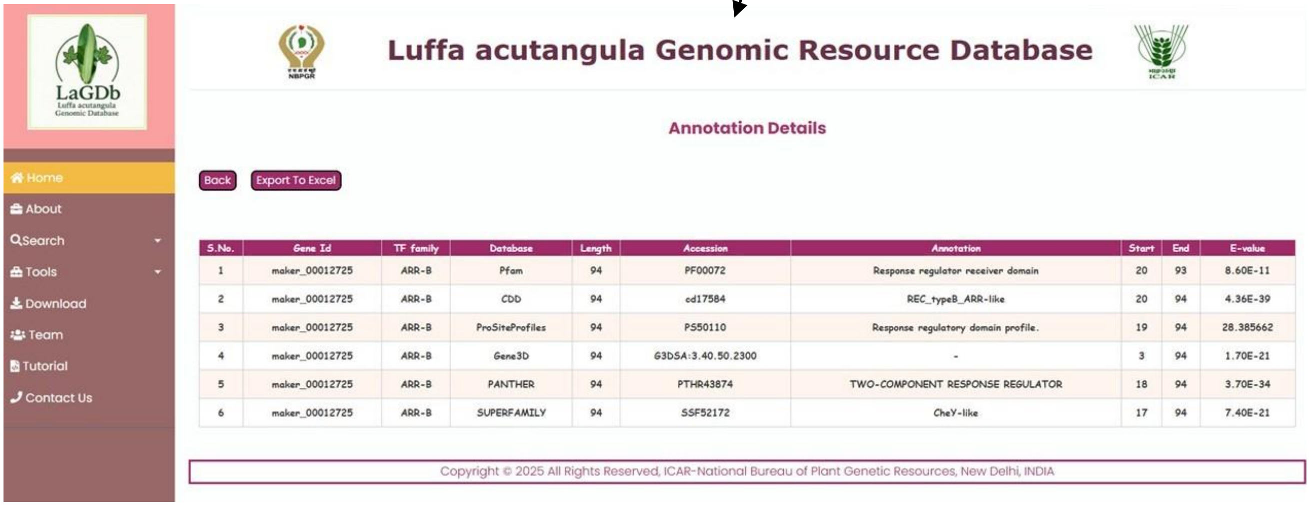


Luffa acutangula Genomic Resource Database

Detail Information

S.No.	Gene Id	Seq_info	Sequence
1	maker_00006581	TfProteinSeq	>maker_00006581 MAKMATLNPKPPSSSSSEREKMRGINGVVKKALGEMEFTAGGGAINWFPGHMAAATRAIR DRLKLADMVIEVRDSRIPLSSANQDLQPHLSSKRRIIALNKKDLANPNIMHKWMHFFDSC NQDCIPINAHSKSSVRK
2	maker_00006581	TfCDSSeq	>maker_00006581 ATGGCAAAAATGGCCACCTTAAACCCTAAACCTCCGTCGTCGTCATCGTCGGAGAGGGAGAAGATGAGGG GGATCAATGGAGTGGTGAAGAAGGCTTTAGGGGAGATGGAATTCACTGCCGGCGGTGGAGCCATCAACTG GTTCCCCGGCCACATGGCCGCAGCCACGCGAGCCATTCGCGACAGACTCAAGCTCGCGGATATGGTGATC
3	maker_00006581	TfGeneSeq	>maker_00006581 ATGGCAAAAATGGCCACCTTAAACCCTAAACCTCCGTCGTCGTCATCGTCGGAGAGGGAG AAGATGAGGGGGATCAATGGAGTGGTGAAGAAGGCTTTAGGGGAGATGGAATTCACTGCC GGCGGTGGAGCCATCAACTGGTTCCCCGGCCACATGGCCGCAGCCACGCGAGCCATTCGC

By clicking on the Annotation_Details link, user will get annotation information of selected TF with InterProScan databases.



Luffa acutangula Genomic Resource Database

Annotation Details

S.No.	Gene Id	TF family	Database	Length	Accession	Annotation	Start	End	E-value
1	maker_00012725	ARR-B	Pfam	94	PF00072	Response regulator receiver domain	20	93	8.60E-11
2	maker_00012725	ARR-B	CDD	94	cd17584	REC_typeB_ARR-like	20	94	4.36E-39
3	maker_00012725	ARR-B	ProSiteProfiles	94	PS50110	Response regulatory domain profile.	19	94	28.385662
4	maker_00012725	ARR-B	Gene3D	94	G3DSA:3.40.50.2300	-	3	94	1.70E-21
5	maker_00012725	ARR-B	PANTHER	94	PTHR43874	TWO-COMPONENT RESPONSE REGULATOR	18	94	3.70E-34
6	maker_00012725	ARR-B	SUPERFAMILY	94	SSF52172	CheY-like	17	94	7.40E-21

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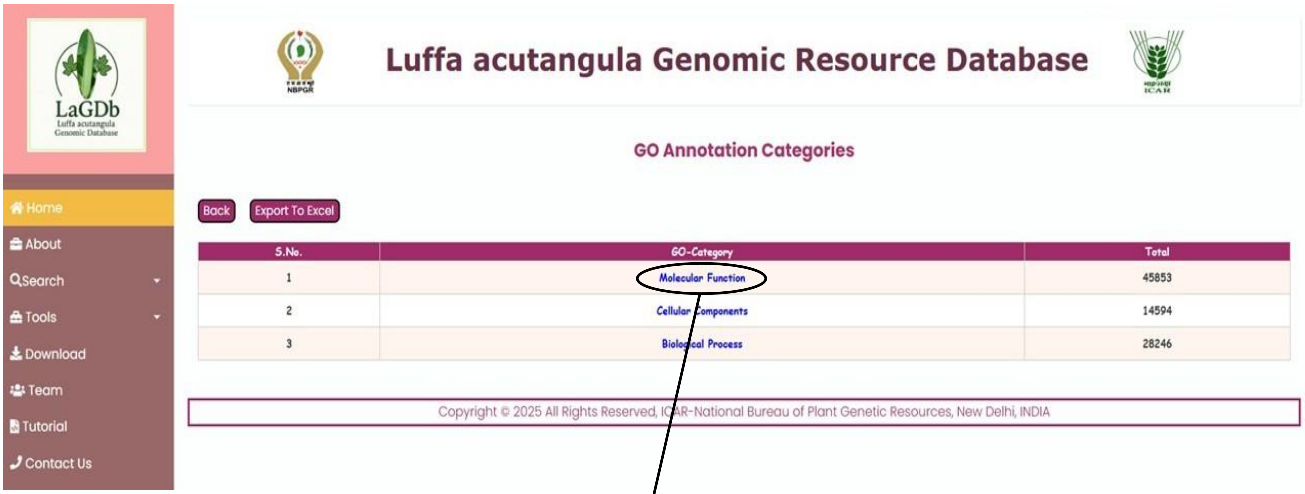
- ❖ By clicking on "More info" tag, under Get GO Annotation block, user will get three categories information with the number details.



Luffa acutangula Genomic Resource Database

GO Annotation Categories

S.No.	GO-Category	Total
1	Molecular Function	45853
2	Cellular Components	14594
3	Biological Process	28246

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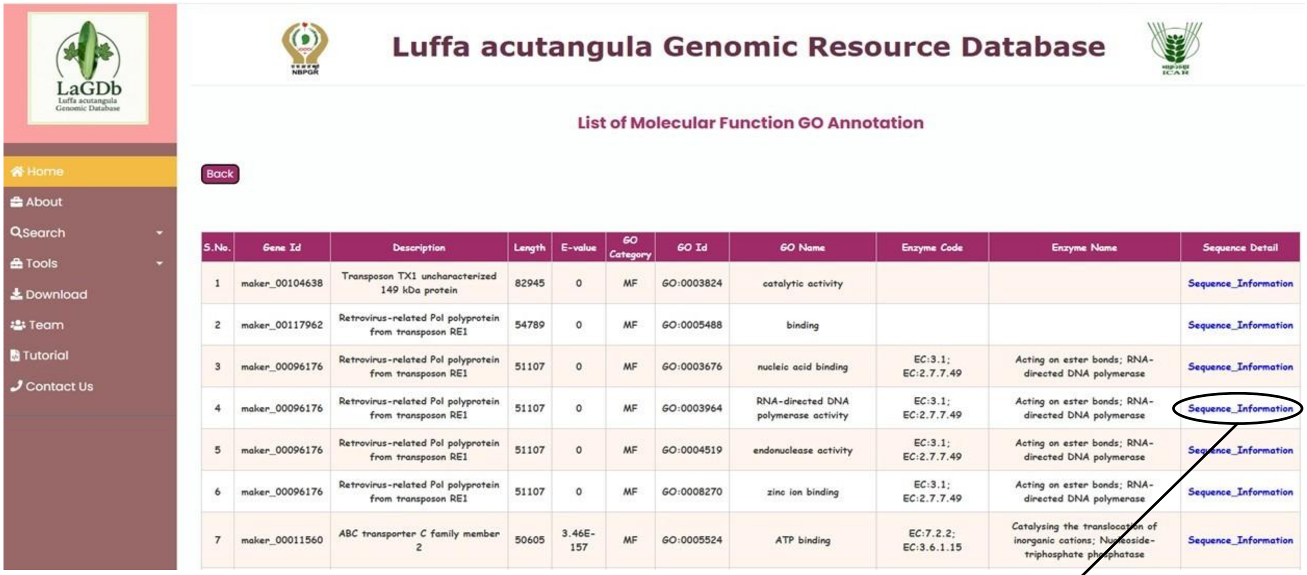
By clicking on the selected category link, user will get list of annotated gene information of this category. User can also get the similar details by clicking on that GO categories displayed on the circular diagram. eg. Molecular Function

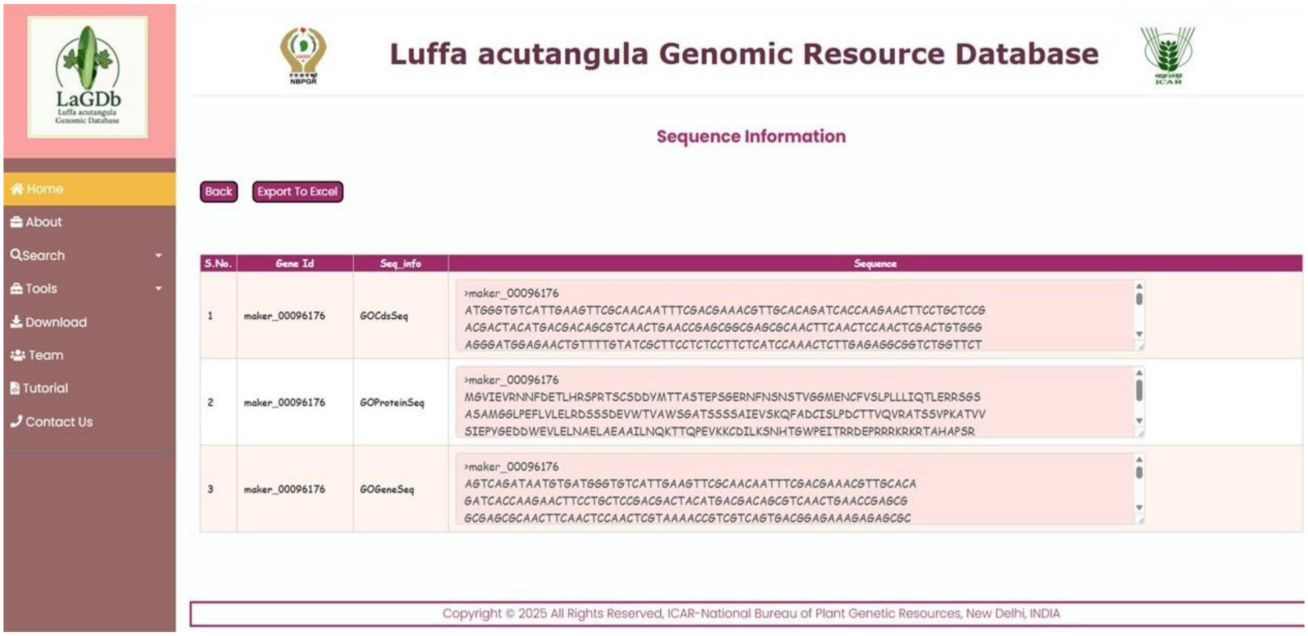


Luffa acutangula Genomic Resource Database

List of Molecular Function GO Annotation

S.No.	Gene Id	Description	Length	E-value	GO Category	GO Id	GO Name	Enzyme Code	Enzyme Name	Sequence Detail
1	maker_00104638	Transposon TX1 uncharacterized 149 kDa protein	82945	0	MF	GO:0003824	catalytic activity			Sequence_Information
2	maker_00117962	Retrovirus-related Pol polyprotein from transposon RE1	54789	0	MF	GO:0005488	binding			Sequence_Information
3	maker_00096176	Retrovirus-related Pol polyprotein from transposon RE1	51107	0	MF	GO:0003676	nucleic acid binding	EC:3.1; EC:2.7.7.49	Acting on ester bonds; RNA-directed DNA polymerase	Sequence_Information
4	maker_00096176	Retrovirus-related Pol polyprotein from transposon RE1	51107	0	MF	GO:0003964	RNA-directed DNA polymerase activity	EC:3.1; EC:2.7.7.49	Acting on ester bonds; RNA-directed DNA polymerase	Sequence_Information
5	maker_00096176	Retrovirus-related Pol polyprotein from transposon RE1	51107	0	MF	GO:0004519	endonuclease activity	EC:3.1; EC:2.7.7.49	Acting on ester bonds; RNA-directed DNA polymerase	Sequence_Information
6	maker_00096176	Retrovirus-related Pol polyprotein from transposon RE1	51107	0	MF	GO:0008270	zinc ion binding	EC:3.1; EC:2.7.7.49	Acting on ester bonds; RNA-directed DNA polymerase	Sequence_Information
7	maker_00011560	ABC transporter C family member 2	50605	3.46E-157	MF	GO:0005524	ATP binding	EC:7.2.2; EC:3.6.1.15	Catalysing the translocation of inorganic cations; Nucleoside-triphosphate phosphatase	Sequence_Information

By clicking on the Sequence_Information link, user will get protein, CDS, and gene sequence information.



Sequence Information

S.No.	Gene Id	Seq_info	Sequence
1	maker_00096176	GOCdsSeq	>maker_00096176 ATGGGTGTCATTGAAGTTCGCAACAATTTCGACGAAACGTTGCACAGATCACCAAGAACTTCCTGCTCCG ACGACTACATGACGACAGCGTCAACTGAACCGAGCGGCGAGCGCAACTTCAACTCCAACTCGACTGTGGG AGGGATGGAGAACTGTTTTGTATCGCTTCCTCTCCTTCTCATCCAAACTCTTGAGAGGCGGTCTGGTTCT
2	maker_00096176	GOProteinSeq	>maker_00096176 MGVIEVRNNFDETLHRSPRTSCSDDYMTTASTEPSGERNFNSNSTVGGMENCFVSLPLLLIQTLERRSGS ASAMGGLPEFLVLELRDSSSDEVWTVAWSGATSSSSAIEVSKQFADCISLPDCTTVQVRATSSVPKATVV SIEPYGEDDWEVLELNAELAEAAILNQKTTQPEVKKCDILKSNHTGWPEITRRDEPRRRKRKRTAHAPSR
3	maker_00096176	GOGeneSeq	>maker_00096176 AGTCAGATAATGTGATGGGTGTCATTGAAGTTCGCAACAATTTCGACGAAACGTTGCACA GATCACCAAGAACTTCCTGCTCCGACGACTACATGACGACAGCGTCAACTGAACCGAGCG GCGAGCGCAACTTCAACTCCAACTCGTAAAACCGTCGTCAGTGACGGAGAAAGAGAGCGC

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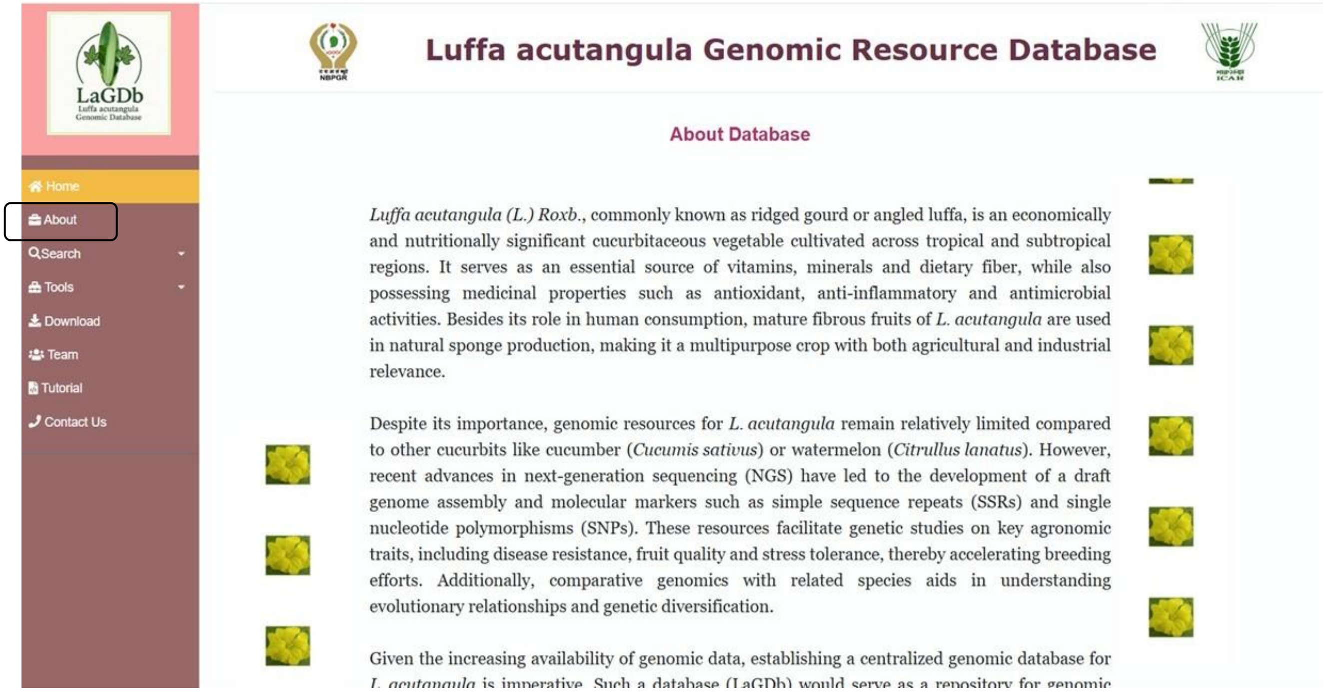
2. **About:** The About page describes the **purpose and background of the database**. It includes details on the project objectives, data source, and the significance of the developed genomic resource for research and crop improvement.



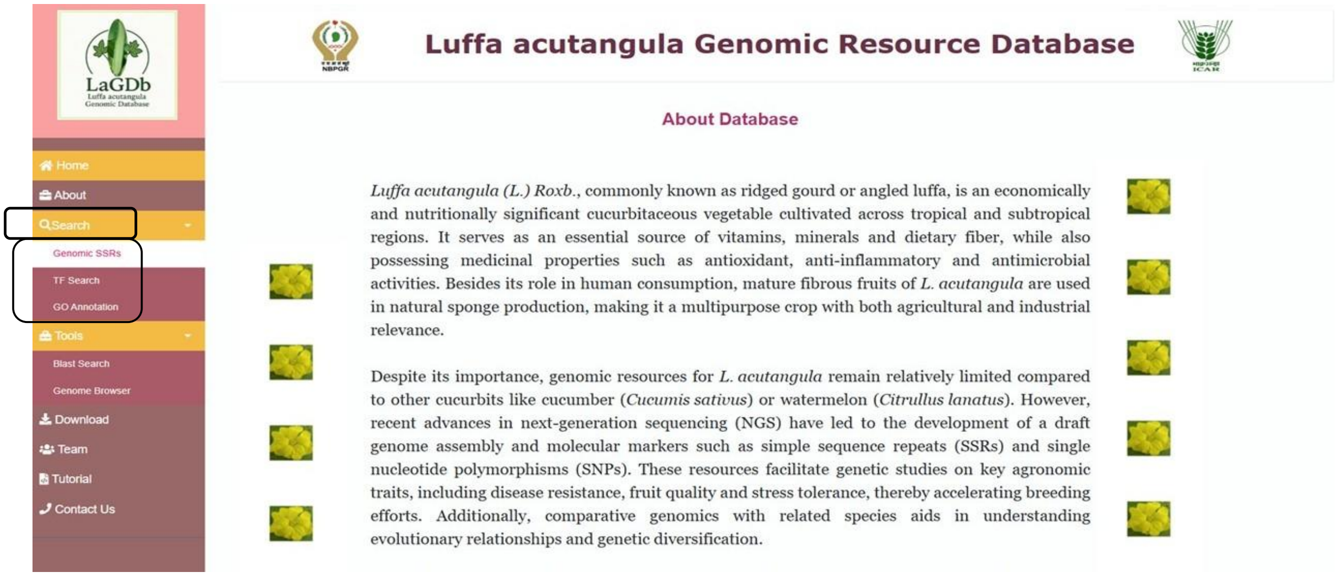
About Database

Luffa acutangula (L.) Roxb., commonly known as ridged gourd or angled luffa, is an economically and nutritionally significant cucurbitaceous vegetable cultivated across tropical and subtropical regions. It serves as an essential source of vitamins, minerals and dietary fiber, while also possessing medicinal properties such as antioxidant, anti-inflammatory and antimicrobial activities. Besides its role in human consumption, mature fibrous fruits of *L. acutangula* are used in natural sponge production, making it a multipurpose crop with both agricultural and industrial relevance.

Despite its importance, genomic resources for *L. acutangula* remain relatively limited compared to other cucurbits like cucumber (*Cucumis sativus*) or watermelon (*Citrullus lanatus*). However, recent advances in next-generation sequencing (NGS) have led to the development of a draft genome assembly and molecular markers such as simple sequence repeats (SSRs) and single nucleotide polymorphisms (SNPs). These resources facilitate genetic studies on key agronomic traits, including disease resistance, fruit quality and stress tolerance, thereby accelerating breeding efforts. Additionally, comparative genomics with related species aids in understanding evolutionary relationships and genetic diversification.

Given the increasing availability of genomic data, establishing a centralized genomic database for *L. acutangula* is imperative. Such a database (LaGDb) would serve as a repository for genomic

3. **Search:** The Search section allows users to query based search for different datasets such as **genomic SSRs**, **transcription factors (TFs),** and **GO annotation** search.



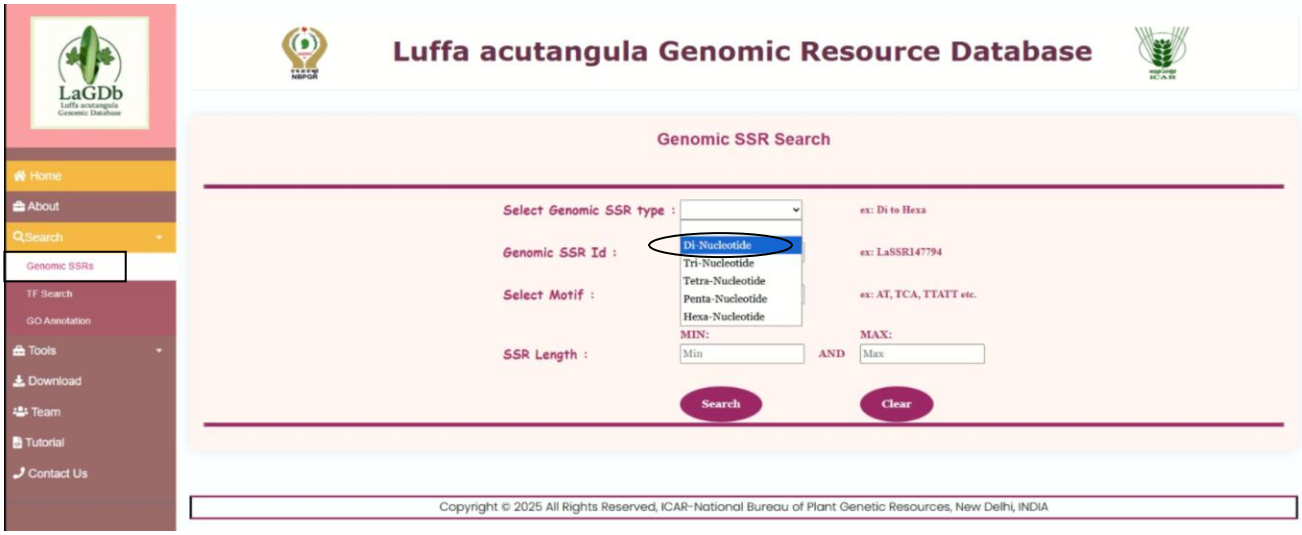
Luffa acutangula Genomic Resource Database

About Database

Luffa acutangula (L.) Roxb., commonly known as ridged gourd or angled luffa, is an economically and nutritionally significant cucurbitaceous vegetable cultivated across tropical and subtropical regions. It serves as an essential source of vitamins, minerals and dietary fiber, while also possessing medicinal properties such as antioxidant, anti-inflammatory and antimicrobial activities. Besides its role in human consumption, mature fibrous fruits of *L. acutangula* are used in natural sponge production, making it a multipurpose crop with both agricultural and industrial relevance.

Despite its importance, genomic resources for *L. acutangula* remain relatively limited compared to other cucurbits like cucumber (*Cucumis sativus*) or watermelon (*Citrullus lanatus*). However, recent advances in next-generation sequencing (NGS) have led to the development of a draft genome assembly and molecular markers such as simple sequence repeats (SSRs) and single nucleotide polymorphisms (SNPs). These resources facilitate genetic studies on key agronomic traits, including disease resistance, fruit quality and stress tolerance, thereby accelerating breeding efforts. Additionally, comparative genomics with related species aids in understanding evolutionary relationships and genetic diversification.

- **Genomic SSR Search:** Search for genomic SSRs using different search parameters such as by selecting SSR Type; search by SSR Id, Sequence motif, Min and Max sequence lengths etc. eg. Select SSR Type from dropdown list



Luffa acutangula Genomic Resource Database

Genomic SSR Search

Select Genomic SSR type : ex: Di to Hexa

Genomic SSR Id : ex: LaSSR147794

Select Motif : ex: AT, TCA, TTATT etc.

SSR Length : MIN: Min AND MAX: Max

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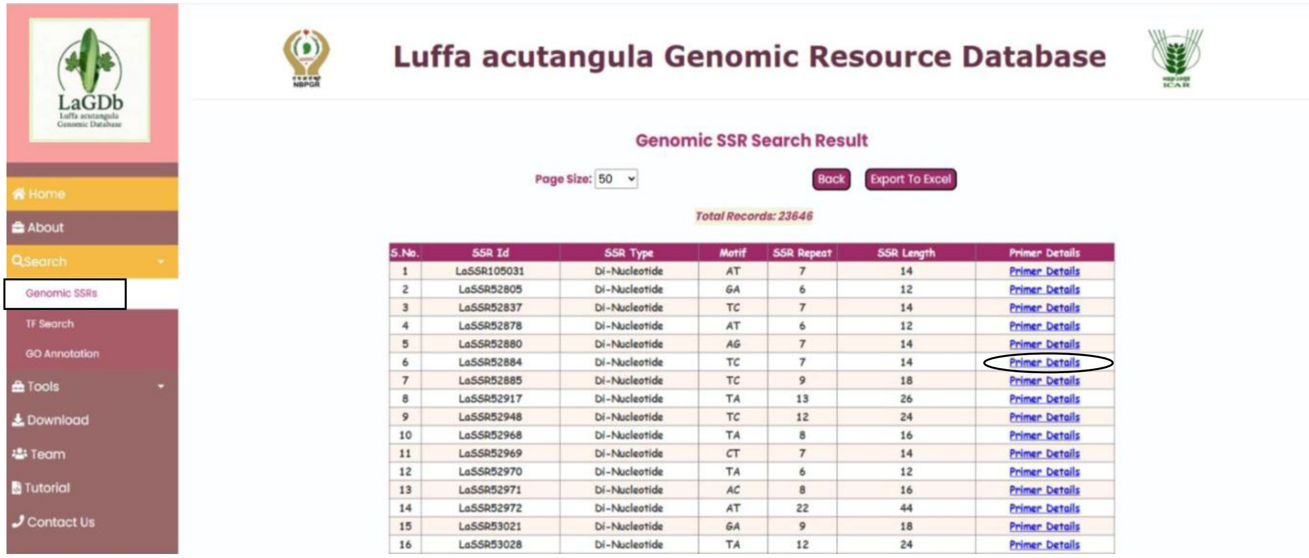
By selecting Di-Nucleotide from dropdown list and click on search button, it will display list of Di-Nucleotide type of genomic SSRs with a link of Primer_Details.



Luffa acutangula Genomic Resource Database

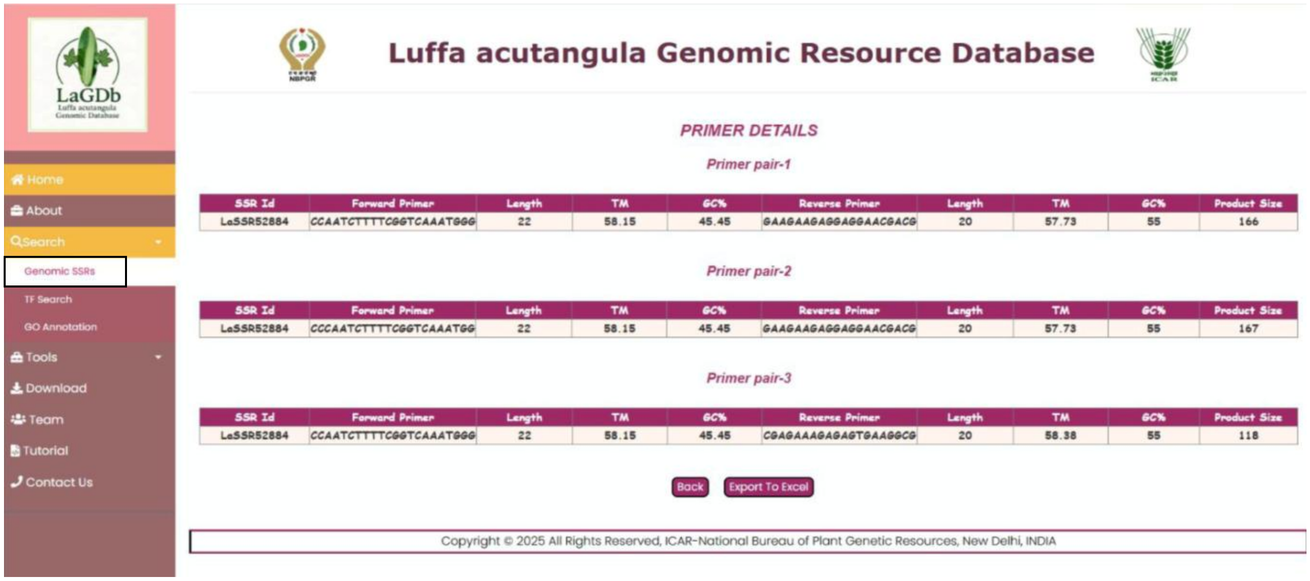
Genomic SSR Search Result

Page Size: 50

Total Records: 23646

S.No.	SSR Id	SSR Type	Motif	SSR Repeat	SSR Length	Primer Details
1	LaSSR105031	Di-Nucleotide	AT	7	14	Primer Details
2	LaSSR52805	Di-Nucleotide	GA	6	12	Primer Details
3	LaSSR52837	Di-Nucleotide	TC	7	14	Primer Details
4	LaSSR52878	Di-Nucleotide	AT	6	12	Primer Details
5	LaSSR52880	Di-Nucleotide	AG	7	14	Primer Details
6	LaSSR52884	Di-Nucleotide	TC	7	14	Primer Details
7	LaSSR52885	Di-Nucleotide	TC	9	18	Primer Details
8	LaSSR52917	Di-Nucleotide	TA	13	26	Primer Details
9	LaSSR52948	Di-Nucleotide	TC	12	24	Primer Details
10	LaSSR52968	Di-Nucleotide	TA	8	16	Primer Details
11	LaSSR52969	Di-Nucleotide	CT	7	14	Primer Details
12	LaSSR52970	Di-Nucleotide	TA	6	12	Primer Details
13	LaSSR52971	Di-Nucleotide	AC	8	16	Primer Details
14	LaSSR52972	Di-Nucleotide	AT	22	44	Primer Details
15	LaSSR53021	Di-Nucleotide	GA	9	18	Primer Details
16	LaSSR53028	Di-Nucleotide	TA	12	24	Primer Details

By clicking on the Primer Details link, it will give three primer pair information of selected genomic SSR.



Luffa acutangula Genomic Resource Database

PRIMER DETAILS

Primer pair-1

SSR Id	Forward Primer	Length	TM	GC%	Reverse Primer	Length	TM	GC%	Product Size
LaSSR52884	CCAATCTTTTCGGTCAAATGGG	22	58.15	45.45	GAAGAAGAGGAGGAACGACG	20	57.73	55	166

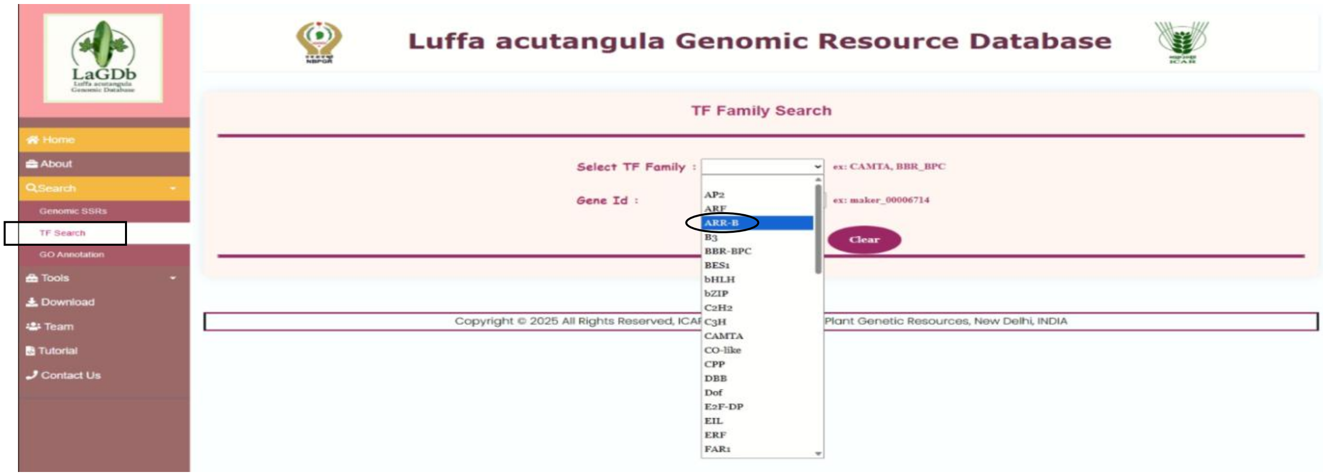
Primer pair-2

SSR Id	Forward Primer	Length	TM	GC%	Reverse Primer	Length	TM	GC%	Product Size
LaSSR52884	CCCAATCTTTTCGGTCAAATGG	22	58.15	45.45	GAAGAAGAGGAGGAACGACG	20	57.73	55	167

Primer pair-3

SSR Id	Forward Primer	Length	TM	GC%	Reverse Primer	Length	TM	GC%	Product Size
LaSSR52884	CCAATCTTTTCGGTCAAATGGG	22	58.15	45.45	CGAGAAAGAGAGTGAAGGCG	20	58.38	55	118

❖ **Transcription Factors (TFs) Search:** Search for TFs using different search parameters such as by selecting TF family and search by Gene Id.



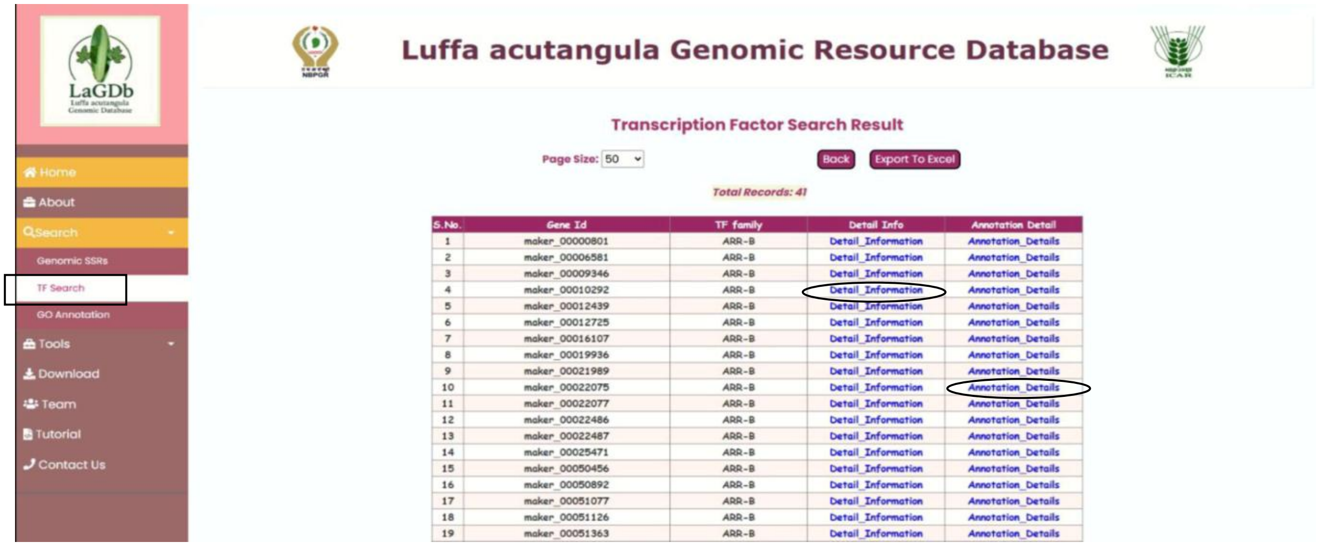
Luffa acutangula Genomic Resource Database

TF Family Search

Select TF Family : ex: CAMTA, BBR_BPC

Gene Id : ex: maker_00006714

By selecting TF family from dropdown list and click on search button, it will display list of TFs in that selected category with a links Detail_Information and Annotation_Details.



Luffa acutangula Genomic Resource Database

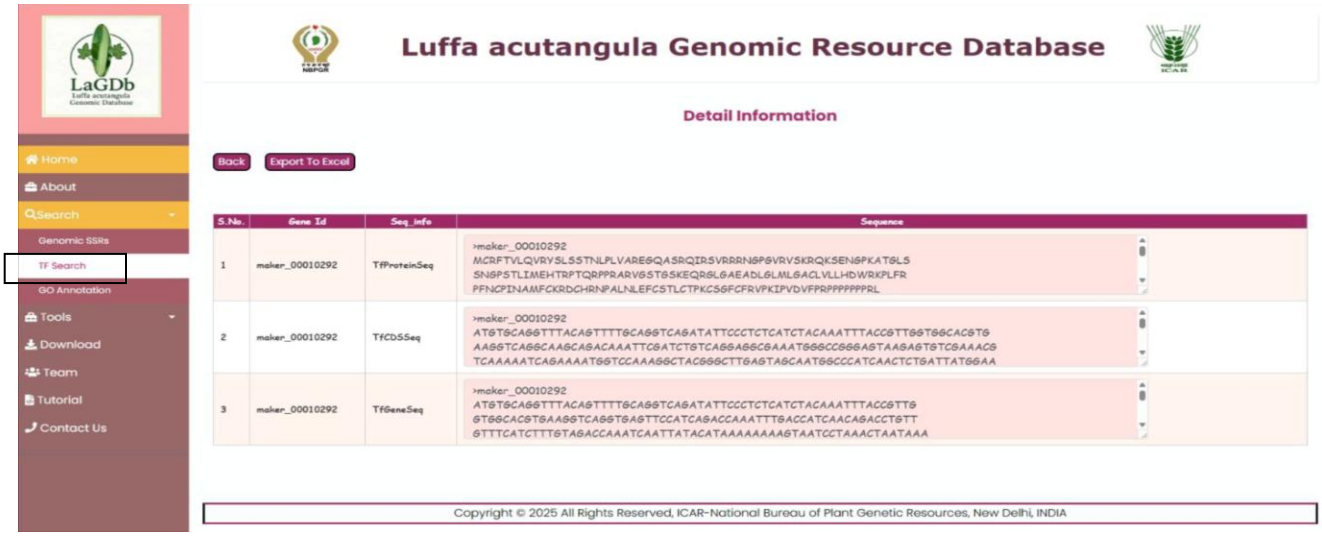
Transcription Factor Search Result

Page Size: 50

Total Records: 41

S.No.	Gene Id	TF family	Detail Info	Annotation Detail
1	maker_00000801	ARR-B	Detail_Information	Annotation_Details
2	maker_00006581	ARR-B	Detail_Information	Annotation_Details
3	maker_00009346	ARR-B	Detail_Information	Annotation_Details
4	maker_00010292	ARR-B	Detail_Information	Annotation_Details
5	maker_00012439	ARR-B	Detail_Information	Annotation_Details
6	maker_00012725	ARR-B	Detail_Information	Annotation_Details
7	maker_00016107	ARR-B	Detail_Information	Annotation_Details
8	maker_00019936	ARR-B	Detail_Information	Annotation_Details
9	maker_00021989	ARR-B	Detail_Information	Annotation_Details
10	maker_00022075	ARR-B	Detail_Information	Annotation_Details
11	maker_00022077	ARR-B	Detail_Information	Annotation_Details
12	maker_00022486	ARR-B	Detail_Information	Annotation_Details
13	maker_00022487	ARR-B	Detail_Information	Annotation_Details
14	maker_00025471	ARR-B	Detail_Information	Annotation_Details
15	maker_00050456	ARR-B	Detail_Information	Annotation_Details
16	maker_00050892	ARR-B	Detail_Information	Annotation_Details
17	maker_00051077	ARR-B	Detail_Information	Annotation_Details
18	maker_00051126	ARR-B	Detail_Information	Annotation_Details
19	maker_00051363	ARR-B	Detail_Information	Annotation_Details

By clicking on the Detail_Information link, it will give protein, CDS, and gene sequences of selected TF.



Luffa acutangula Genomic Resource Database

Detail Information

S.No.	Gene Id	Seq_info	Sequence
1	maker_00010292	TfProteinSeq	>maker_00010292 MCRFTVLQVRYSLSSTNLPLVAREGQASRQIRSVRRRNGPGVRVSKRQKSENGPKATGLS SNGPSTLIMEHTRPTQRPPRARVGSTGSKEQRGLGAEADLGLMLGACLVLLHDWRKPLFR PFNCPINAMFCKRDCHRNPALNLEFCSTLCTPKCSGFCFRVPKIPVDVFPRPPPPPPPRL
2	maker_00010292	TfCDSSeq	>maker_00010292 ATGTGCAGGTTTACAGTTTTGCAGGTCAGATATTCCCTCTCATCTACAAATTTACCGTTGGTGGCACGTG AAGGTCAGGCAAGCAGACAAATTCGATCTGTCAGGAGGCGAAATGGGCCGGGAGTAAGAGTGTCGAAACG TCAAAAATCAGAAAATGGTCCAAAGGCTACGGGCTTGAGTAGCAATGGCCCATCAACTCTGATTATGGAA
3	maker_00010292	TfGeneSeq	>maker_00010292 ATGTGCAGGTTTACAGTTTTGCAGGTCAGATATTCCCTCTCATCTACAAATTTACCGTTG GTGGCACGTGAAGGTCAGGTGAGTTCCATCAGACCAAATTTGACCATCAACAGACCTGTT GTTTCATCTTTGTAGACCAAATCAATTATACATAAAAAAAAGTAATCCTAAACTAATAAA

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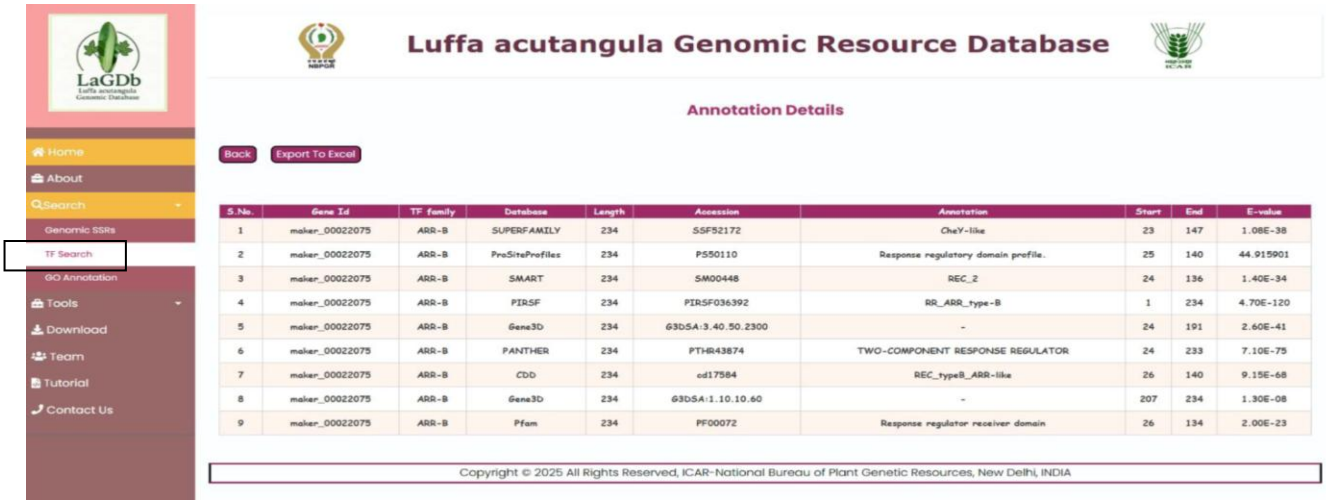
By clicking on the Annotation_Details link, user will get annotation information of selected TF with InterProScan databases.



Luffa acutangula Genomic Resource Database

Annotation Details

S.No.	Gene Id	TF family	Database	Length	Accession	Annotation	Start	End	E-value
1	maker_00022075	ARR-B	SUPERFAMILY	234	SSF52172	CheY-like	23	147	1.08E-38
2	maker_00022075	ARR-B	ProSiteProfiles	234	PS50110	Response regulatory domain profile.	25	140	44.915901
3	maker_00022075	ARR-B	SMART	234	SM00448	REC_2	24	136	1.40E-34
4	maker_00022075	ARR-B	PIRSF	234	PIRSF036392	RR_ARR_type-B	1	234	4.70E-120
5	maker_00022075	ARR-B	Gene3D	234	G3DSA:3.40.50.2300	-	24	191	2.60E-41
6	maker_00022075	ARR-B	PANTHER	234	PTHR43874	TWO-COMPONENT RESPONSE REGULATOR	24	233	7.10E-75
7	maker_00022075	ARR-B	CDD	234	cd17584	REC_typeB_ARR-like	26	140	9.15E-68
8	maker_00022075	ARR-B	Gene3D	234	G3DSA:1.10.10.60	-	207	234	1.30E-08
9	maker_00022075	ARR-B	Pfam	234	PF00072	Response regulator receiver domain	26	134	2.00E-23

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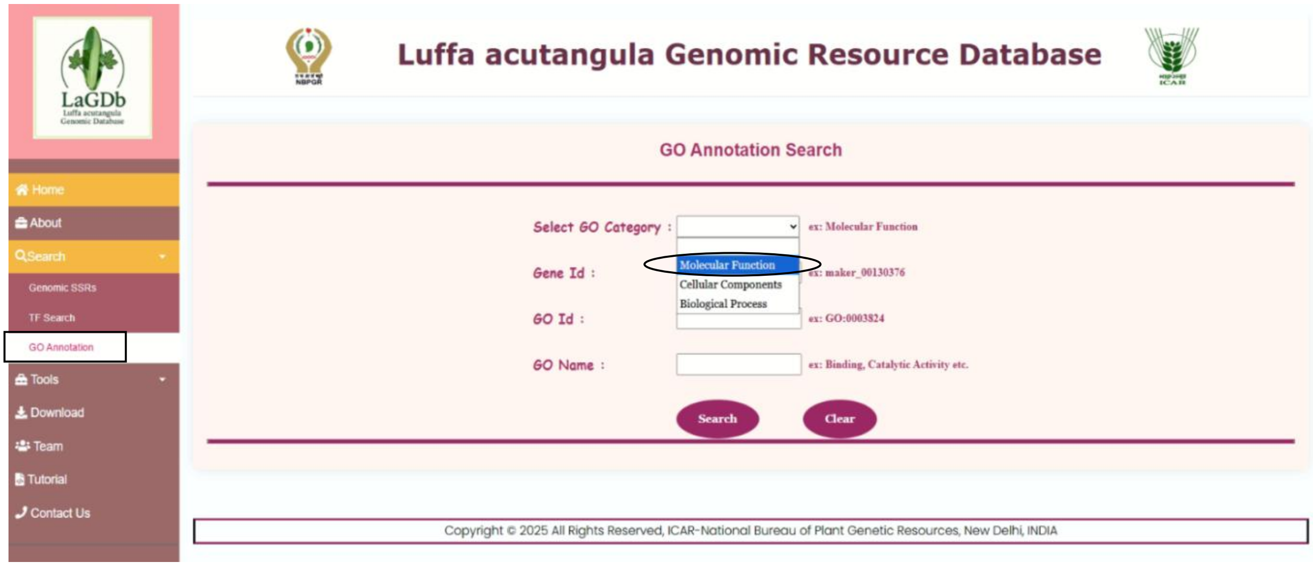
❖ **Gene Ontology (GO) Search:** Search gene ontology based functional annotation using different search parameters such as by selecting GO category, search by Gene Id, GO Id, and GO names.



Luffa acutangula Genomic Resource Database

GO Annotation Search

Select GO Category : ex: Molecular Function
Gene Id : ex: maker_00130376
GO Id : ex: GO:0003824
GO Name : ex: Binding, Catalytic Activity etc.

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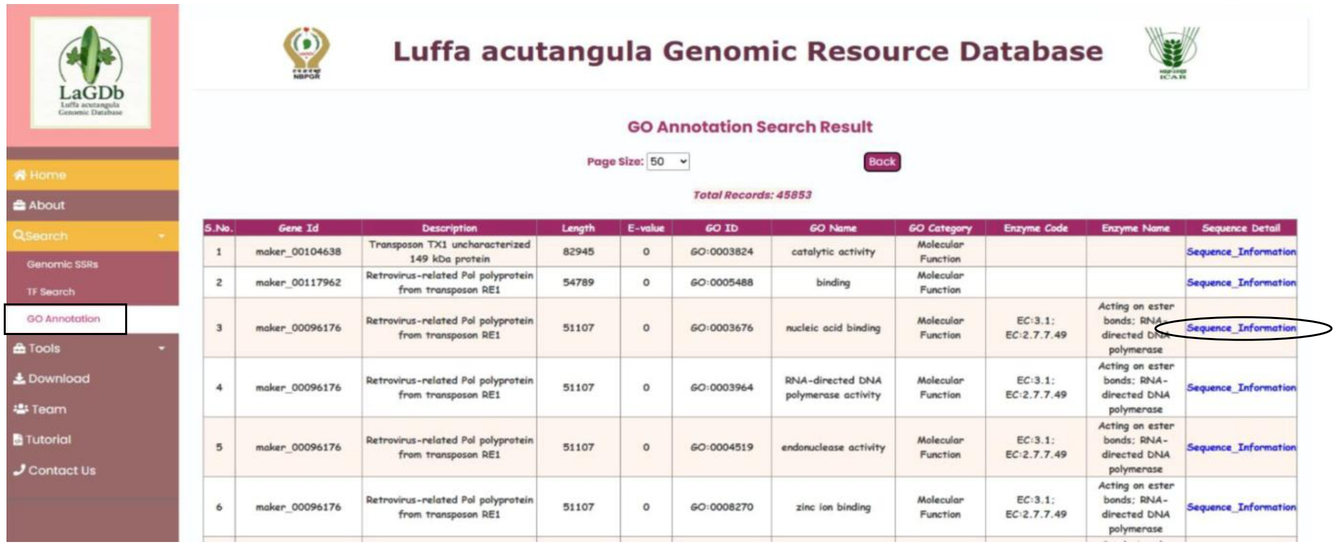
By selecting GO category from the dropdown list and click on search button, it will display list of genes functionally annotated in that selected category with a link of Sequence_Information.



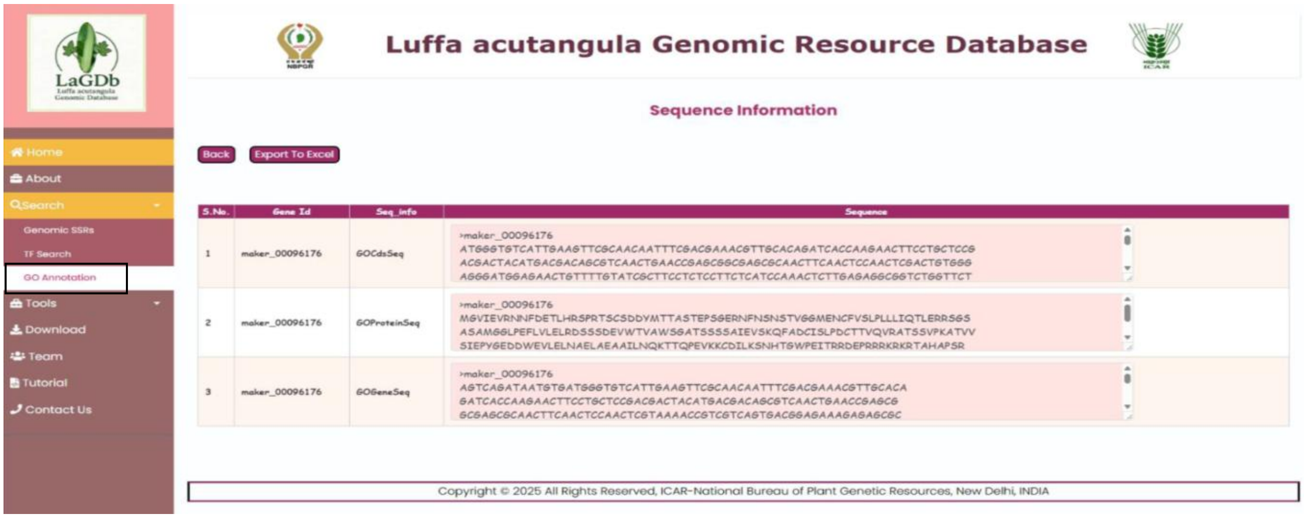
Luffa acutangula Genomic Resource Database

GO Annotation Search Result

Total Records: 45853

S.No.	Gene Id	Description	Length	E-value	GO ID	GO Name	GO Category	Enzyme Code	Enzyme Name	Sequence Detail
1	maker_00104638	Transposon TX1 uncharacterized 149 kDa protein	82945	0	GO:0003824	catalytic activity	Molecular Function			Sequence_Information
2	maker_00117962	Retrovirus-related Pol polyprotein from transposon RE1	54789	0	GO:0005488	binding	Molecular Function			Sequence_Information
3	maker_00096176	Retrovirus-related Pol polyprotein from transposon RE1	51107	0	GO:0003676	nucleic acid binding	Molecular Function	EC:3.1; EC:2.7.7.49	Acting on ester bonds; RNA-directed DNA polymerase	Sequence_Information
4	maker_00096176	Retrovirus-related Pol polyprotein from transposon RE1	51107	0	GO:0003964	RNA-directed DNA polymerase activity	Molecular Function	EC:3.1; EC:2.7.7.49	Acting on ester bonds; RNA-directed DNA polymerase	Sequence_Information
5	maker_00096176	Retrovirus-related Pol polyprotein from transposon RE1	51107	0	GO:0004519	endonuclease activity	Molecular Function	EC:3.1; EC:2.7.7.49	Acting on ester bonds; RNA-directed DNA polymerase	Sequence_Information
6	maker_00096176	Retrovirus-related Pol polyprotein from transposon RE1	51107	0	GO:0008270	zinc ion binding	Molecular Function	EC:3.1; EC:2.7.7.49	Acting on ester bonds; RNA-directed DNA polymerase	Sequence_Information

By clicking on the Sequence_Information link, user will get protein, CDS, and gene sequence information.



Luffa acutangula Genomic Resource Database

Sequence Information

S.No.	Gene Id	Seq_info	Sequence
1	maker_00096176	GOCdsSeq	>maker_00096176 ATGGGTGTCATTGAAGTTCGCAACAATTTCGACGAAACGTTGCACAGATCACCAAGAACTTCCTGCTCCG ACGACTACATGACGACAGCGTCAACTGAACCGAGCGGCGAGCGCAACTTCAACTCCAACTCGACTGTGGG AGGGATGGAGAACTGTTTTGTATCGCTTCCTCTCCTTCTCATCCAAACTCTTGAGAGGCGGTCTGGTTCT
2	maker_00096176	GOProteinSeq	>maker_00096176 MGVIEVRNNFDETLHRSPRTSCSDDYMTTASTEPSGERNFNSNSTVGGMENCFVSLPLLLIQTLERRSGS ASAMGGLPEFLVLELRDSSSDEVWTVAWSGATSSSSAIEVSKQFADCISLPDCTTVQVRATSSVPKATVV SIEPYGEDDWEVLELNAELAEAAILNQKTTQPEVKKCDILKSNHTGWPEITRRDEPRRRKRKRTAHAPSR
3	maker_00096176	GOGeneSeq	>maker_00096176 AGTCAGATAATGTGATGGGTGTCATTGAAGTTCGCAACAATTTCGACGAAACGTTGCACA GATCACCAAGAACTTCCTGCTCCGACGACTACATGACGACAGCGTCAACTGAACCGAGCG GCGAGCGCAACTTCAACTCCAACTCGTAAAACCGTCGTCAGTGACGGAGAAAGAGAGCGC

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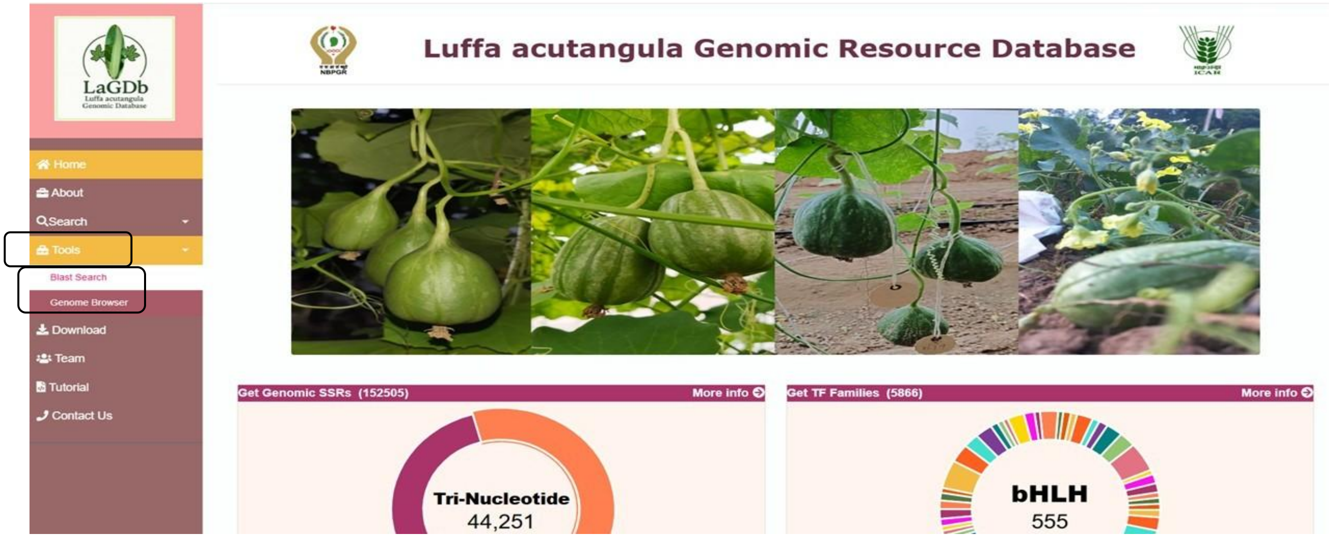
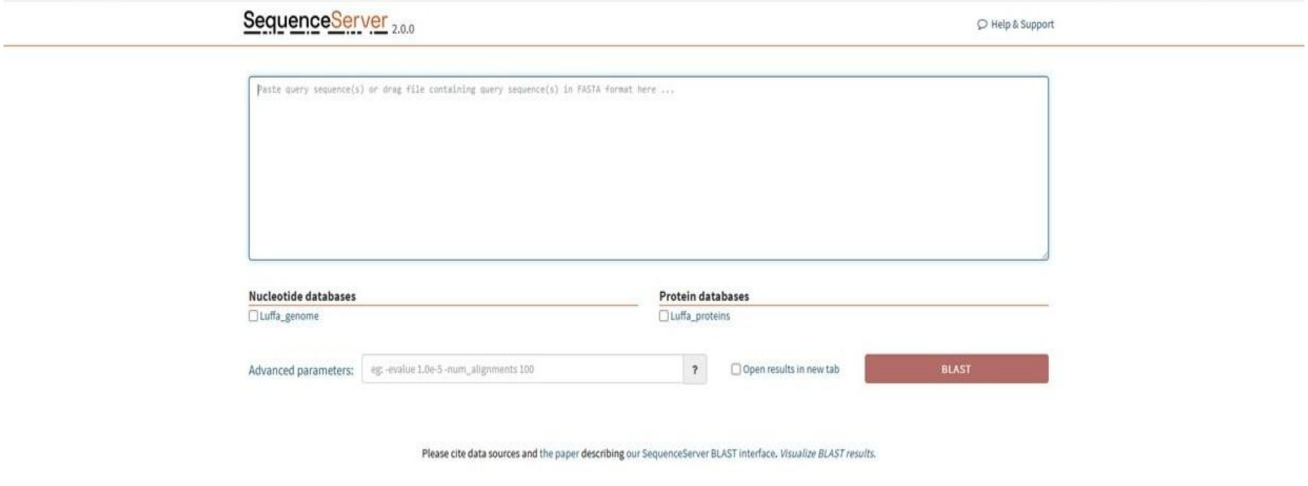
4. **Tools:** The Tools page integrates external bioinformatics applications with the database such as BLAST Search and Genome Browser (JBrowse).

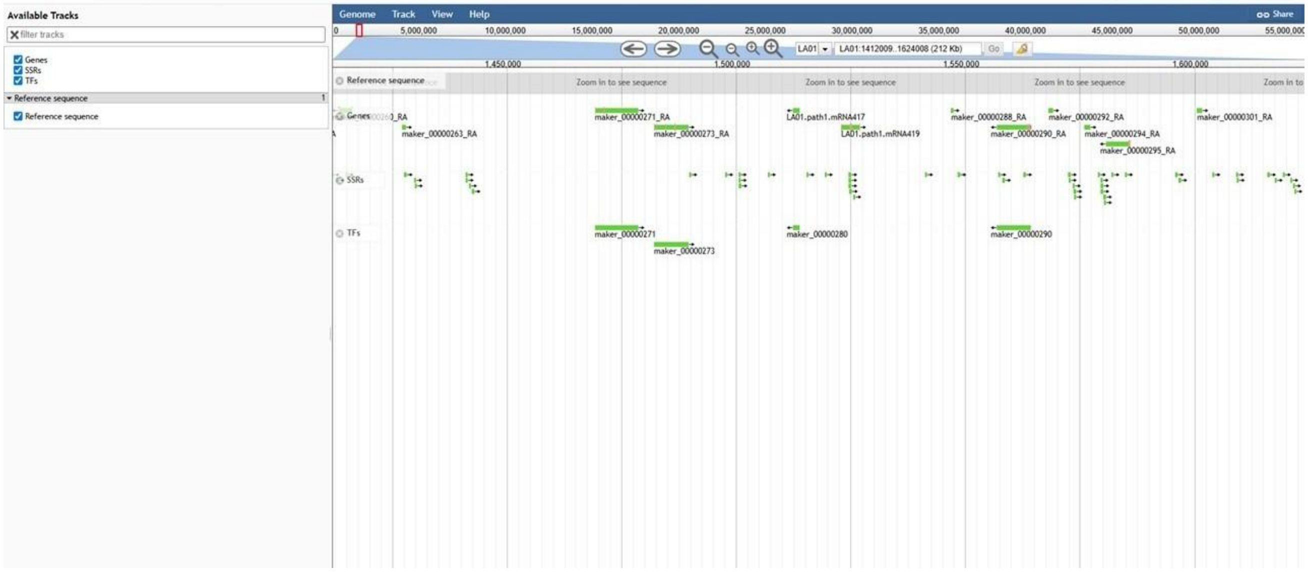


- **BLAST Search:** It performs sequence similarity searches against *Luffa acutangula* genome and proteome datasets.

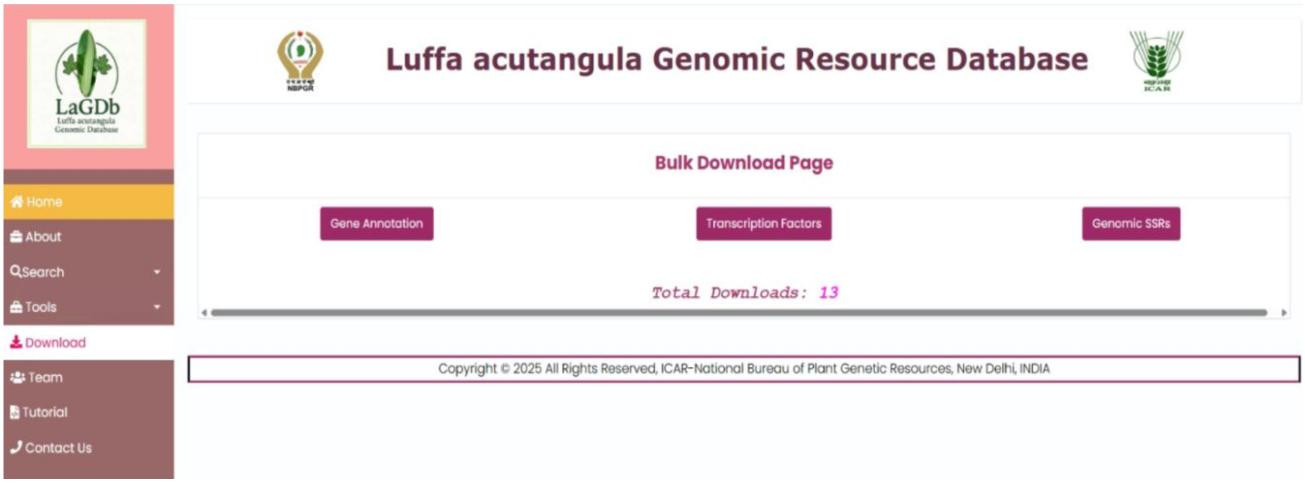


Please cite data sources and the paper describing our SequenceServer BLAST interface. *Visualize BLAST results.*

- **Genome Browser:** It visualizes genomic regions, genes, genomic SSRs, TFs interactively.



5. **Downloads:** The Download section provides direct access to datasets, including genomic SSRs, TFs, and GO annotations. User can download curated files for offline analysis and their research use.



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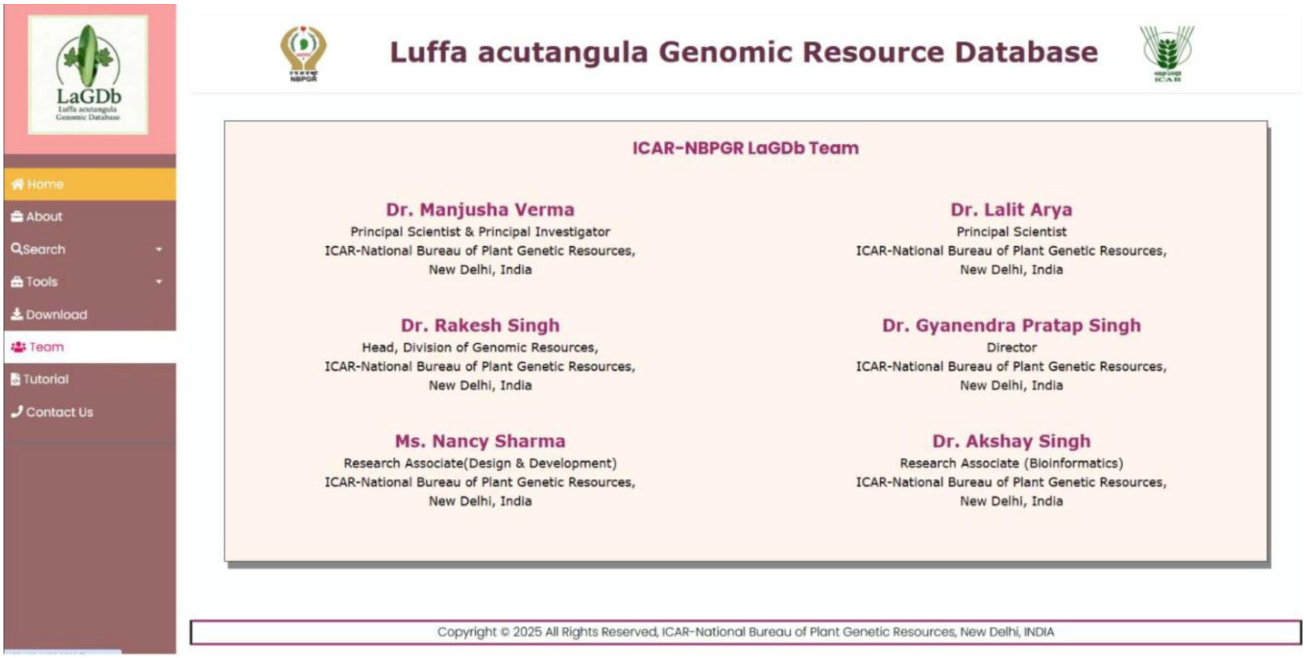
6. **Team:** The Download section provides direct access to datasets, including genomic SSRs, TFs, and GO annotations. User can download curated files for offline analysis and their research use.



Luffa acutangula Genomic Resource Database

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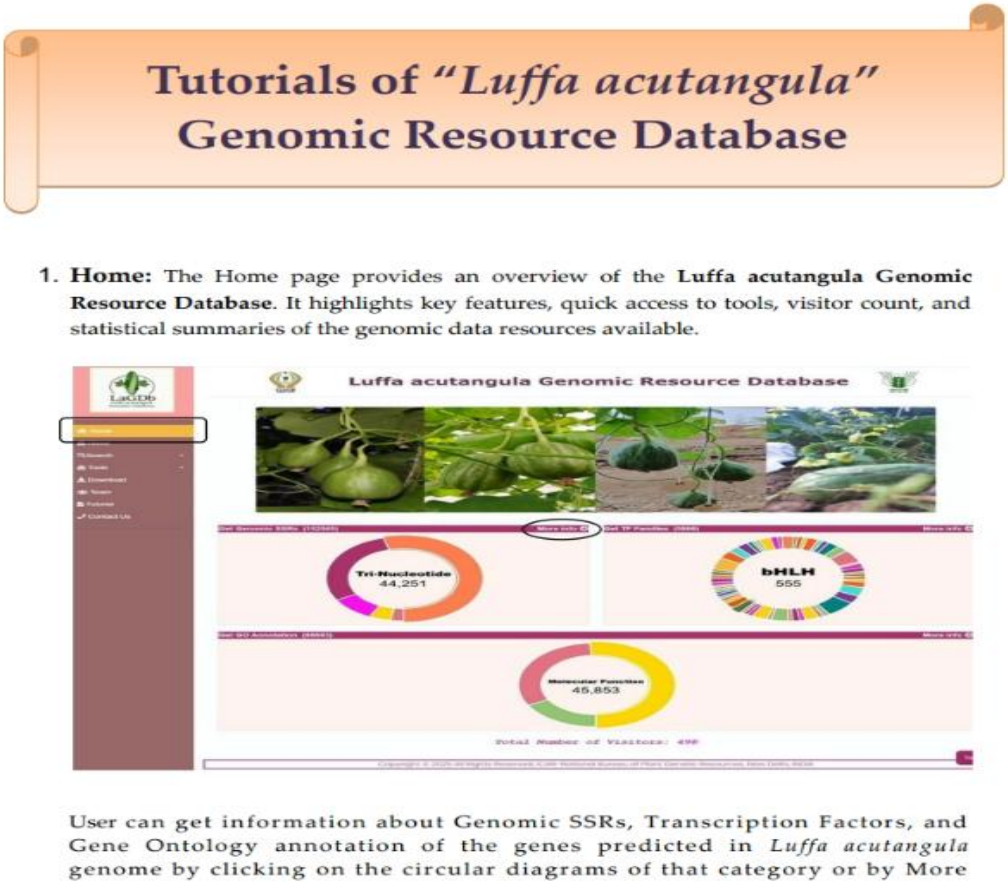
7. **Tutorials:** The Tutorial page offers a step-by-step guide on how to use the database effectively. It includes instructions with screenshots or examples for searching, browsing, downloading data, and using integrated tools like BLAST.



Tutorials of "*Luffa acutangula*"
Genomic Resource Database

1. **Home:** The Home page provides an overview of the **Luffa acutangula Genomic Resource Database**. It highlights key features, quick access to tools, visitor count, and statistical summaries of the genomic data resources available.

User can get information about Genomic SSRs, Transcription Factors, and Gene Ontology annotation of the genes predicted in *Luffa acutangula* genome by clicking on the circular diagrams of that category or by More

8. **Contact Us:** The Contact page provides information on how to reach the database administrators and research team.

Luffa acutangula Genomic Resource Database

Contact Us

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