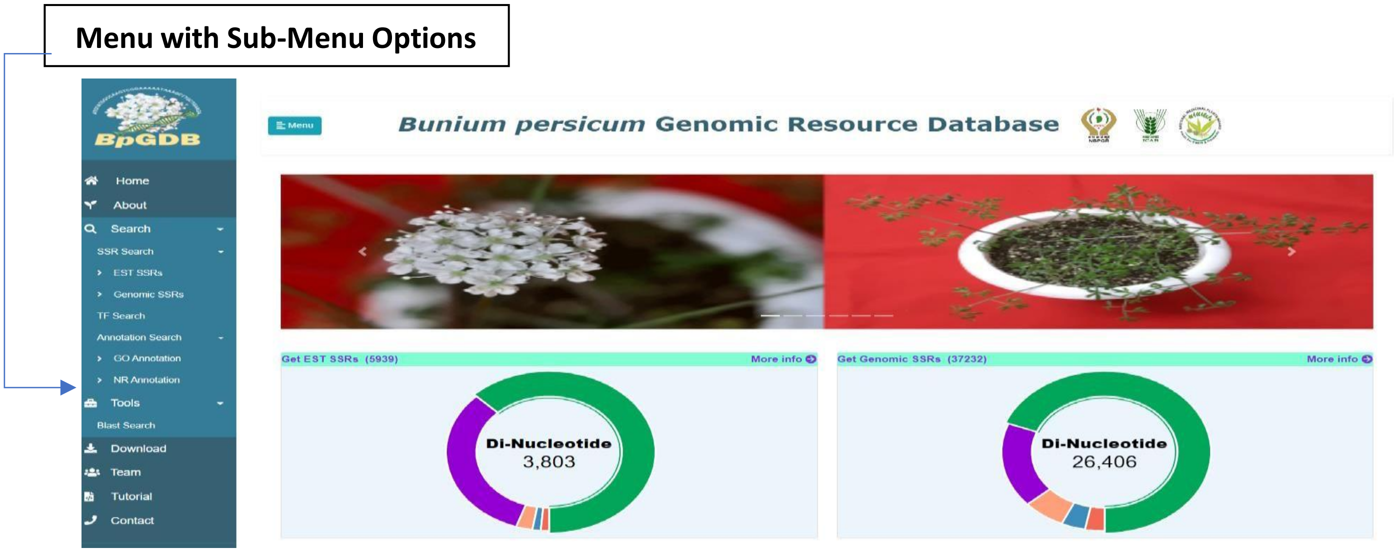
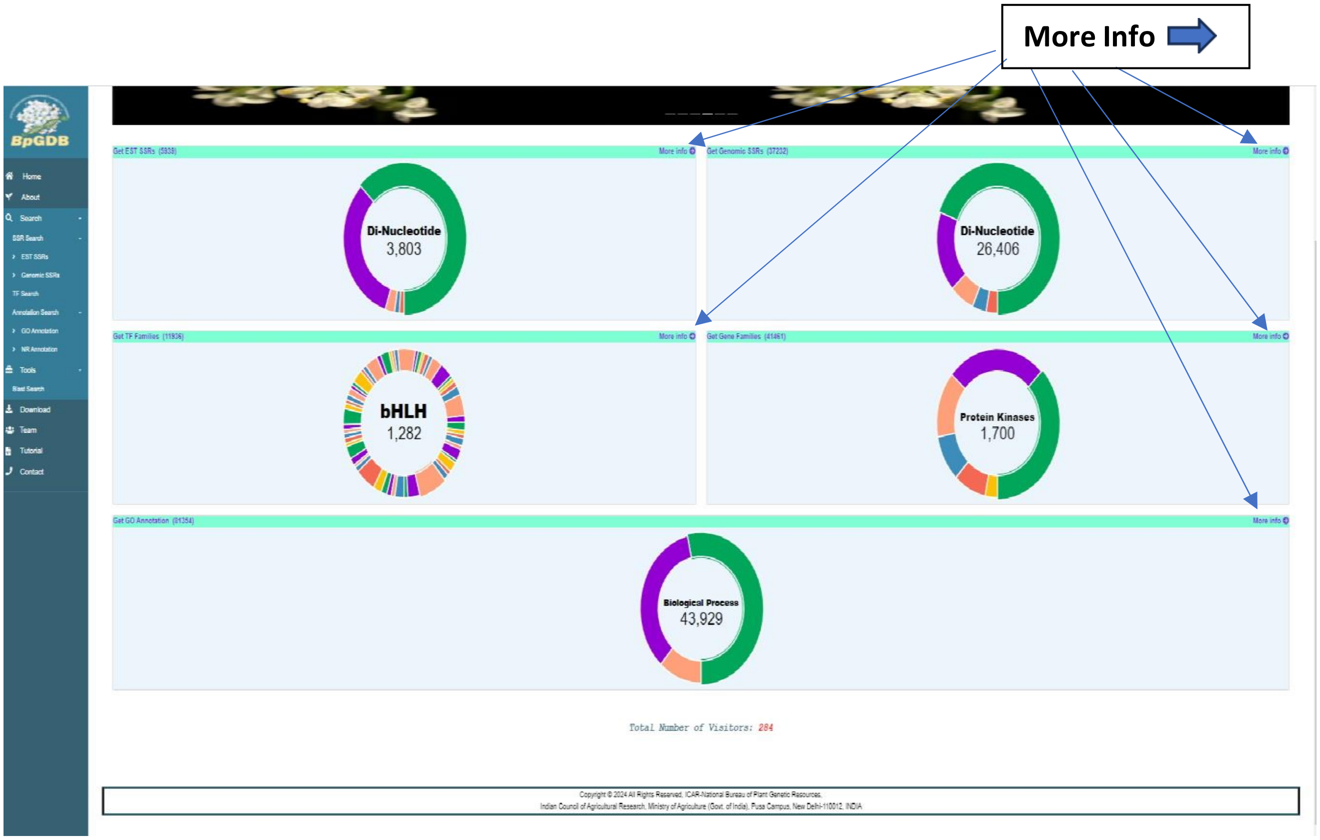
TUTORIALS of "Bunium *persicum*" Genomic Resource Database

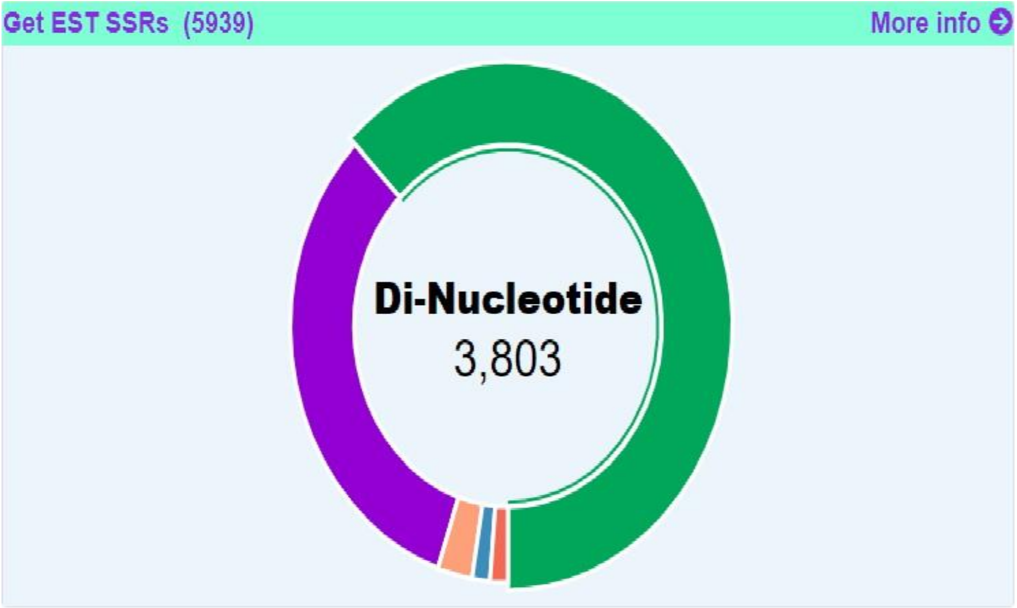
1. **HOME Page** consists information about the database with different Menu options to access the database efficiently.



1.(a).By Clicking on More Info Link, user will get further details.

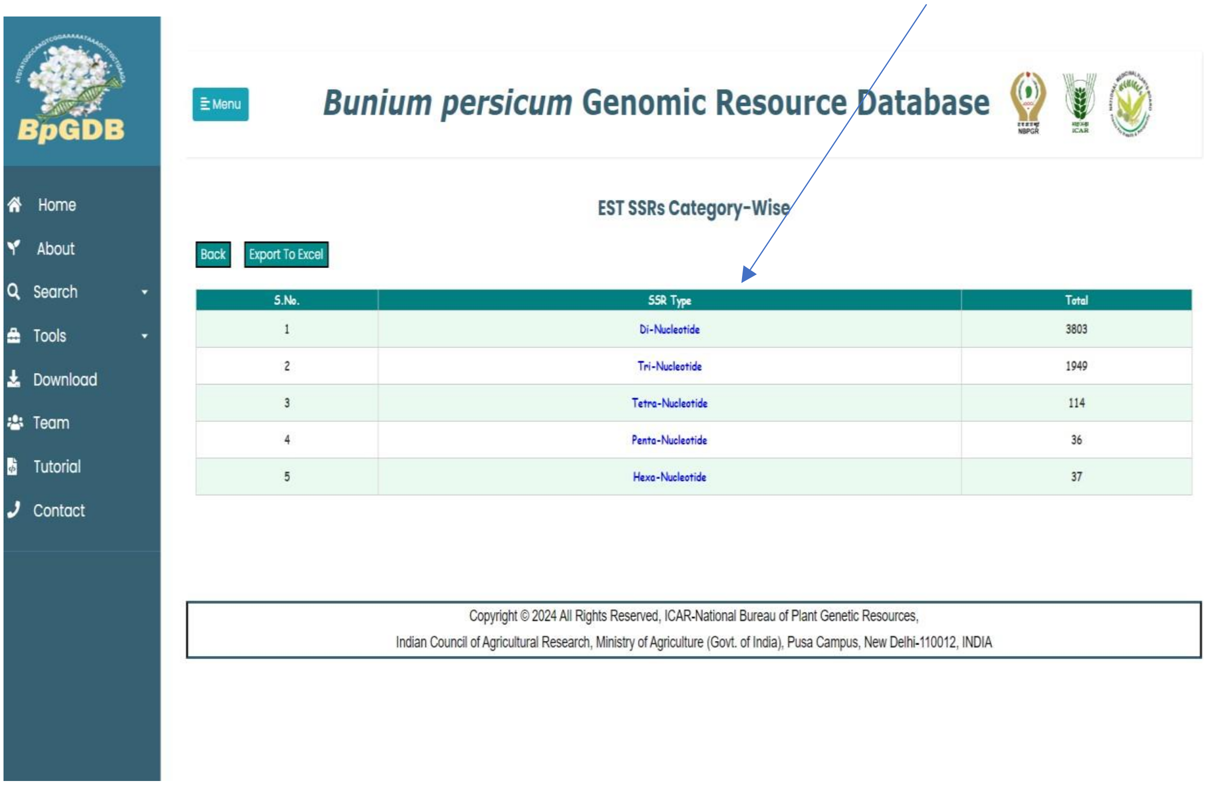


2. By-Clicking on Get EST SSRs Circle, the user will get particular Category Detail.



2.(a). By-Clicking on “More info” link, user will get all EST SSRs Categories.

EST SSRs Name Link



EST SSRs Category-Wise

S.No.	SSR Type	Total
1	Di-Nucleotide	3803
2	Tri-Nucleotide	1949
3	Tetra-Nucleotide	114
4	Penta-Nucleotide	36
5	Hexa-Nucleotide	37

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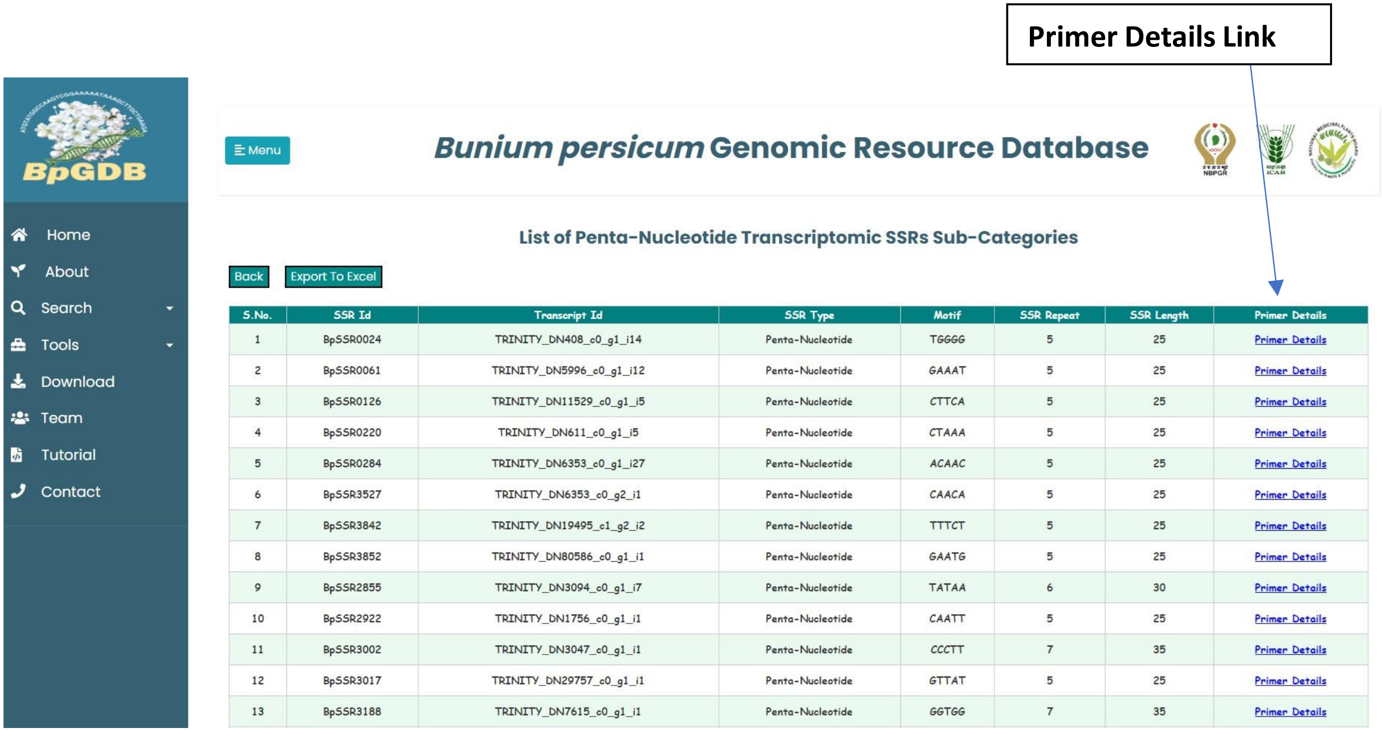
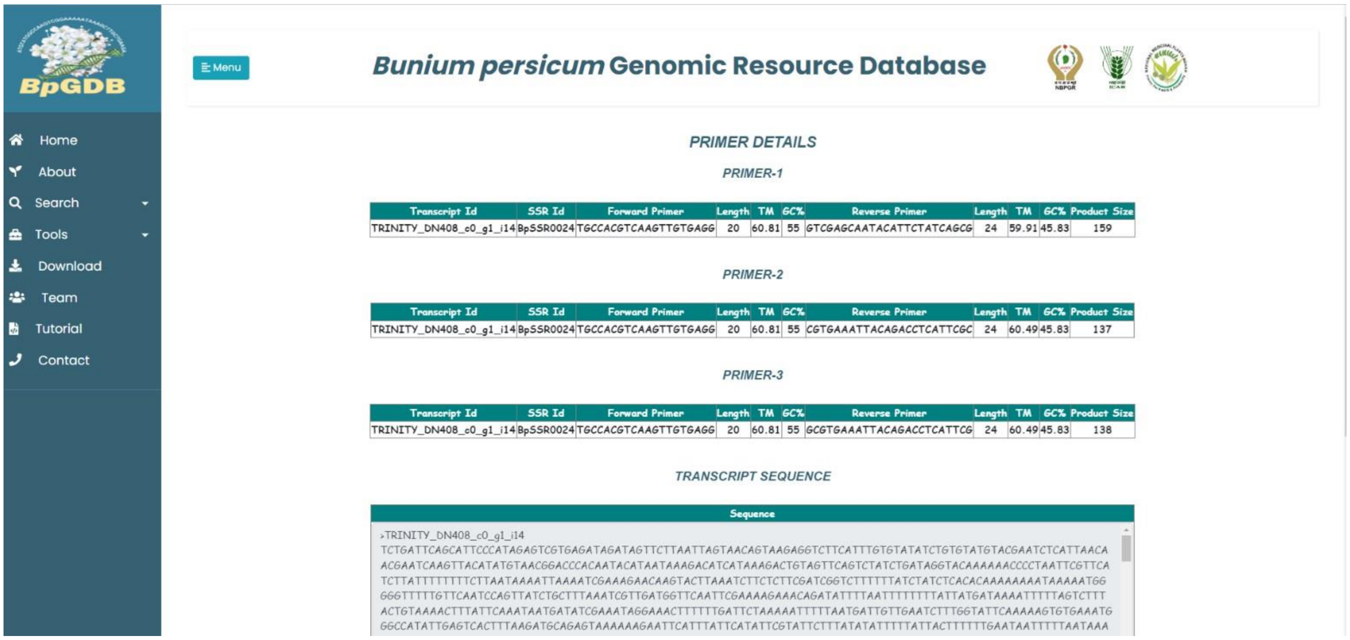
2.(b). User will get particular SSRs Sub-Categories which consists of SSR Id, Transcript Id, SSR Type, Motif, SSR Repeat, SSR Length & Primer Details Link with Export to Excel Facility Function.



List of Penta-Nucleotide Transcriptomic SSRs Sub-Categories

S.No.	SSR Id	Transcript Id	SSR Type	Motif	SSR Repeat	SSR Length	Primer Details
1	BpSSR0024	TRINITY_DN408_c0_g1_i14	Penta-Nucleotide	TGGGG	5	25	Primer Details
2	BpSSR0061	TRINITY_DN5996_c0_g1_i12	Penta-Nucleotide	GAAAT	5	25	Primer Details
3	BpSSR0126	TRINITY_DN11529_c0_g1_i5	Penta-Nucleotide	CTTCA	5	25	Primer Details
4	BpSSR0220	TRINITY_DN611_c0_g1_i5	Penta-Nucleotide	CTAAA	5	25	Primer Details
5	BpSSR0284	TRINITY_DN6353_c0_g1_i27	Penta-Nucleotide	ACAAC	5	25	Primer Details
6	BpSSR3527	TRINITY_DN6353_c0_g2_i1	Penta-Nucleotide	CAACA	5	25	Primer Details
7	BpSSR3842	TRINITY_DN19495_c1_g2_i2	Penta-Nucleotide	TTTCT	5	25	Primer Details
8	BpSSR3852	TRINITY_DN80586_c0_g1_i1	Penta-Nucleotide	GAATG	5	25	Primer Details
9	BpSSR2855	TRINITY_DN3094_c0_g1_i7	Penta-Nucleotide	TATAA	6	30	Primer Details
10	BpSSR2922	TRINITY_DN1756_c0_g1_i1	Penta-Nucleotide	CAATT	5	25	Primer Details
11	BpSSR3002	TRINITY_DN3047_c0_g1_i1	Penta-Nucleotide	CCCTT	7	35	Primer Details
12	BpSSR3017	TRINITY_DN29757_c0_g1_i1	Penta-Nucleotide	GTTAT	5	25	Primer Details
13	BpSSR3188	TRINITY_DN7615_c0_g1_i1	Penta-Nucleotide	GGTGG	7	35	Primer Details

2.(c). By-clicking on Primer Details link, the user will get Primer-1,2,3 details along with Transcript Sequence with Export to Excel Facility Function.



PRIMER DETAILS

PRIMER-1

Transcript Id	SSR Id	Forward Primer	Length	TM	GC%	Reverse Primer	Length	TM	GC%	Product Size
TRINITY_DN408_c0_g1_i14	BpSSR0024	TGCCACGTCAAGTTGTGAGG	20	60.81	55	GTCGAGCAATACATTCTATCAGCG	24	59.91	45.83	159

PRIMER-2

Transcript Id	SSR Id	Forward Primer	Length	TM	GC%	Reverse Primer	Length	TM	GC%	Product Size
TRINITY_DN408_c0_g1_i14	BpSSR0024	TGCCACGTCAAGTTGTGAGG	20	60.81	55	CGTGAAATTACAGACCTCATTCGC	24	60.49	45.83	137

PRIMER-3

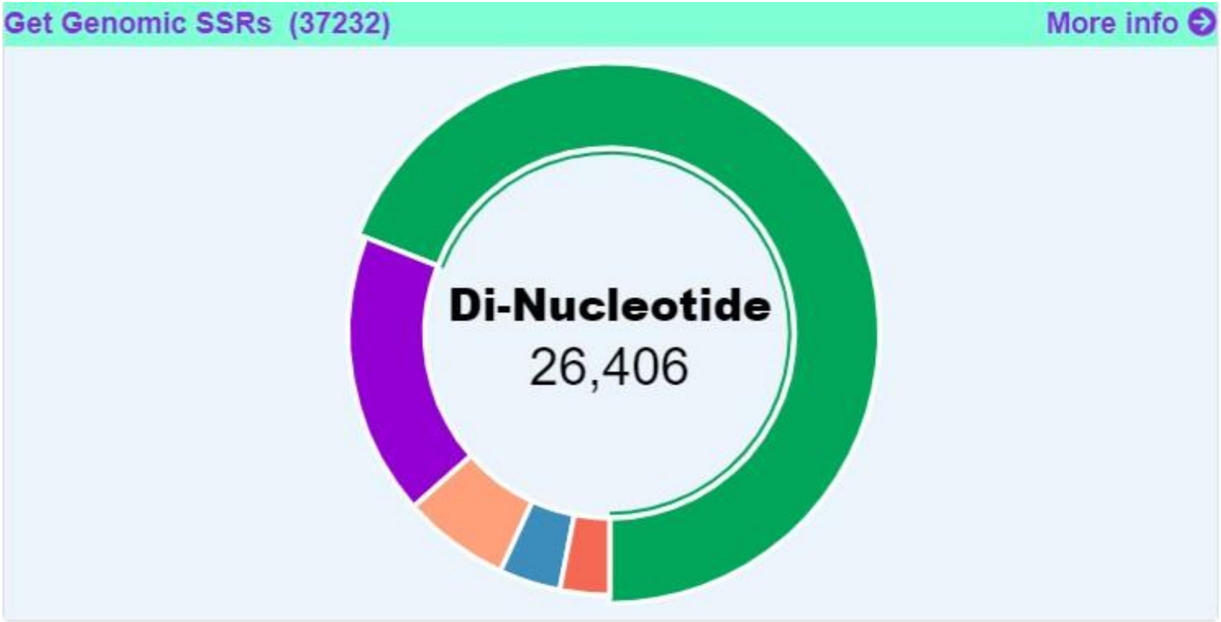
Transcript Id	SSR Id	Forward Primer	Length	TM	GC%	Reverse Primer	Length	TM	GC%	Product Size
TRINITY_DN408_c0_g1_i14	BpSSR0024	TGCCACGTCAAGTTGTGAGG	20	60.81	55	GCGTGAAATTACAGACCTCATTCG	24	60.49	45.83	138

TRANSCRIPT SEQUENCE

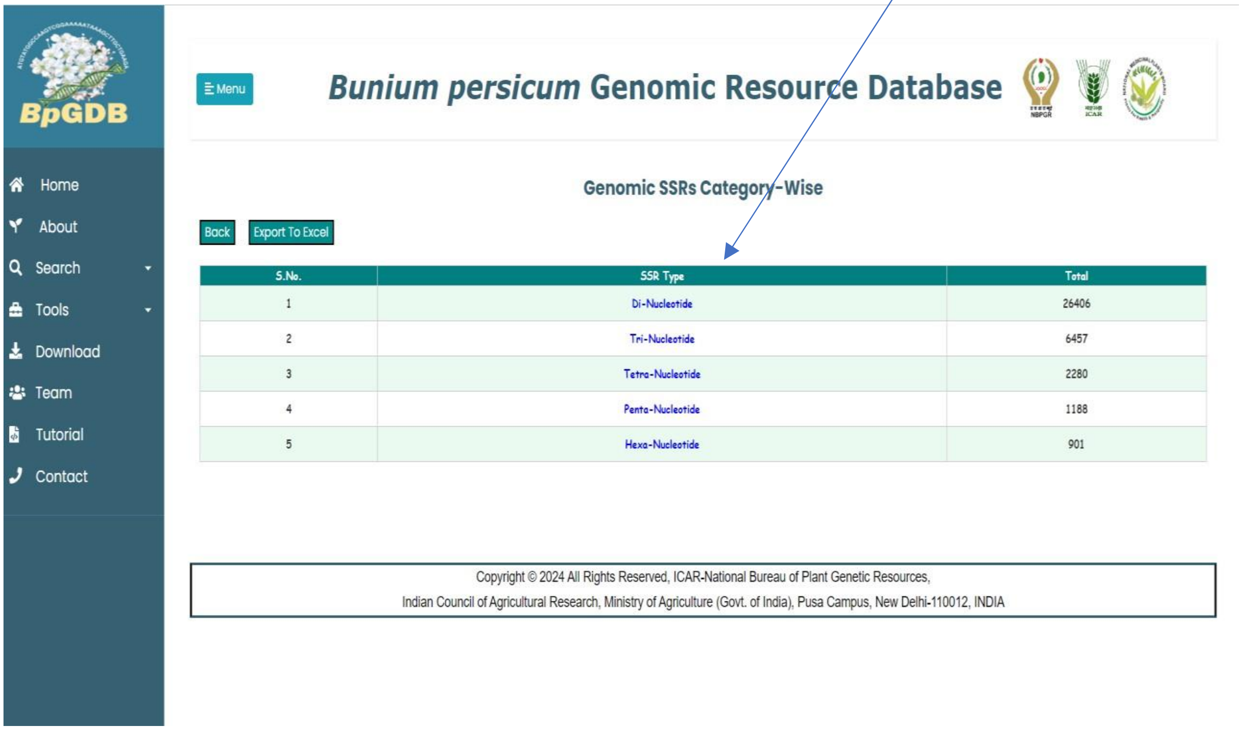
Sequence

```
>TRINITY_DN408_c0_g1_i14
TCTGATTCAGCATTCCCATAGAGTCGTGAGATAGATAGTTCTTAATTAGTAACAGTAAGAGGTCTTCATTTGTGTATATCTGTGTATGTACGAATCTCATTAACA
ACGAATCAAGTTACATATGTAACGGACCCACAATACATAATAAAGACATCATAAAGACTGTAGTTCAGTCTATCTGATAGGTACAAAAAACCCCTAATTCGTTCA
TCTTATTTTTTTTCTTAATAAAATTAAAATCGAAAGAACAAGTACTTAAATCTTCTCTTCGATCGGTCTTTTTTATCTATCTCACACAAAAAAAATAAAAATGG
GGGTTTTTGTTCAATCCAGTTATCTGCTTTAAATCGTTGATGGTTCAATTCGAAAAGAAACAGATATTTTAATTTTTTTTTATTATGATAAAATTTTTAGTCTTT
ACTGTAAAACTTTATTCAAATAATGATATCGAAATAGGAAACTTTTTTGATTCTAAAAATTTTTAATGATTGTTGAATCTTTGGTATTCAAAAAGTGTGAAATG
GGCCATATTGAGTCACTTTAAGATGCAGAGTAAAAAAGAATTCATTTATTCATATTCGTATTCTTTATATATTTTTATTACTTTTTTGAATAATTTTTAATAAA
```

3. By-Clicking on Get Genomic SSRs Circle, the user will get particular Category Detail.



3.(a). By-Clicking on “More info” link, user will get all Genomic SSRs Categories.



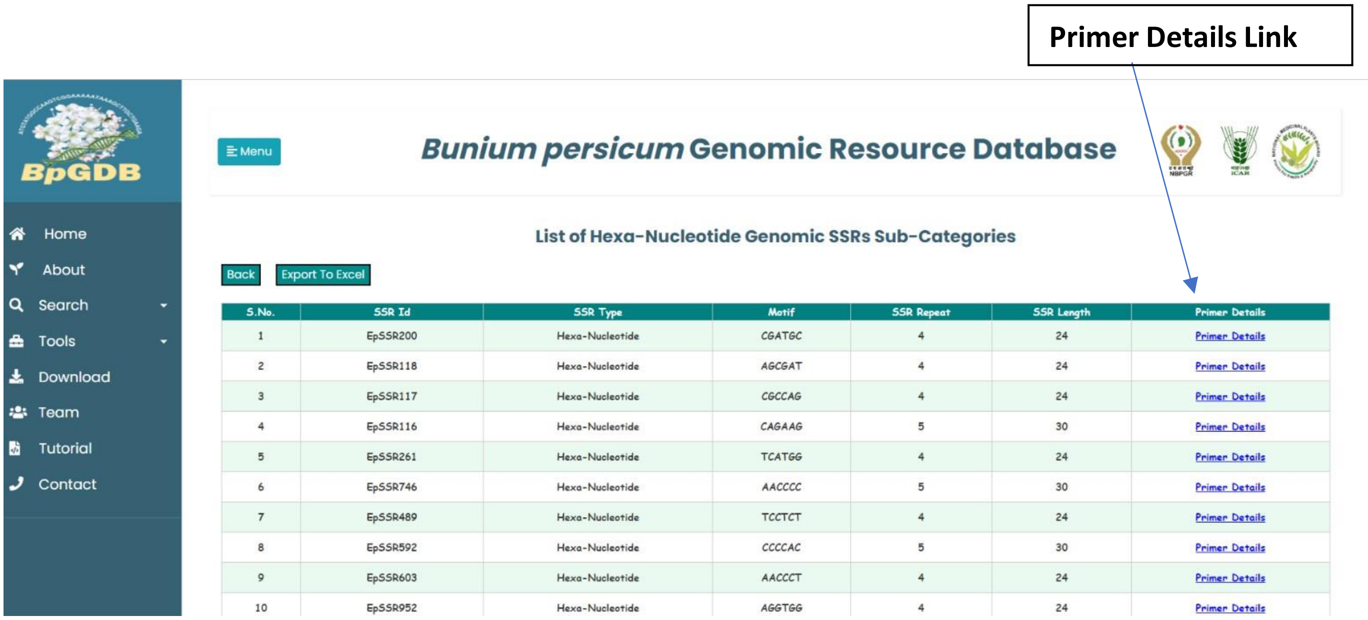
Genomic SSRs Name Link

Bunium persicum Genomic Resource Database

Genomic SSRs Category-Wise

S.No.	SSR Type	Total
1	Di-Nucleotide	26406
2	Tri-Nucleotide	6457
3	Tetra-Nucleotide	2280
4	Penta-Nucleotide	1188
5	Hexa-Nucleotide	901

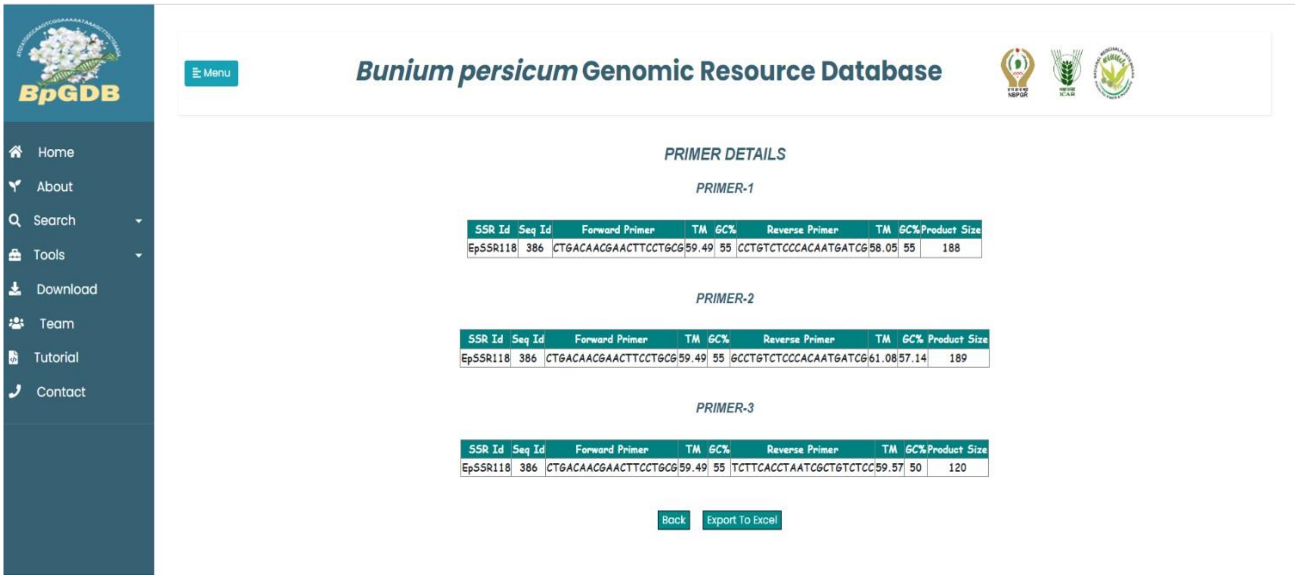
3.(b). User will get particular SSRs Sub-Categories which consists of SSR Id, SSR Type, Motif, SSR Repeat, SSR Length & Primer Details Link with Export to Excel Facility Function.


Primer Details Link

List of Hexa-Nucleotide Genomic SSRs Sub-Categories

S.No.	SSR Id	SSR Type	Motif	SSR Repeat	SSR Length	Primer Details
1	EpSSR200	Hexa-Nucleotide	CGATGC	4	24	Primer Details
2	EpSSR118	Hexa-Nucleotide	AGCGAT	4	24	Primer Details
3	EpSSR117	Hexa-Nucleotide	CGCCAG	4	24	Primer Details
4	EpSSR116	Hexa-Nucleotide	CAGAAG	5	30	Primer Details
5	EpSSR261	Hexa-Nucleotide	TCATGG	4	24	Primer Details
6	EpSSR746	Hexa-Nucleotide	AACCCC	5	30	Primer Details
7	EpSSR489	Hexa-Nucleotide	TCCTCT	4	24	Primer Details
8	EpSSR592	Hexa-Nucleotide	CCCCAC	5	30	Primer Details
9	EpSSR603	Hexa-Nucleotide	AACCCT	4	24	Primer Details
10	EpSSR952	Hexa-Nucleotide	AGGTGG	4	24	Primer Details

3.(c). By-clicking on Primer Details link, the user will get Primer-1,2,3 details with Export to Excel Facility Function.



PRIMER DETAILS

PRIMER-1

SSR Id	Seq Id	Forward Primer	TM	GC%	Reverse Primer	TM	GC%	Product Size
EpSSR118	386	CTGACAACGAACTTCCTGCG	59.49	55	CCTGTCTCCCACAATGATCG	58.05	55	188

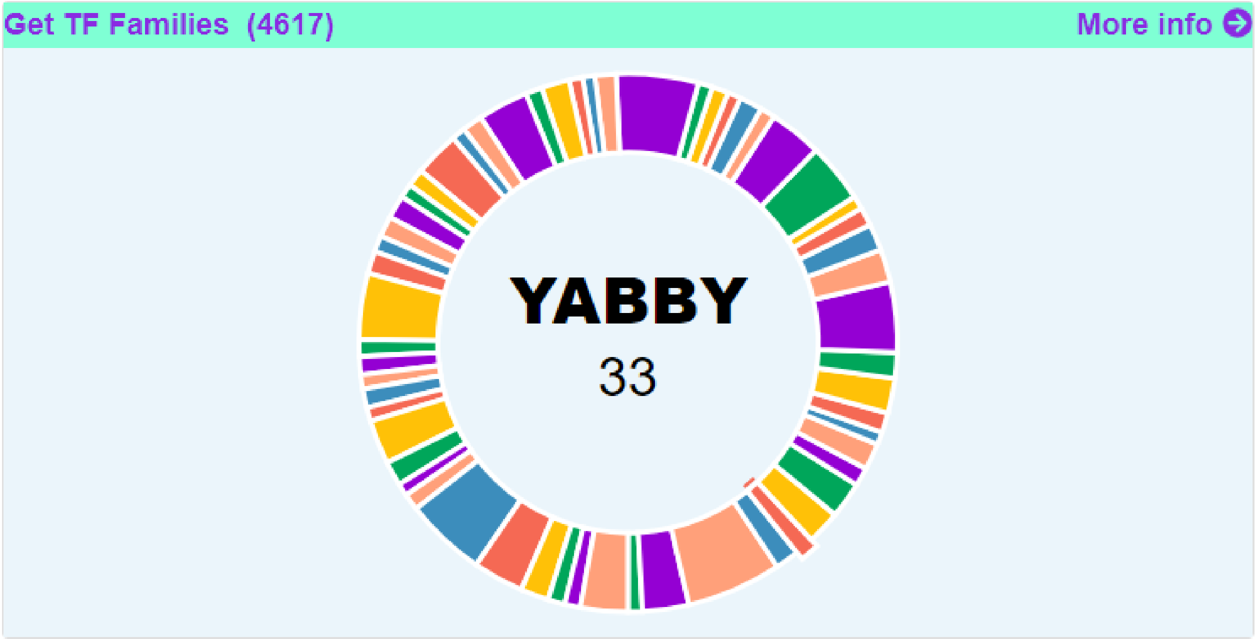
PRIMER-2

SSR Id	Seq Id	Forward Primer	TM	GC%	Reverse Primer	TM	GC%	Product Size
EpSSR118	386	CTGACAACGAACTTCCTGCG	59.49	55	GCCTGTCTCCCACAATGATCG	61.08	57.14	189

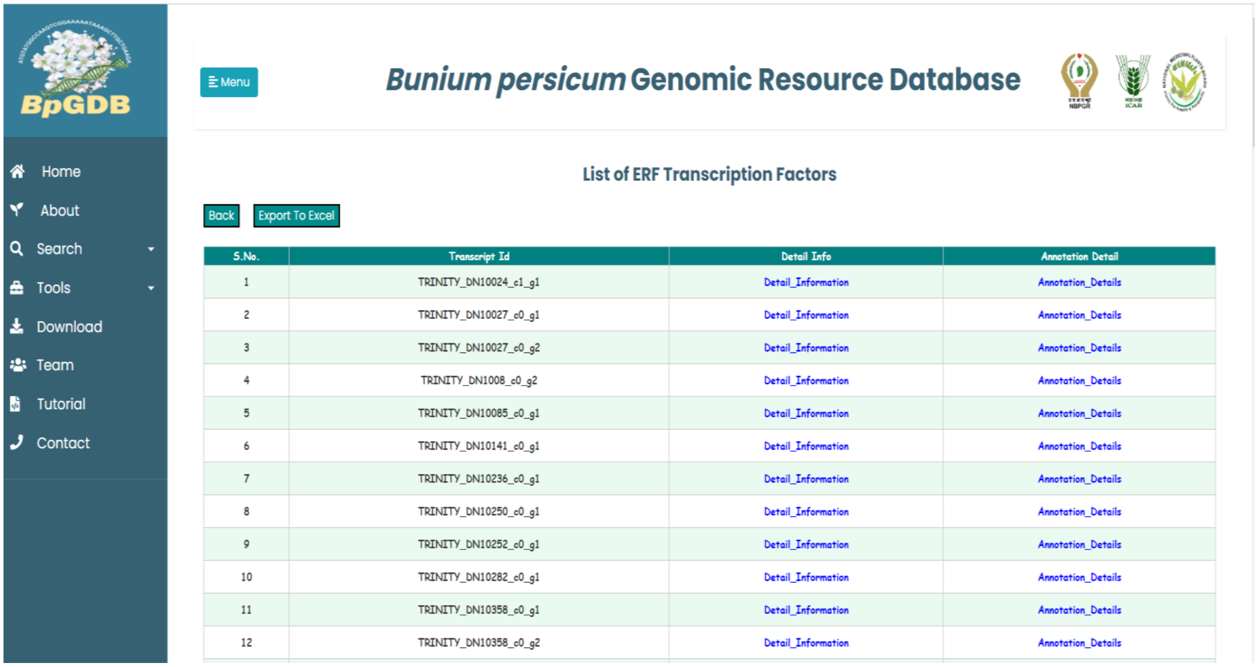
PRIMER-3

SSR Id	Seq Id	Forward Primer	TM	GC%	Reverse Primer	TM	GC%	Product Size
EpSSR118	386	CTGACAACGAACTTCCTGCG	59.49	55	TCTTCACCTAATCGCTGTCTCC	59.57	50	120

4. By-Clicking on Get TF Families Circle, the user will get particular Family Detail.



4.(a).User will get List of Particular Family Transcription Factors with Export to Excel Facility Function.

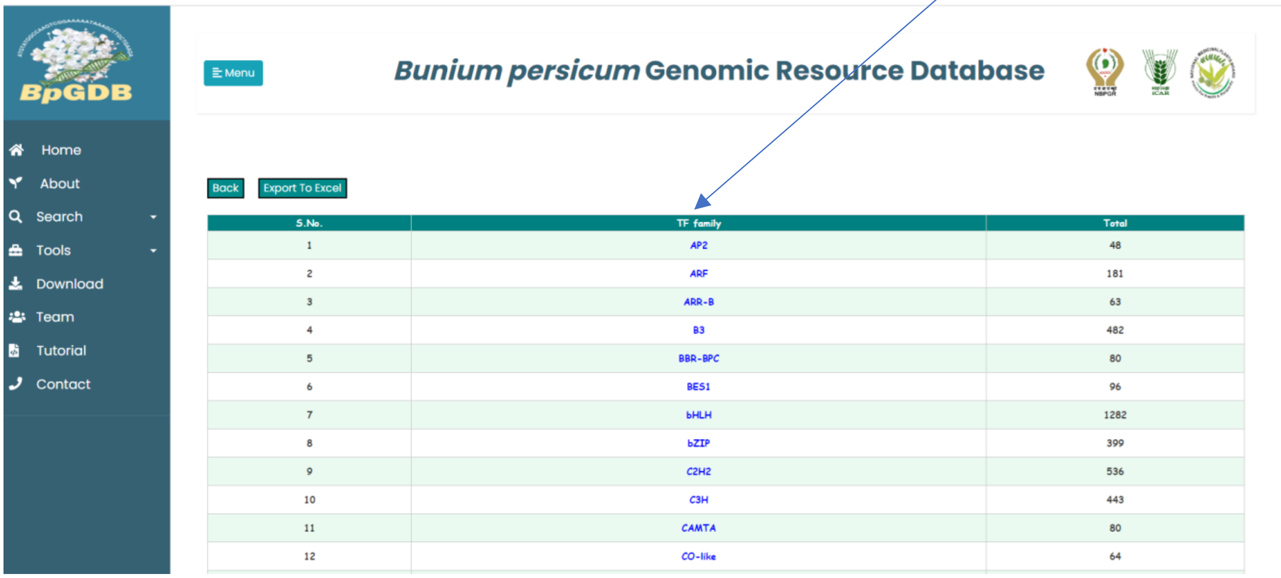


Bunium persicum Genomic Resource Database

List of ERF Transcription Factors

S.No.	Transcript Id	Detail Info	Annotation Detail
1	TRINITY_DN10024_c1_g1	Detail_Information	Annotation_Details
2	TRINITY_DN10027_c0_g1	Detail_Information	Annotation_Details
3	TRINITY_DN10027_c0_g2	Detail_Information	Annotation_Details
4	TRINITY_DN1008_c0_g2	Detail_Information	Annotation_Details
5	TRINITY_DN10085_c0_g1	Detail_Information	Annotation_Details
6	TRINITY_DN10141_c0_g1	Detail_Information	Annotation_Details
7	TRINITY_DN10236_c0_g1	Detail_Information	Annotation_Details
8	TRINITY_DN10250_c0_g1	Detail_Information	Annotation_Details
9	TRINITY_DN10252_c0_g1	Detail_Information	Annotation_Details
10	TRINITY_DN10282_c0_g1	Detail_Information	Annotation_Details
11	TRINITY_DN10358_c0_g1	Detail_Information	Annotation_Details
12	TRINITY_DN10358_c0_g2	Detail_Information	Annotation_Details

4.(b). By-Clicking on “More info” link, User will Get TF Family List Details (which are clickable to get further details) with Export to Excel Facility Function.

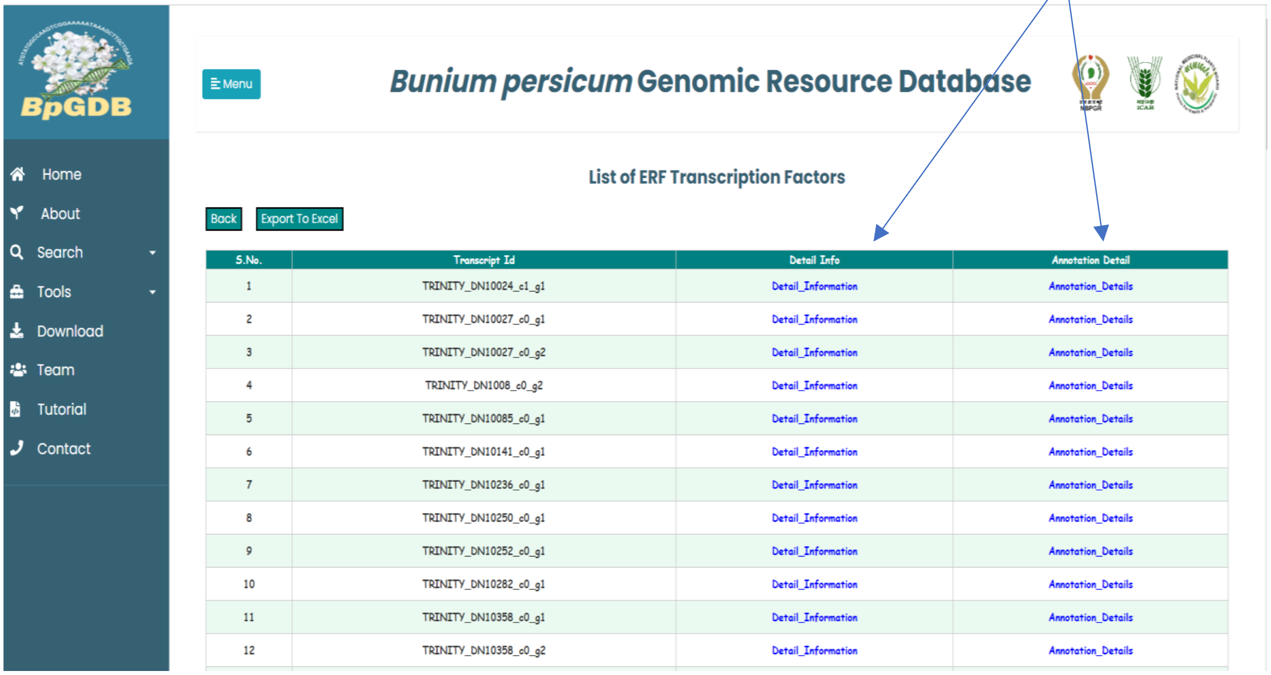


Family-wise Links

S.No.	TF family	Total
1	AP2	48
2	ARF	181
3	ARR-B	63
4	B3	482
5	BBR-BPC	80
6	BES1	96
7	bHLH	1282
8	bZIP	399
9	C2H2	536
10	C3H	443
11	CAMTA	80
12	CO-like	64

4.(c). By clicking on Family-Names, User will get detail like Transcript ID, Detail Information & Annotation Detail with Export to Excel Facility Function.

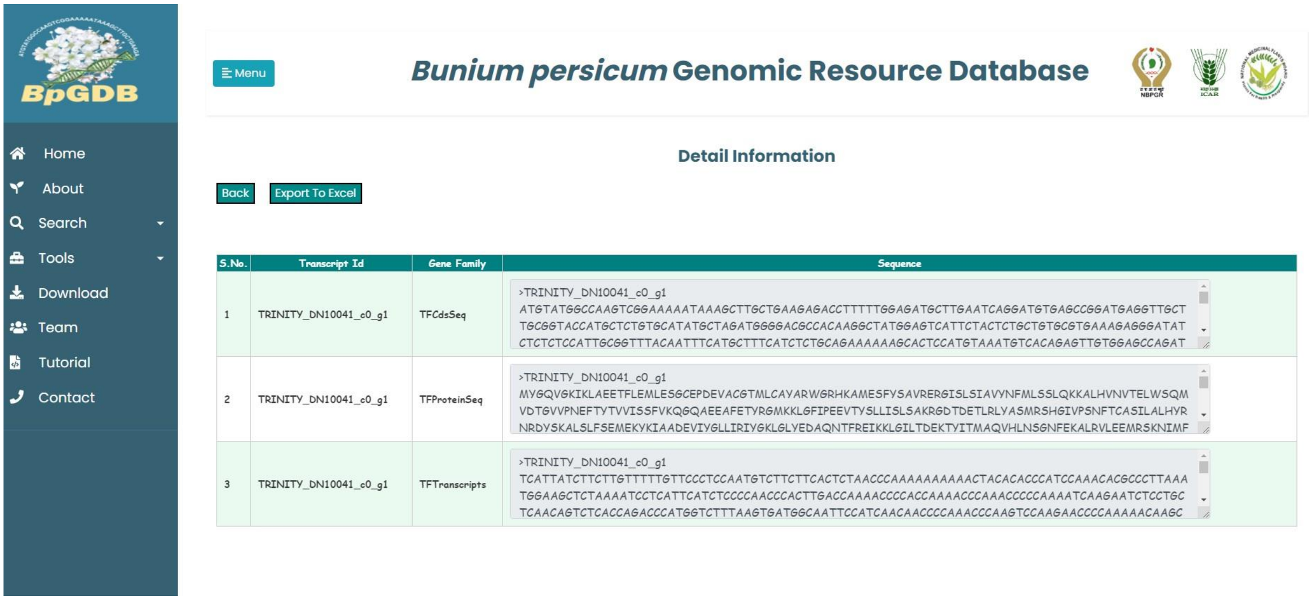
Detail information & Annotation Detail Page Links



List of ERF Transcription Factors

S.No.	Transcript Id	Detail Info	Annotation Detail
1	TRINITY_DN10024_c1_g1	Detail_Information	Annotation_Details
2	TRINITY_DN10027_c0_g1	Detail_Information	Annotation_Details
3	TRINITY_DN10027_c0_g2	Detail_Information	Annotation_Details
4	TRINITY_DN1008_c0_g2	Detail_Information	Annotation_Details
5	TRINITY_DN10085_c0_g1	Detail_Information	Annotation_Details
6	TRINITY_DN10141_c0_g1	Detail_Information	Annotation_Details
7	TRINITY_DN10236_c0_g1	Detail_Information	Annotation_Details
8	TRINITY_DN10250_c0_g1	Detail_Information	Annotation_Details
9	TRINITY_DN10252_c0_g1	Detail_Information	Annotation_Details
10	TRINITY_DN10282_c0_g1	Detail_Information	Annotation_Details
11	TRINITY_DN10358_c0_g1	Detail_Information	Annotation_Details
12	TRINITY_DN10358_c0_g2	Detail_Information	Annotation_Details

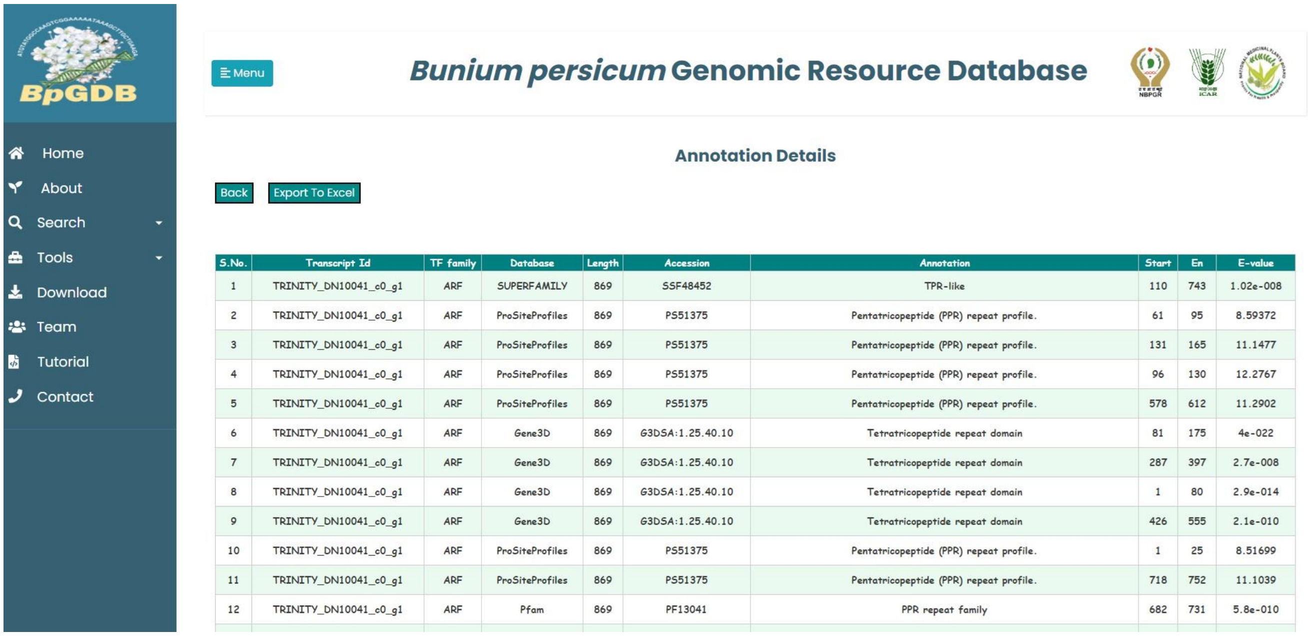
4.(d). By-Clicking on Detail_Information Link, User will get Transcript Id, Gene Family & Sequence Details with Export to Excel Facility Function.



Detail Information

S.No.	Transcript Id	Gene Family	Sequence
1	TRINITY_DN10041_c0_g1	TFCdsSeq	>TRINITY_DN10041_c0_g1 ATGTATGGCCAAGTCGGAAAAATAAAGCTTGCTGAAGAGACCTTTTTGGAGATGCTTGAATCAGGATGTGAGCCGGATGAGGTTGCT TGCGGTACCATGCTCTGTGCATATGCTAGATGGGGACGCCACAAGGCTATGGAGTCATTCTACTCTGCTGTGCGTGAAAGAGGGATAT CTCTCTCCATTGCGGTTTACAATTTCATGCTTTCATCTCTGCAGAAAAAAGCACTCCATGTAAATGTCACAGAGTTGTGGAGCCAGAT
2	TRINITY_DN10041_c0_g1	TFProteinSeq	>TRINITY_DN10041_c0_g1 MYGQVGKIKLAEETFLEMLESGCEPDEVACGTMLCAYARWGRHKAMESFYSAVRERGISLSIAVYNFMLSSLQKKALHVNVTELWSQM VDTGVVPNEFTYTVVISSFVKQGQAEEAFETYRGMKKLGFIPEEVTYSLLISLSAKRGDTDETLRLYASMRSHGIVPSNFTCASILALHYR NRDYSKALSLFSEMEKYKIAADEVIYGLLIRIYGKLGLYEDAQNTFREIKKLGILTDEKTYITMAQVHLNSGNFEKALRVLEEMRSKNIMF
3	TRINITY_DN10041_c0_g1	TFTranscripts	>TRINITY_DN10041_c0_g1 TCATTATCTTCTTGTTTTTGTTCCCTCCAATGTCTTCTTCACTCTAACCCAAAAAAAAAACTACACACCCATCCAAACACGCCCTTAAA TGGAAGCTCTAAAATCCTCATTCATCTCCCCAACCCACTTGACCAAAACCCCACCAAAACCCAAACCCCCAAAATCAAGAATCTCCTGC TCAACAGTCTCACCAGACCCATGGTCTTTAAGTGATGGCAATTCCATCAACAACCCCAAACCCAAGTCCAAGAACCCCAAAAACAAGC

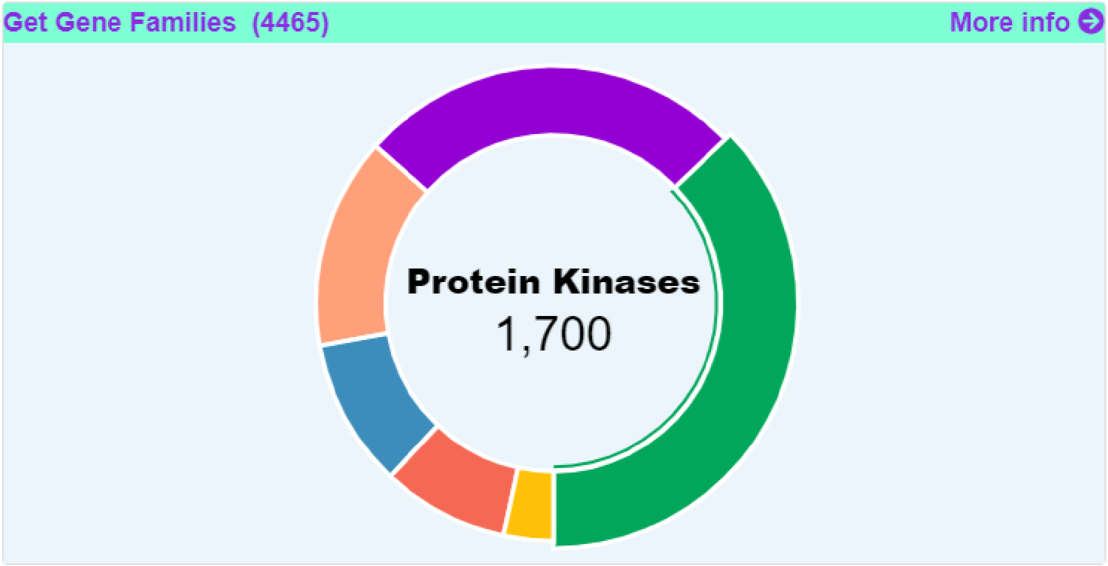
4.(e). By-Clicking on Annotation-Detail Link, User will get Transcript Id, Tf family, Database, Length, Accession, Annotation, start, en, E-value etc. with Export to Excel Facility Function.



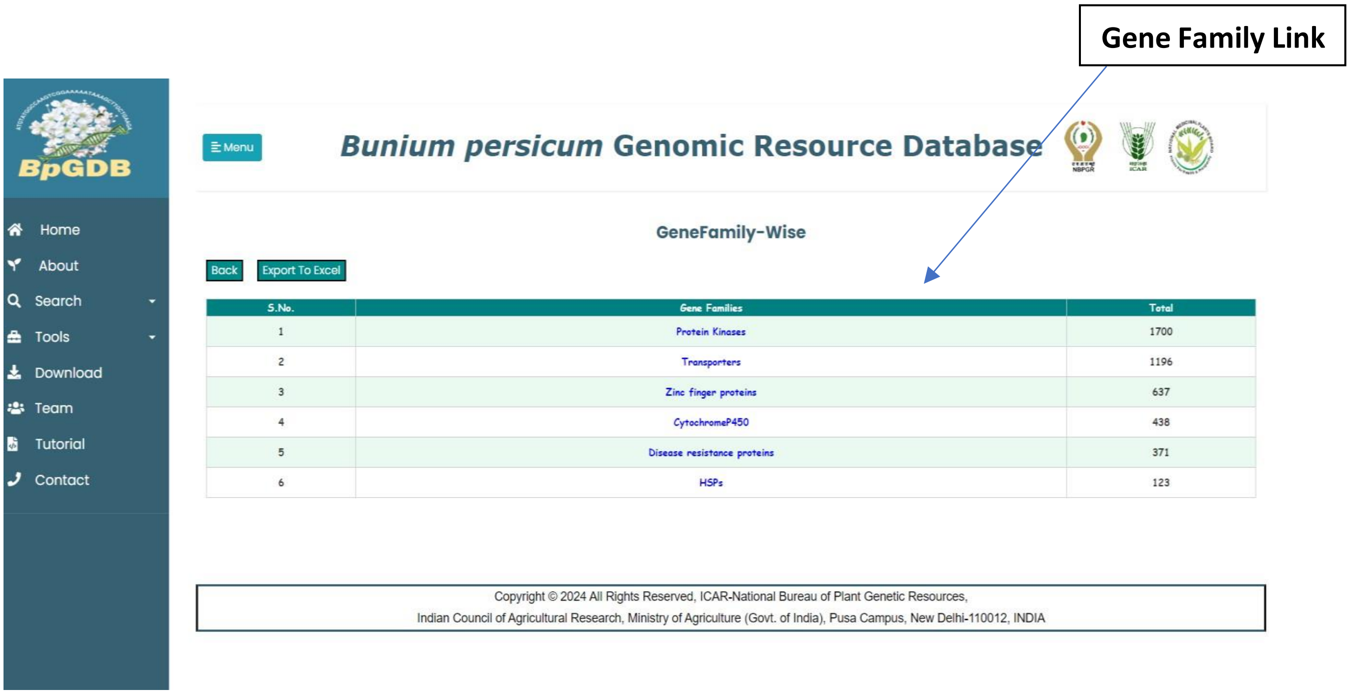
Annotation Details

S.No.	Transcript Id	TF family	Database	Length	Accession	Annotation	Start	En	E-value
1	TRINITY_DN10041_c0_g1	ARF	SUPERFAMILY	869	SSF48452	TPR-like	110	743	1.02e-008
2	TRINITY_DN10041_c0_g1	ARF	ProSiteProfiles	869	PS51375	Pentatricopeptide (PPR) repeat profile.	61	95	8.59372
3	TRINITY_DN10041_c0_g1	ARF	ProSiteProfiles	869	PS51375	Pentatricopeptide (PPR) repeat profile.	131	165	11.1477
4	TRINITY_DN10041_c0_g1	ARF	ProSiteProfiles	869	PS51375	Pentatricopeptide (PPR) repeat profile.	96	130	12.2767
5	TRINITY_DN10041_c0_g1	ARF	ProSiteProfiles	869	PS51375	Pentatricopeptide (PPR) repeat profile.	578	612	11.2902
6	TRINITY_DN10041_c0_g1	ARF	Gene3D	869	G3DSA:1.25.40.10	Tetratricopeptide repeat domain	81	175	4e-022
7	TRINITY_DN10041_c0_g1	ARF	Gene3D	869	G3DSA:1.25.40.10	Tetratricopeptide repeat domain	287	397	2.7e-008
8	TRINITY_DN10041_c0_g1	ARF	Gene3D	869	G3DSA:1.25.40.10	Tetratricopeptide repeat domain	1	80	2.9e-014
9	TRINITY_DN10041_c0_g1	ARF	Gene3D	869	G3DSA:1.25.40.10	Tetratricopeptide repeat domain	426	555	2.1e-010
10	TRINITY_DN10041_c0_g1	ARF	ProSiteProfiles	869	PS51375	Pentatricopeptide (PPR) repeat profile.	1	25	8.51699
11	TRINITY_DN10041_c0_g1	ARF	ProSiteProfiles	869	PS51375	Pentatricopeptide (PPR) repeat profile.	718	752	11.1039
12	TRINITY_DN10041_c0_g1	ARF	Pfam	869	PF13041	PPR repeat family	682	731	5.8e-010

5. By-Clicking on Get Gene Families Circle, the user will get particular Gene Family Detail.



5.(a). By-Clicking on “More info” link, user will get all Gene Name Family-wise details with Export to Excel Facility Function.

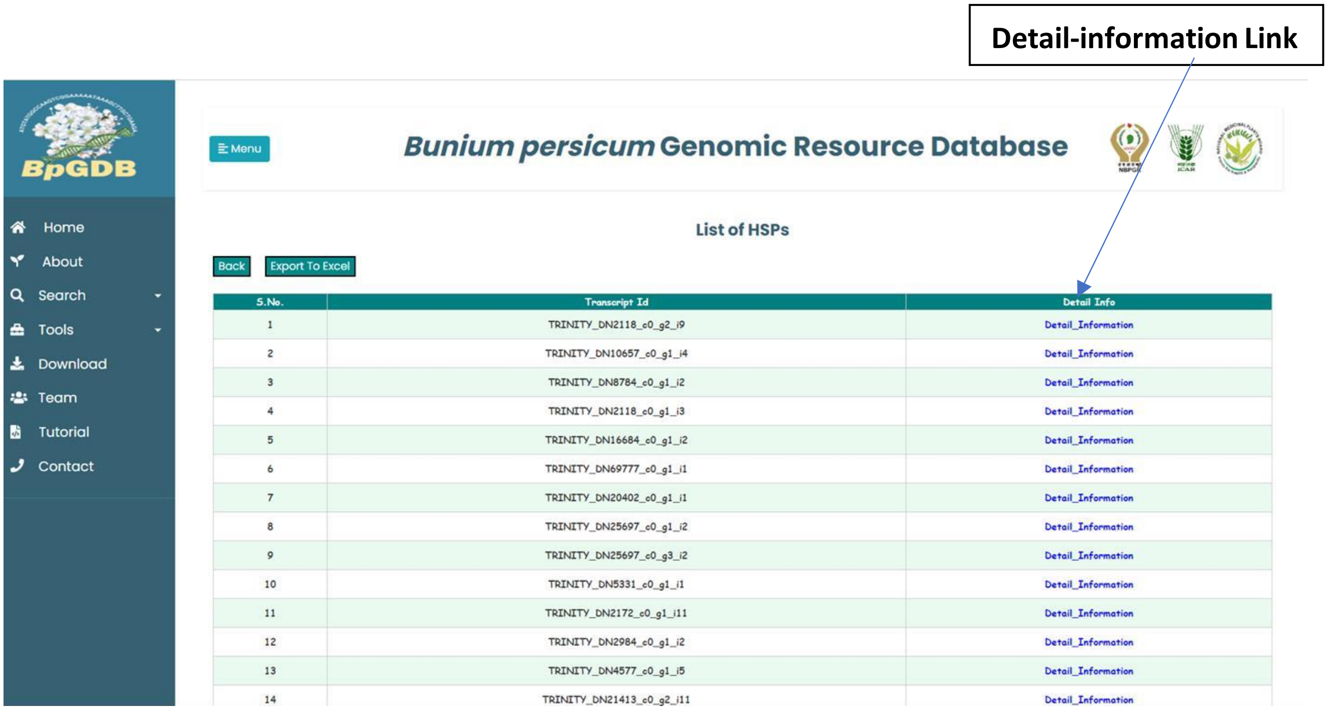

Gene Family Link

Bunium persicum Genomic Resource Database

GeneFamily-Wise

S.No.	Gene Families	Total
1	Protein Kinases	1700
2	Transporters	1196
3	Zinc finger proteins	637
4	CytochromeP450	438
5	Disease resistance proteins	371
6	HSPs	123

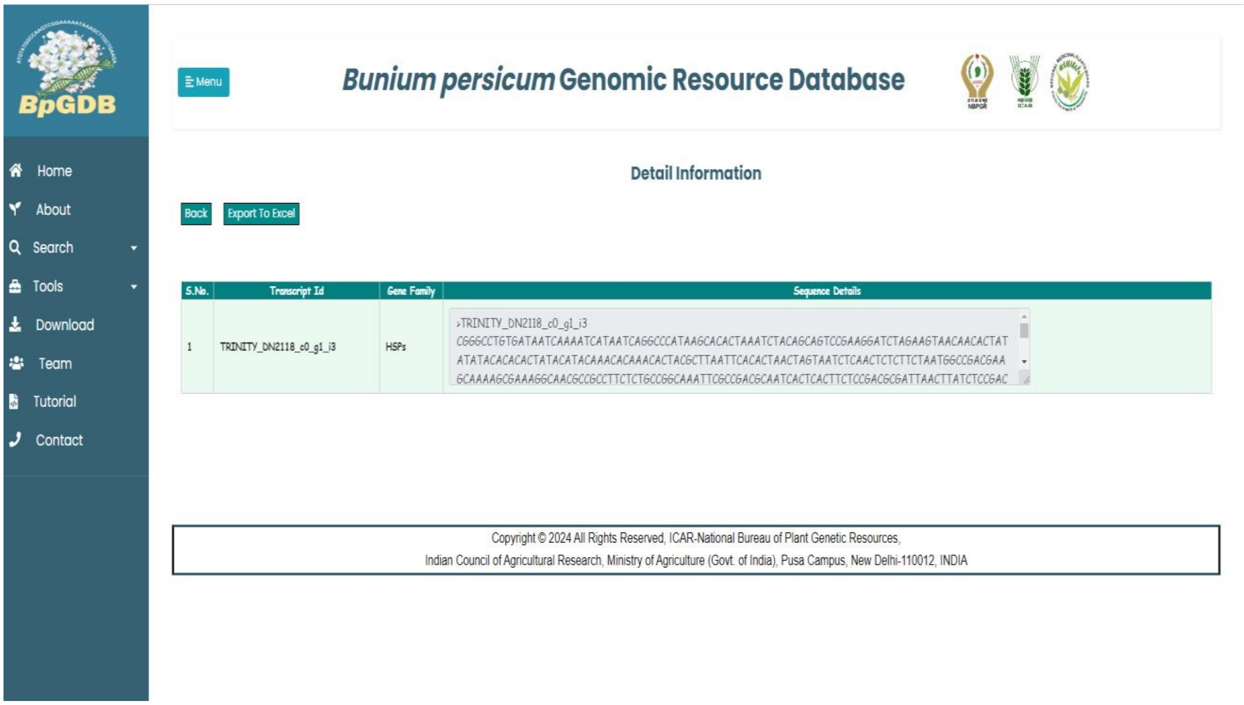
5.(b). By-Clicking on Gene Names, user will get Transcript Id and Detail-Information Link with Export to Excel Facility Function.


Detail-information Link

List of HSPs

S.No.	Transcript Id	Detail Info
1	TRINITY_DN2118_c0_g2_i9	Detail_Information
2	TRINITY_DN10657_c0_g1_i4	Detail_Information
3	TRINITY_DN8784_c0_g1_i2	Detail_Information
4	TRINITY_DN2118_c0_g1_i3	Detail_Information
5	TRINITY_DN16684_c0_g1_i2	Detail_Information
6	TRINITY_DN69777_c0_g1_i1	Detail_Information
7	TRINITY_DN20402_c0_g1_i1	Detail_Information
8	TRINITY_DN25697_c0_g1_i2	Detail_Information
9	TRINITY_DN25697_c0_g3_i2	Detail_Information
10	TRINITY_DN5331_c0_g1_i1	Detail_Information
11	TRINITY_DN2172_c0_g1_i11	Detail_Information
12	TRINITY_DN2984_c0_g1_i2	Detail_Information
13	TRINITY_DN4577_c0_g1_i5	Detail_Information
14	TRINITY_DN21413_c0_g2_i11	Detail_Information

5.(c). By-Clicking on Detail-information link, user will get Transcript Id, Gene family and Sequence details with Export to Excel Facility Function.



Detail Information

S.No.	Transcript Id	Gene Family	Sequence Details
1	TRINITY_DN2118_c0_g1_i3	HSPs	>TRINITY_DN2118_c0_g1_i3 CGGGCCTGTGATAATCAAAATCATAATCAGGCCCATAAGCACACTAAATCTACAGCAGTCCGAAGGATCTAGAAGTAACAACACTAT ATATACACACACTATACATACAAACACAAACACTACGCTTAATTCACACTAACTAGTAATCTCAACTCTCTTCTAATGGCCGACGAA GCAAAAGCGAAAGGCAACGCCGCCTTCTCTGCCGGCAAATTCGCCGACGCAATCACTCACTTCTCCGACGCGATTAACTTATCTCCGAC

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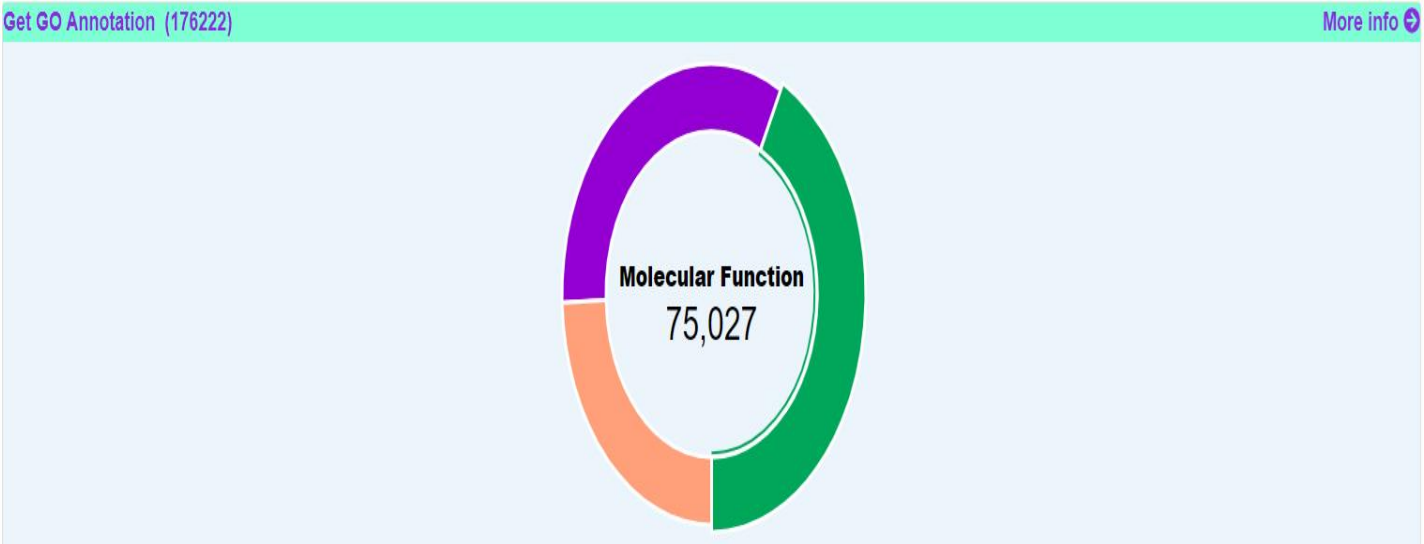
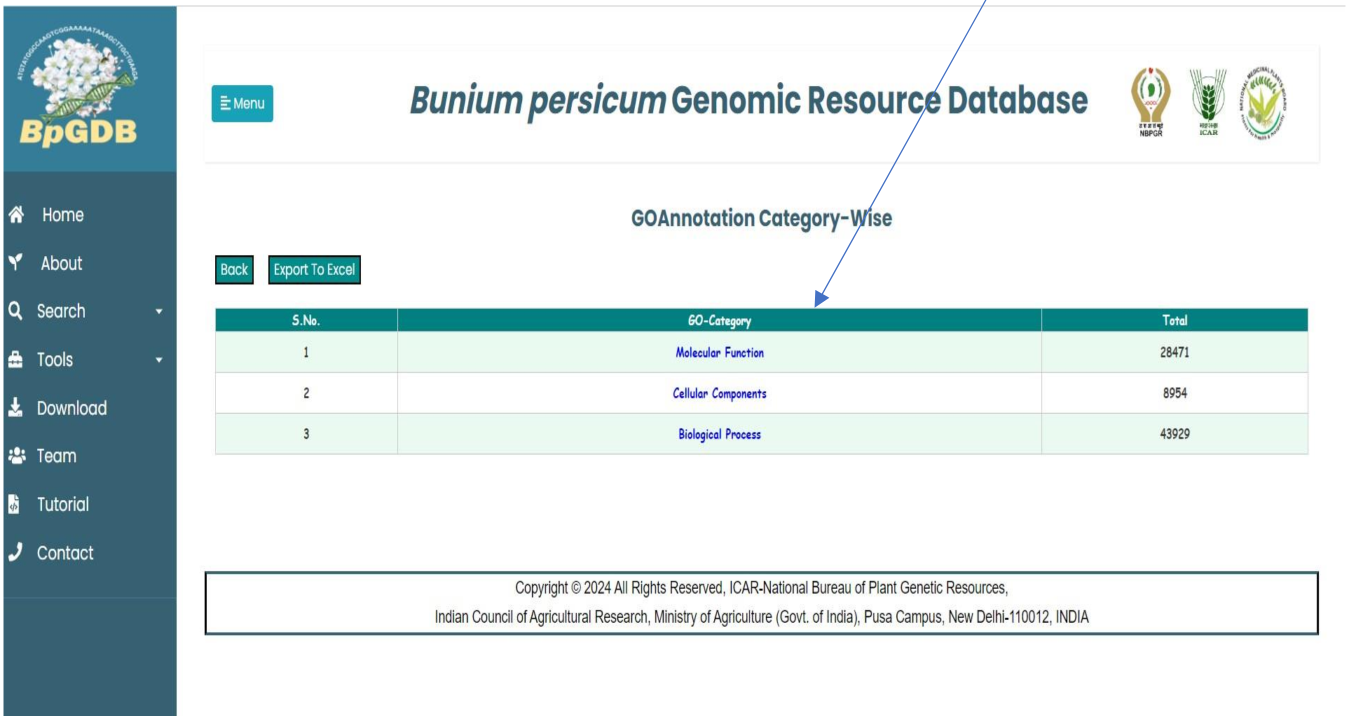
Indian Council of Agricultural Research, Ministry of Agriculture (Govt. of India), Pusa Campus, New Delhi-110012, INDIA

6. By-Clicking on Get GO Annotation Circle, the user will get particular Go Name Detail.



6.(a). By-Clicking on "More info" link, user will get all GO-Annotation Categories with Export to Excel Facility Function.

GO-Categories Link



Bunium persicum Genomic Resource Database

GOAnnotation Category-Wise

S.No.	GO-Category	Total
1	Molecular Function	28471
2	Cellular Components	8954
3	Biological Process	43929

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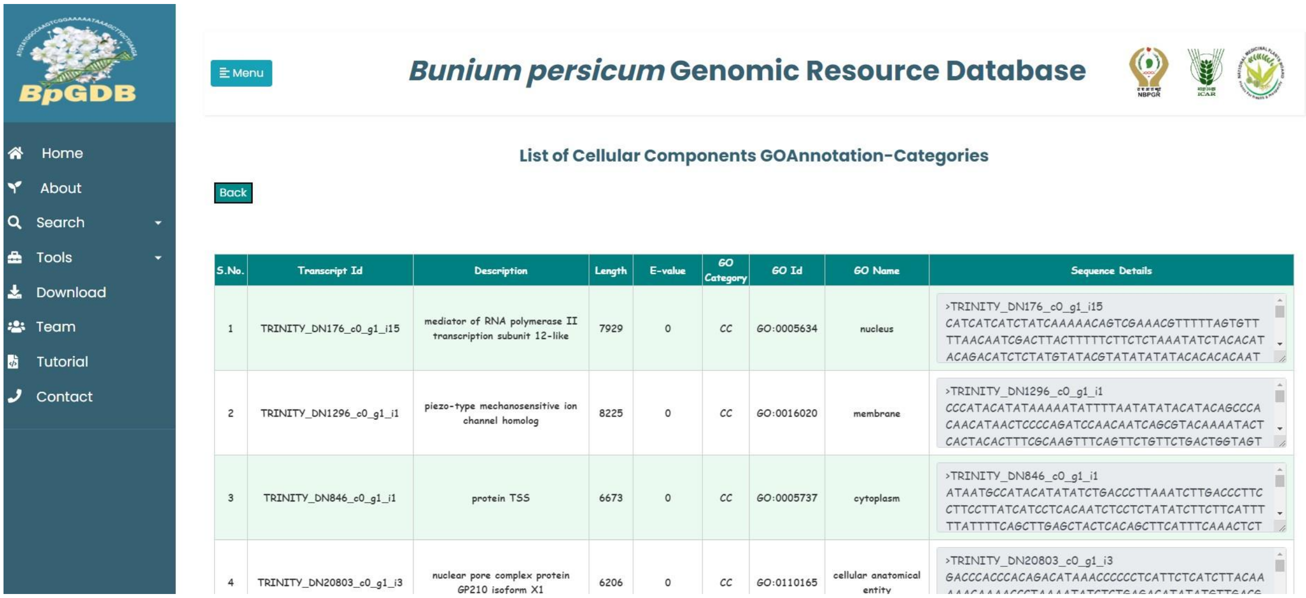
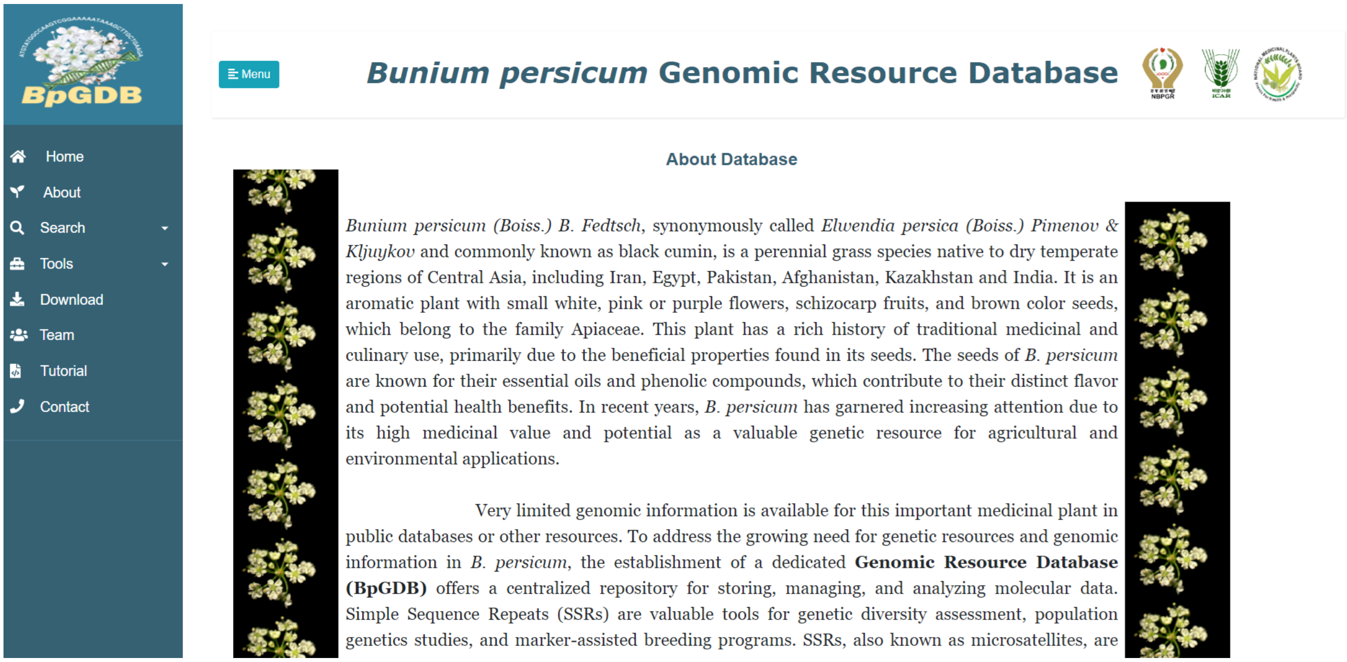
6.(b). By-Clicking on Go-Name Link, user will get Transcript Id, Description, Length, E-value, Go category, Go Id, Go Name with Sequence Details.



List of Cellular Components GOAnnotation-Categories

S.No.	Transcript Id	Description	Length	E-value	GO Category	GO Id	GO Name	Sequence Details
1	TRINITY_DN176_c0_g1_i15	mediator of RNA polymerase II transcription subunit 12-like	7929	0	CC	GO:0005634	nucleus	>TRINITY_DN176_c0_g1_i15 CATCATCATCTATCAAAAACAGTCGAAACGTTTTTAGTGTT TTAACAATCGACTTACTTTTTCTTCTCTAAATATCTACACAT ACAGACATCTCTATGTATACGTATATATATACACACACAAT
2	TRINITY_DN1296_c0_g1_i1	piezo-type mechanosensitive ion channel homolog	8225	0	CC	GO:0016020	membrane	>TRINITY_DN1296_c0_g1_i1 CCCATACATATAAAAATATTTTAATATATACATACAGCCCA CAACATAACTCCCCAGATCCAACAATCAGCGTACAAAATACT CACTACACTTTCGCAAGTTTCAGTTCTGTTCTGACTGGTAGT
3	TRINITY_DN846_c0_g1_i1	protein TSS	6673	0	CC	GO:0005737	cytoplasm	>TRINITY_DN846_c0_g1_i1 ATAATGCCATACATATATCTGACCCTTAAATCTTGACCCTTC CTTCCTTATCATCCTCACAATCTCCTCTATATCTTCTTCATTT TTATTTTCAGCTTGAGCTACTCACAGCTTCATTTCAAACTCT
4	TRINITY_DN20803_c0_g1_i3	nuclear pore complex protein GP210 isoform X1	6206	0	CC	GO:0110165	cellular anatomical entity	>TRINITY_DN20803_c0_g1_i3 GACCCACCCACAGACATAAACCCCCCTCATTCTCATCTTACAA

7. **About Page** of “*Bunium persicum*”.

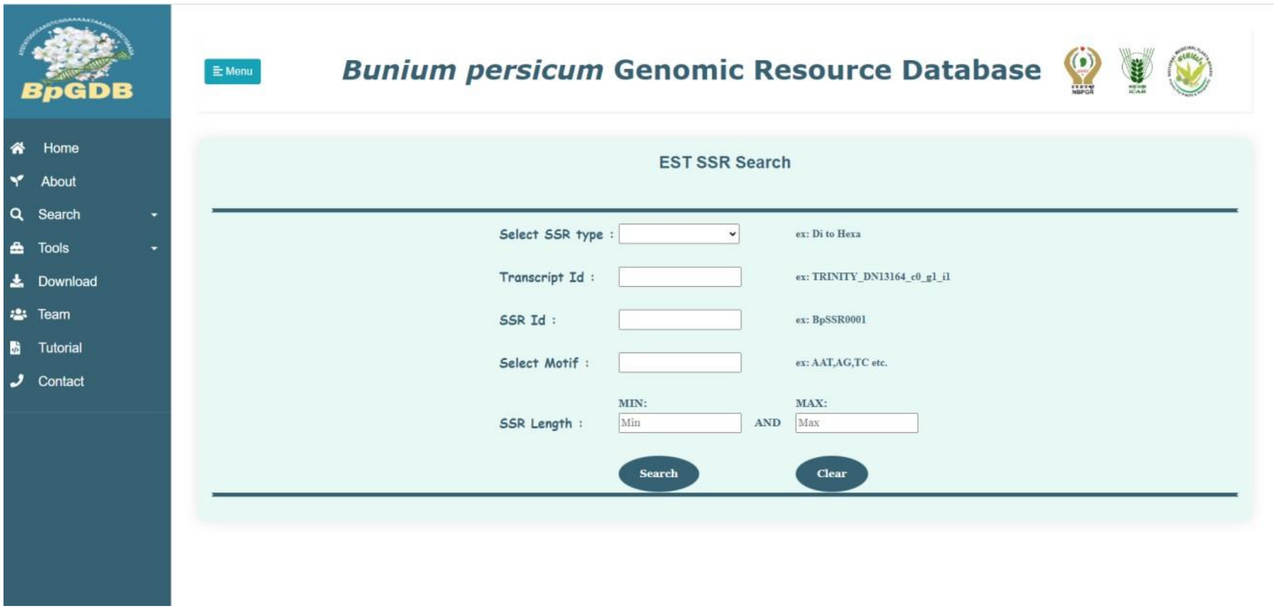


About Database

Bunium persicum (Boiss.) B. Fedtsch, synonymously called *Elwendia persica (Boiss.) Pimenov & Kljuykov* and commonly known as black cumin, is a perennial grass species native to dry temperate regions of Central Asia, including Iran, Egypt, Pakistan, Afghanistan, Kazakhstan and India. It is an aromatic plant with small white, pink or purple flowers, schizocarp fruits, and brown color seeds, which belong to the family Apiaceae. This plant has a rich history of traditional medicinal and culinary use, primarily due to the beneficial properties found in its seeds. The seeds of *B. persicum* are known for their essential oils and phenolic compounds, which contribute to their distinct flavor and potential health benefits. In recent years, *B. persicum* has garnered increasing attention due to its high medicinal value and potential as a valuable genetic resource for agricultural and environmental applications.

Very limited genomic information is available for this important medicinal plant in public databases or other resources. To address the growing need for genetic resources and genomic information in *B. persicum*, the establishment of a dedicated **Genomic Resource Database (BpGDB)** offers a centralized repository for storing, managing, and analyzing molecular data. Simple Sequence Repeats (SSRs) are valuable tools for genetic diversity assessment, population genetics studies, and marker-assisted breeding programs. SSRs, also known as microsatellites, are

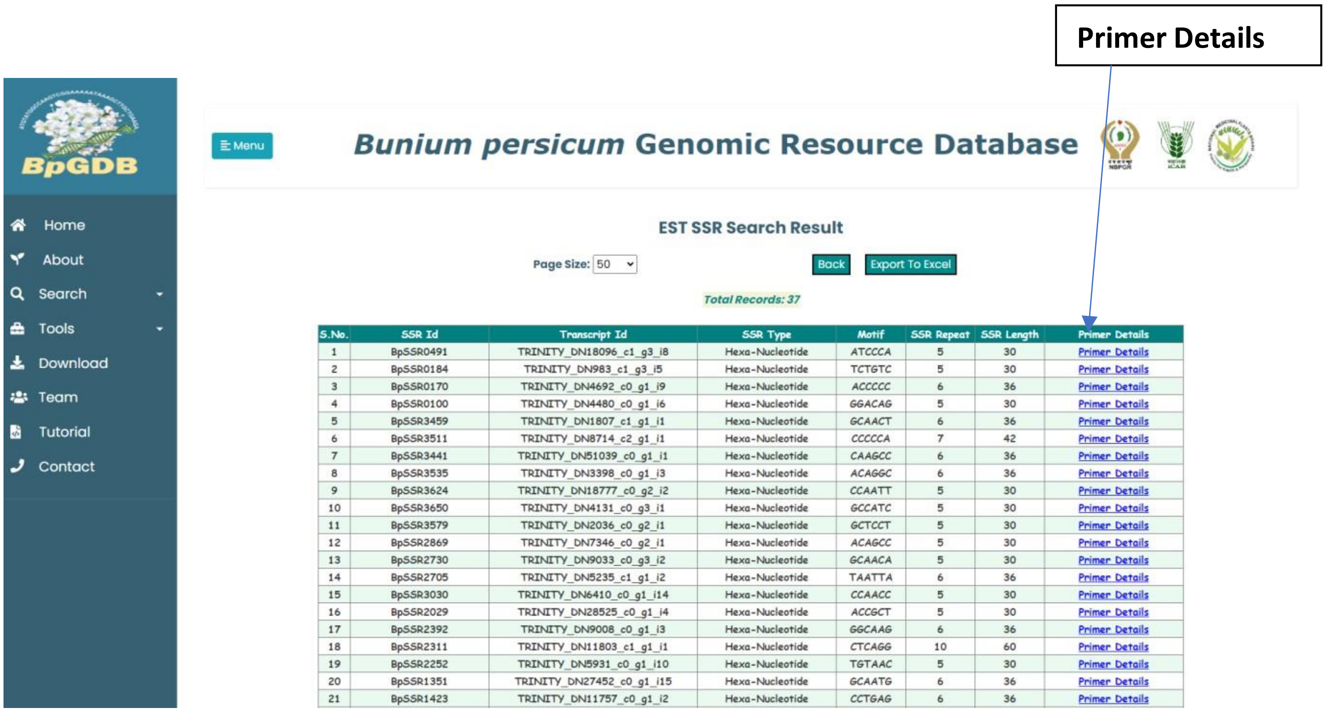
8. **SSR EST Search Page** which helps the user to search database on different parameters like SSR type, Transcript Id, SSR Id, Motif, SSR Length etc.



EST SSR Search

Select SSR type : ex: Di to Hexa
Transcript Id : ex: TRINITY_DN13164_c0_g1_i1
SSR Id : ex: BpSSR0001
Select Motif : ex: AAT,AG,TC etc.
SSR Length : MIN: Min AND MAX: Max

8.(a). Search Result Page consists further detail like SSR Id, Transcript Id, SSR type, Motif, SSR Repeat, SSR Length, Primer Details link with Export to Excel Facility Function.



Primer Details

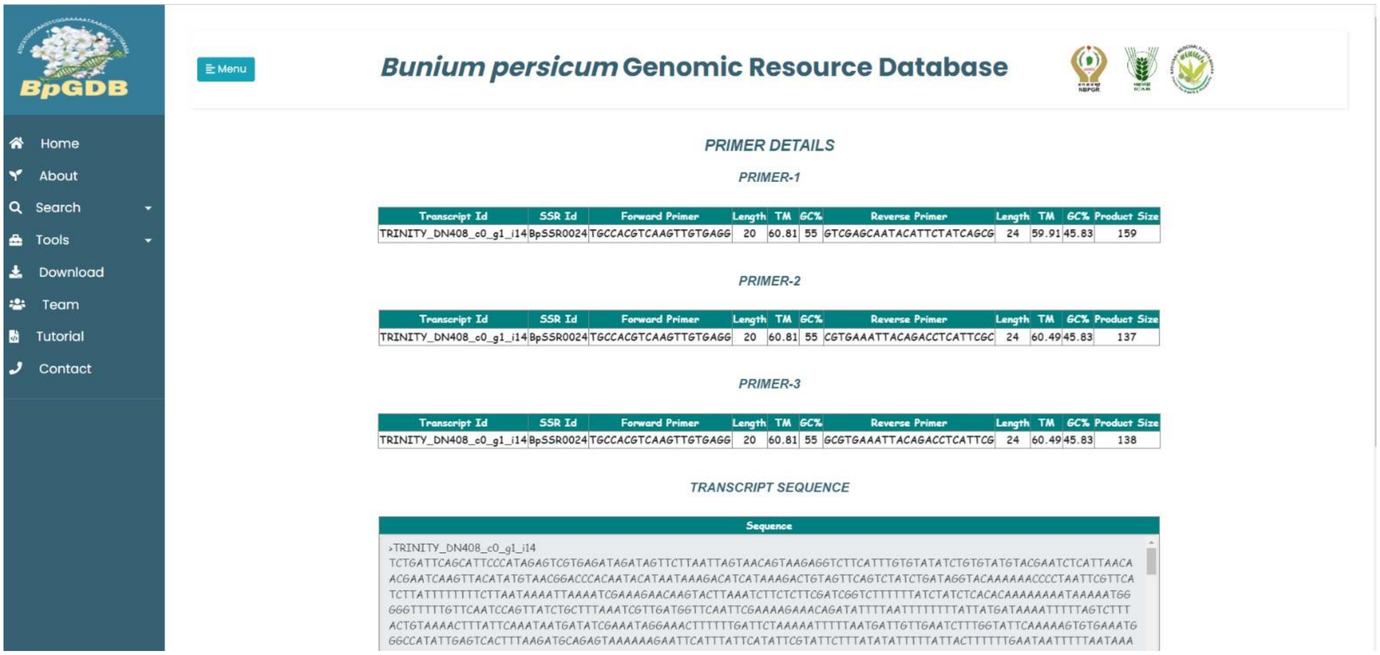
EST SSR Search Result

Page Size: 50

Total Records: 37

S.No.	SSR Id	Transcript Id	SSR Type	Motif	SSR Repeat	SSR Length	Primer Details
1	BpSSR0491	TRINITY_DN18096_c1_g3_i8	Hexa-Nucleotide	ATCCCA	5	30	Primer Details
2	BpSSR0184	TRINITY_DN983_c1_g3_i5	Hexa-Nucleotide	TCTGTC	5	30	Primer Details
3	BpSSR0170	TRINITY_DN4692_c0_g1_i9	Hexa-Nucleotide	ACCCCC	6	36	Primer Details
4	BpSSR0100	TRINITY_DN4480_c0_g1_i6	Hexa-Nucleotide	GGACAG	5	30	Primer Details
5	BpSSR3459	TRINITY_DN1807_c1_g1_i1	Hexa-Nucleotide	GCAACT	6	36	Primer Details
6	BpSSR3511	TRINITY_DN8714_c2_g1_i1	Hexa-Nucleotide	CCCCCA	7	42	Primer Details
7	BpSSR3441	TRINITY_DN51039_c0_g1_i1	Hexa-Nucleotide	CAAGCC	6	36	Primer Details
8	BpSSR3535	TRINITY_DN3398_c0_g1_i3	Hexa-Nucleotide	ACAGGC	6	36	Primer Details
9	BpSSR3624	TRINITY_DN18777_c0_g2_i2	Hexa-Nucleotide	CCAATT	5	30	Primer Details
10	BpSSR3650	TRINITY_DN4131_c0_g3_i1	Hexa-Nucleotide	GCCATC	5	30	Primer Details
11	BpSSR3579	TRINITY_DN2036_c0_g2_i1	Hexa-Nucleotide	GCTCCT	5	30	Primer Details
12	BpSSR2869	TRINITY_DN7346_c0_g2_i1	Hexa-Nucleotide	ACAGCC	5	30	Primer Details
13	BpSSR2730	TRINITY_DN9033_c0_g3_i2	Hexa-Nucleotide	GCAACA	5	30	Primer Details
14	BpSSR2705	TRINITY_DN5235_c1_g1_i2	Hexa-Nucleotide	TAATTA	6	36	Primer Details
15	BpSSR3030	TRINITY_DN6410_c0_g1_i14	Hexa-Nucleotide	CCAACC	5	30	Primer Details
16	BpSSR2029	TRINITY_DN28525_c0_g1_i4	Hexa-Nucleotide	ACCGCT	5	30	Primer Details
17	BpSSR2392	TRINITY_DN9008_c0_g1_i3	Hexa-Nucleotide	GGCAAG	6	36	Primer Details
18	BpSSR2311	TRINITY_DN11803_c1_g1_i1	Hexa-Nucleotide	CTCAGG	10	60	Primer Details
19	BpSSR2252	TRINITY_DN5931_c0_g1_i10	Hexa-Nucleotide	TGTAAC	5	30	Primer Details
20	BpSSR1351	TRINITY_DN27452_c0_g1_i15	Hexa-Nucleotide	GCAATG	6	36	Primer Details
21	BpSSR1423	TRINITY_DN11757_c0_g1_i2	Hexa-Nucleotide	CCTGAG	6	36	Primer Details

8.(b). Primer Details Link page consists further detail of Primer-1,2,3 & Transcript Sequence with Export to Excel Facility.



PRIMER DETAILS

PRIMER-1

Transcript Id	SSR Id	Forward Primer	Length	TM	GC%	Reverse Primer	Length	TM	GC%	Product Size
TRINITY_DN408_c0_g1_i14	BpSSR0024	TGCCACGTCAAGTTGTGAGG	20	60.81	55	GTCGAGCAATACATTCTATCAGCG	24	59.91	45.83	159

PRIMER-2

Transcript Id	SSR Id	Forward Primer	Length	TM	GC%	Reverse Primer	Length	TM	GC%	Product Size
TRINITY_DN408_c0_g1_i14	BpSSR0024	TGCCACGTCAAGTTGTGAGG	20	60.81	55	CGTGAAATTACAGACCTCATTCGC	24	60.49	45.83	137

PRIMER-3

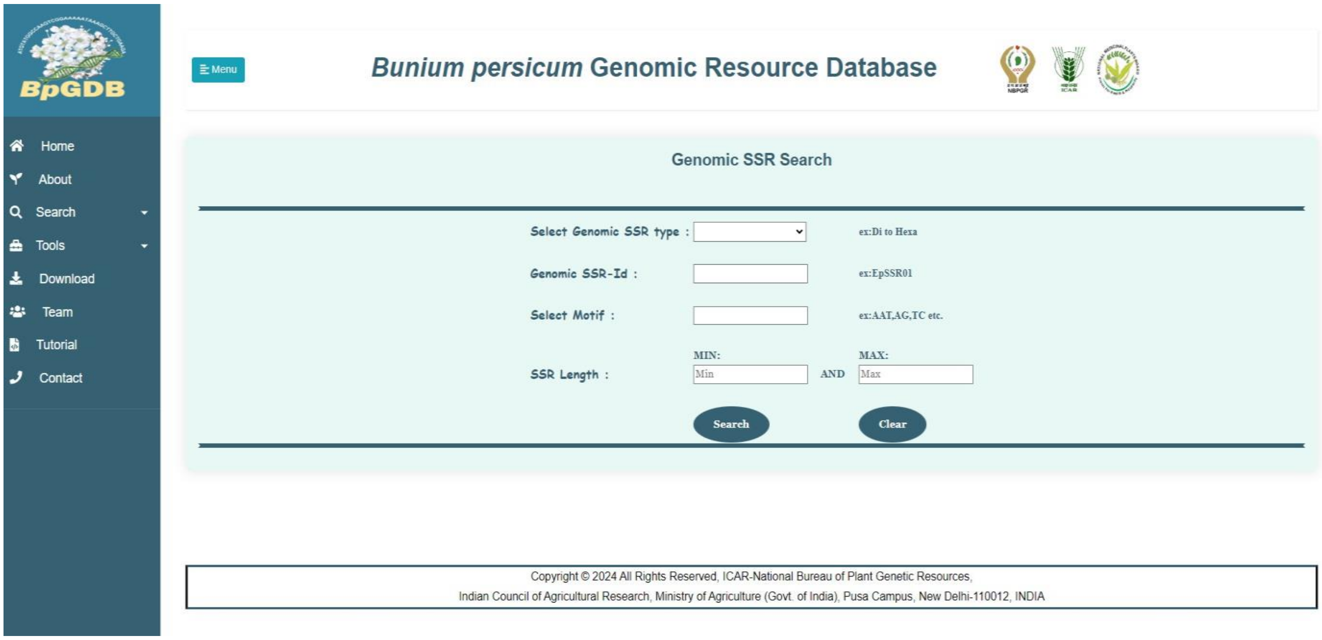
Transcript Id	SSR Id	Forward Primer	Length	TM	GC%	Reverse Primer	Length	TM	GC%	Product Size
TRINITY_DN408_c0_g1_i14	BpSSR0024	TGCCACGTCAAGTTGTGAGG	20	60.81	55	GCGTGAAATTACAGACCTCATTCG	24	60.49	45.83	138

TRANSCRIPT SEQUENCE

Sequence

```
>TRINITY_DN408_c0_g1_i14
TCTGATTCAGCATTCCCATAGAGTCGTGAGATAGATAGTTCTTAATTAGTAACAGTAAGAGGTCTTCATTTGTGTATATCTGTGTATGTACGAATCTCATTAACA
ACGAATCAAGTTACATATGTAACGGACCCACAATACATAATAAAGACATCATAAAGACTGTAGTTCAGTCTATCTGATAGGTACAAAAAACCCCTAATTCGTTCA
TCTTATTTTTTTTTCTTAATAAAATTAAAATCGAAAGAACAAGTACTTAAATCTTCTCTTCGATCGGTCTTTTTTATCTATCTCACACAAAAAAAAATAAAAATGG
GGGTTTTTGTTCAATCCAGTTATCTGCTTTAAATCGTTGATGGTTCAATTCGAAAAGAAACAGATATTTTAATTTTTTTTATTATGATAAAATTTTTAGTCTTT
ACTGTAAAACTTTATTCAAATAATGATATCGAAATAGGAAACTTTTTTGATTCTAAAAATTTTTAATGATTGTTGAATCTTTGGTATTCAAAAAGTGTGAAATG
GGCCATATTGAGTCACTTTAAGATGCAGAGTAAAAAAGAATTCATTTATTCATATTCGTATTCTTTATATATTTTTATTACTTTTTTGAATAATTTTTAATAAA
```

9. **SSR Genomic Search Page** which helps the user to search database on different parameters like Genomic SSR type, Genomic SSR Id, Motif, SSR Length etc.



Genomic SSR Search

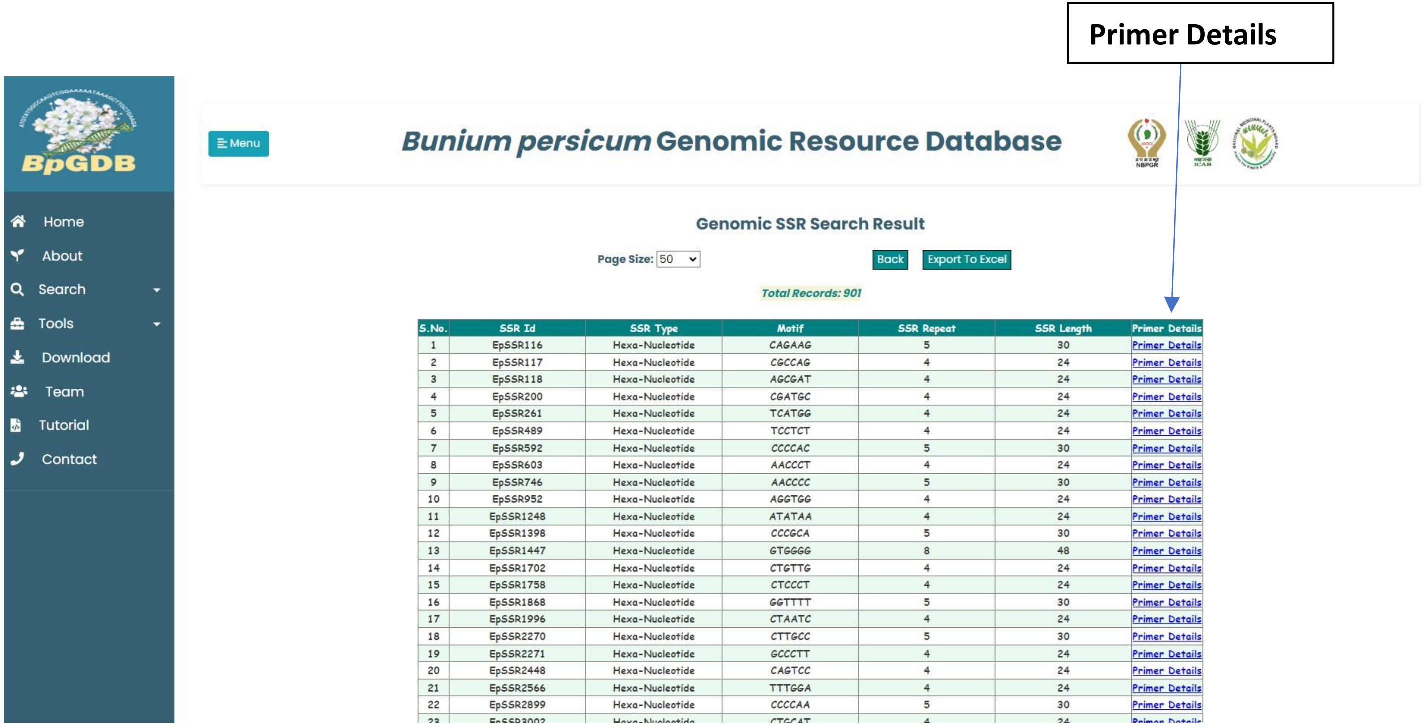
Select Genomic SSR type : ex:Di to Hexa

Genomic SSR-Id : ex:EpSSR01

Select Motif : ex:AAT,AG,TC etc.

SSR Length : MIN: Min AND MAX: Max

9.(a). Search Result Page consists further detail like SSR Id, SSR Type, Motif, SSR Repeat, SSR Length, Primer Details link with Export to Excel Facility Function.



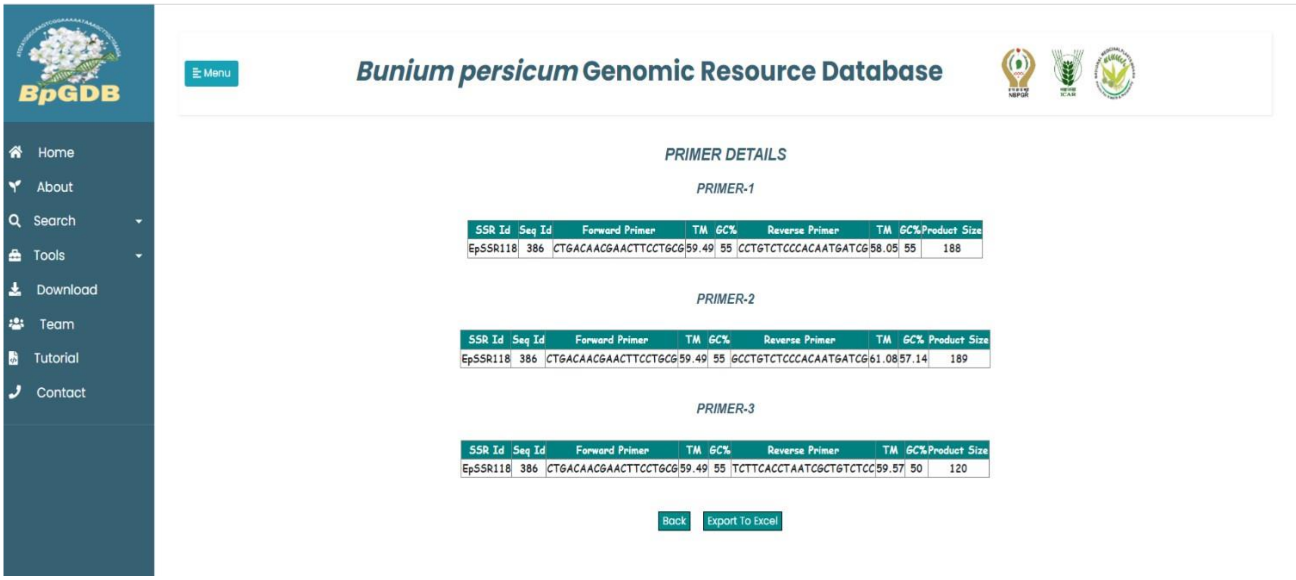
Genomic SSR Search Result

Page Size: 50

Total Records: 901

S.No.	SSR Id	SSR Type	Motif	SSR Repeat	SSR Length	Primer Details
1	EpSSR116	Hexa-Nucleotide	CAGAAG	5	30	Primer Details
2	EpSSR117	Hexa-Nucleotide	CGCCAG	4	24	Primer Details
3	EpSSR118	Hexa-Nucleotide	AGCGAT	4	24	Primer Details
4	EpSSR200	Hexa-Nucleotide	CGATGC	4	24	Primer Details
5	EpSSR261	Hexa-Nucleotide	TCATGG	4	24	Primer Details
6	EpSSR489	Hexa-Nucleotide	TCCTCT	4	24	Primer Details
7	EpSSR592	Hexa-Nucleotide	CCCCAC	5	30	Primer Details
8	EpSSR603	Hexa-Nucleotide	AACCCT	4	24	Primer Details
9	EpSSR746	Hexa-Nucleotide	AACCCC	5	30	Primer Details
10	EpSSR952	Hexa-Nucleotide	AGGTGG	4	24	Primer Details
11	EpSSR1248	Hexa-Nucleotide	ATATAA	4	24	Primer Details
12	EpSSR1398	Hexa-Nucleotide	CCCGCA	5	30	Primer Details
13	EpSSR1447	Hexa-Nucleotide	GTGGGG	8	48	Primer Details
14	EpSSR1702	Hexa-Nucleotide	CTGTTG	4	24	Primer Details
15	EpSSR1758	Hexa-Nucleotide	CTCCCT	4	24	Primer Details
16	EpSSR1868	Hexa-Nucleotide	GGTTTT	5	30	Primer Details
17	EpSSR1996	Hexa-Nucleotide	CTAATC	4	24	Primer Details
18	EpSSR2270	Hexa-Nucleotide	CTTGCC	5	30	Primer Details
19	EpSSR2271	Hexa-Nucleotide	GCCCTT	4	24	Primer Details
20	EpSSR2448	Hexa-Nucleotide	CAGTCC	4	24	Primer Details
21	EpSSR2566	Hexa-Nucleotide	TTTGGA	4	24	Primer Details
22	EpSSR2899	Hexa-Nucleotide	CCCCAA	5	30	Primer Details

9.(b). Primer Details Link page consists further detail of Primer-1,2,3 with Export to Excel Facility Function.



PRIMER DETAILS

PRIMER-1

SSR Id	Seq Id	Forward Primer	TM	GC%	Reverse Primer	TM	GC%	Product Size
EpSSR118	386	CTGACAACGAACTTCCTGCG	59.49	55	CCTGTCTCCCACAATGATCG	58.05	55	188

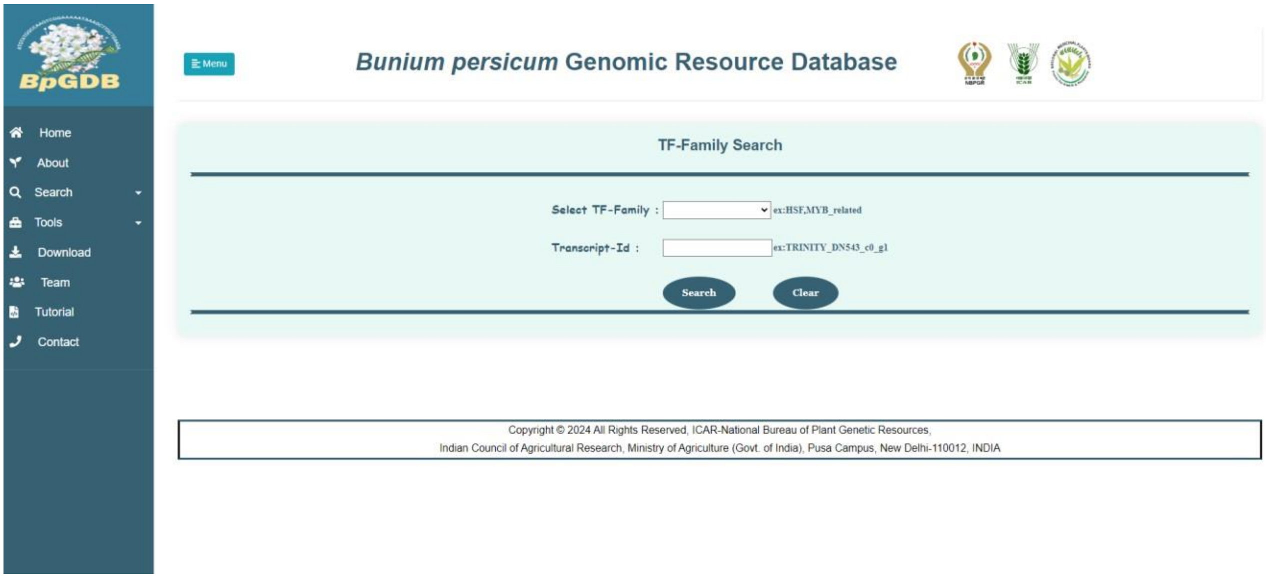
PRIMER-2

SSR Id	Seq Id	Forward Primer	TM	GC%	Reverse Primer	TM	GC%	Product Size
EpSSR118	386	CTGACAACGAACTTCCTGCG	59.49	55	GCCTGTCTCCCACAATGATCG	61.08	57.14	189

PRIMER-3

SSR Id	Seq Id	Forward Primer	TM	GC%	Reverse Primer	TM	GC%	Product Size
EpSSR118	386	CTGACAACGAACTTCCTGCG	59.49	55	TCTTCACCTAATCGCTGTCTCC	59.57	50	120

10. **TF-Family Search Page** which helps the user to search database on different parameters like TF Family and Transcript Id etc.



Bunium persicum Genomic Resource Database

TF-Family Search

Select TF-Family : ex:HSF,MYB_related

Transcript-Id : ex:TRINITY_DN543_c0_g1

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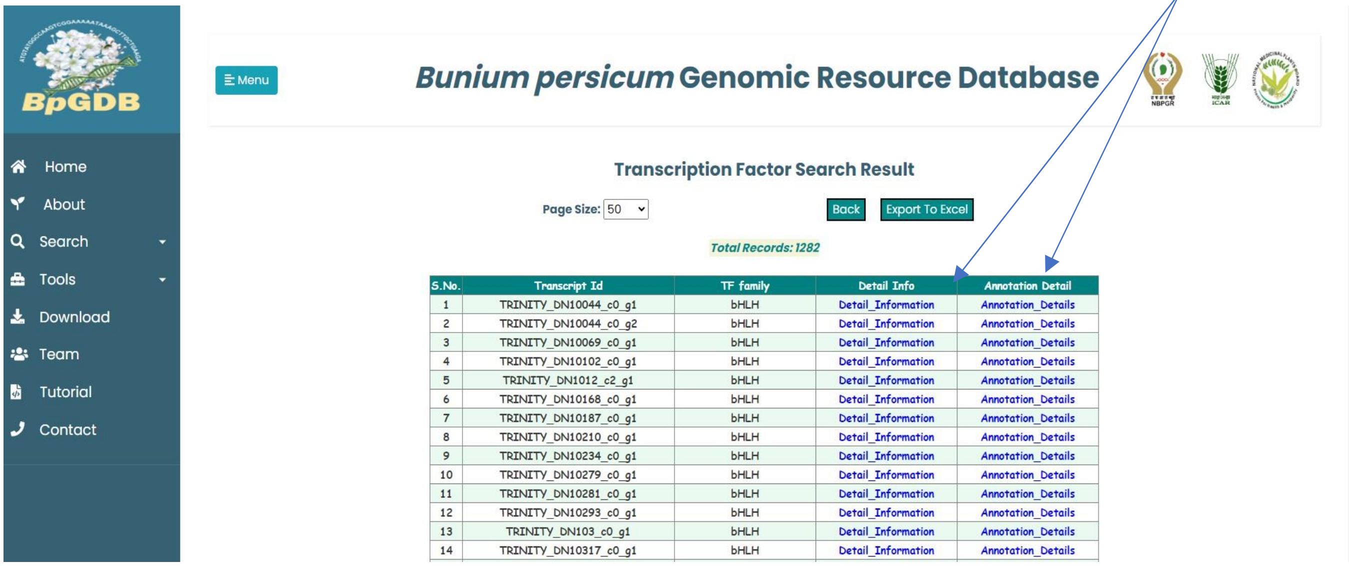
10.(a). Transcripts Factor Search Result Page consists further detail like Transcript Id, TF family, Annotation Detail link, Detail Information link with Export to Excel Facility Function.

Annotation Detail, Detail Information Link



Bunium persicum Genomic Resource Database

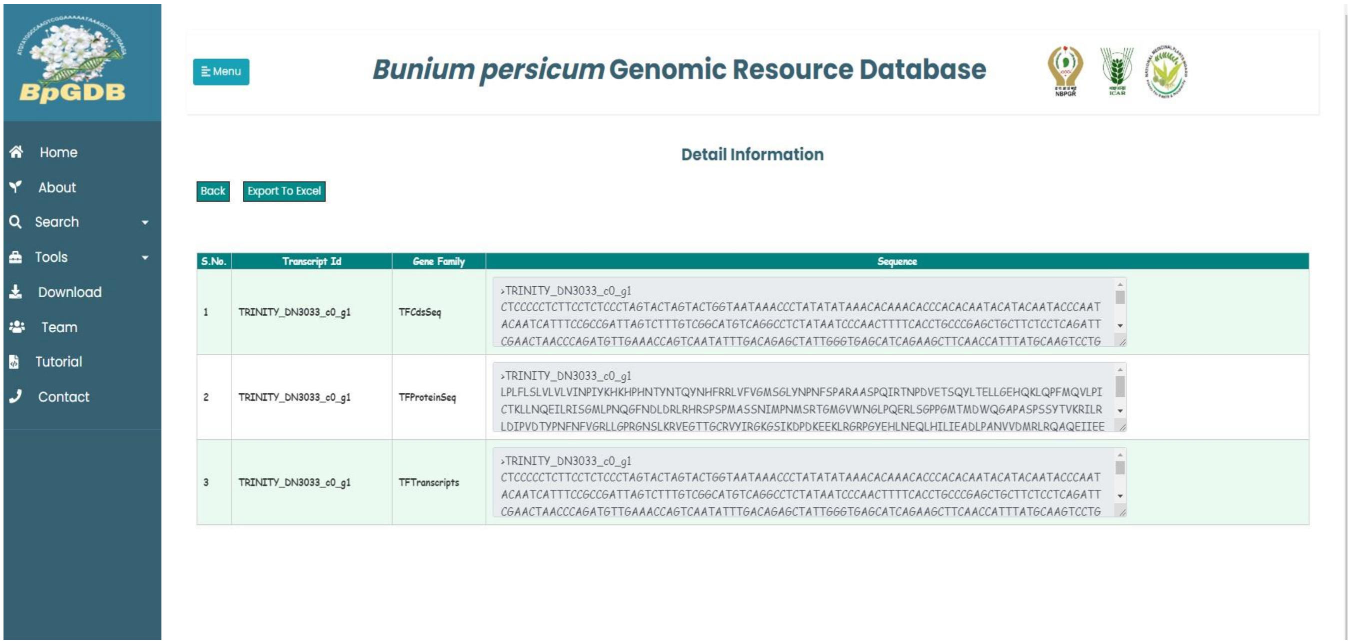
Transcription Factor Search Result

Page Size: 50

Total Records: 1282

S.No.	Transcript Id	TF family	Detail Info	Annotation Detail
1	TRINITY_DN10044_c0_g1	bHLH	Detail_Information	Annotation_Details
2	TRINITY_DN10044_c0_g2	bHLH	Detail_Information	Annotation_Details
3	TRINITY_DN10069_c0_g1	bHLH	Detail_Information	Annotation_Details
4	TRINITY_DN10102_c0_g1	bHLH	Detail_Information	Annotation_Details
5	TRINITY_DN1012_c2_g1	bHLH	Detail_Information	Annotation_Details
6	TRINITY_DN10168_c0_g1	bHLH	Detail_Information	Annotation_Details
7	TRINITY_DN10187_c0_g1	bHLH	Detail_Information	Annotation_Details
8	TRINITY_DN10210_c0_g1	bHLH	Detail_Information	Annotation_Details
9	TRINITY_DN10234_c0_g1	bHLH	Detail_Information	Annotation_Details
10	TRINITY_DN10279_c0_g1	bHLH	Detail_Information	Annotation_Details
11	TRINITY_DN10281_c0_g1	bHLH	Detail_Information	Annotation_Details
12	TRINITY_DN10293_c0_g1	bHLH	Detail_Information	Annotation_Details
13	TRINITY_DN103_c0_g1	bHLH	Detail_Information	Annotation_Details
14	TRINITY_DN10317_c0_g1	bHLH	Detail_Information	Annotation_Details

10.(b). Detail-Information link page consists of further detail like Transcript Id, Gene Family and Sequence with Export to Excel Facility Function.

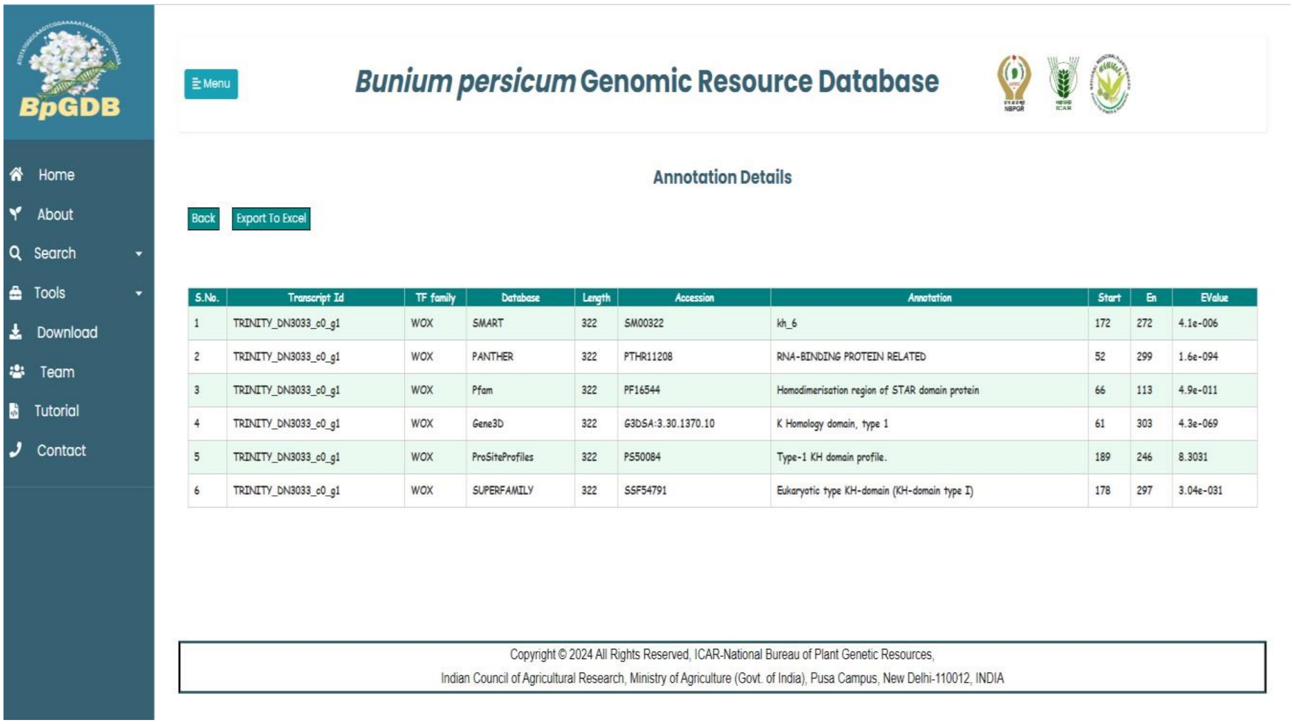


Bunium persicum Genomic Resource Database

Detail Information

S.No.	Transcript Id	Gene Family	Sequence
1	TRINITY_DN3033_c0_g1	TFCdsSeq	>TRINITY_DN3033_c0_g1 CTCCCCCTCTTCCTCTCCCTAGTACTAGTACTGGTAATAAACCCTATATATAAACACAAACACCCACACAATACATACAATACCCAAT ACAATCATTTCCGCCGATTAGTCTTTGTCGGCATGTCAGGCCTCTATAATCCCAACTTTTCACCTGCCCGAGCTGCTTCTCCTCAGATT CGAACTAACCCAGATGTTGAAACCAGTCAATATTTGACAGAGCTATTGGGTGAGCATCAGAAGCTTCAACCATTTATGCAAGTCCTG
2	TRINITY_DN3033_c0_g1	TFProteinSeq	>TRINITY_DN3033_c0_g1 LPLFLSLVLVLVINPIYKHKHPHNTYNTQYNHFRRLVFVGMSGLYNPNFSPARAASPQIRTNPDVETSQYLTELLGEHQKLQPFMQVLPI CTKLLNQEILRISGMLPNQGFNDLDRLRHRSPSPMASSNIMPNMSRTGMGVWNGLPQERLSGPPGMTMDWQGAPASPSSYTVKRILR LDIPVDTYPNFNFVGRLLGPRGNSLKRVEGTTGCRVYIRGKGSIKDPDKEEKLRGRPGYEHLNEQLHILIEADLPANVVDMRLRQAQEIIEE
3	TRINITY_DN3033_c0_g1	TFTranscripts	>TRINITY_DN3033_c0_g1 CTCCCCCTCTTCCTCTCCCTAGTACTAGTACTGGTAATAAACCCTATATATAAACACAAACACCCACACAATACATACAATACCCAAT ACAATCATTTCCGCCGATTAGTCTTTGTCGGCATGTCAGGCCTCTATAATCCCAACTTTTCACCTGCCCGAGCTGCTTCTCCTCAGATT CGAACTAACCCAGATGTTGAAACCAGTCAATATTTGACAGAGCTATTGGGTGAGCATCAGAAGCTTCAACCATTTATGCAAGTCCTG

10.(c). Annotation-Details link page consists of further detail like Transcript Id, TF family, Database, Length, Accession, Annotation, Start, En, E-value with Export to Excel Facility Function.



Bunium persicum Genomic Resource Database

Annotation Details

S.No.	Transcript Id	TF family	Database	Length	Accession	Annotation	Start	En	EValue
1	TRINITY_DN3033_c0_g1	WOX	SMART	322	SM00322	kh_6	172	272	4.1e-006
2	TRINITY_DN3033_c0_g1	WOX	PANTHER	322	PTHR11208	RNA-BINDING PROTEIN RELATED	52	299	1.6e-094
3	TRINITY_DN3033_c0_g1	WOX	Pfam	322	PF16544	Homodimerisation region of STAR domain protein	66	113	4.9e-011
4	TRINITY_DN3033_c0_g1	WOX	Gene3D	322	G3DSA:3.30.1370.10	K Homology domain, type 1	61	303	4.3e-069
5	TRINITY_DN3033_c0_g1	WOX	ProSiteProfiles	322	PS50084	Type-1 KH domain profile.	189	246	8.3031
6	TRINITY_DN3033_c0_g1	WOX	SUPERFAMILY	322	SSF54791	Eukaryotic type KH-domain (KH-domain type I)	178	297	3.04e-031

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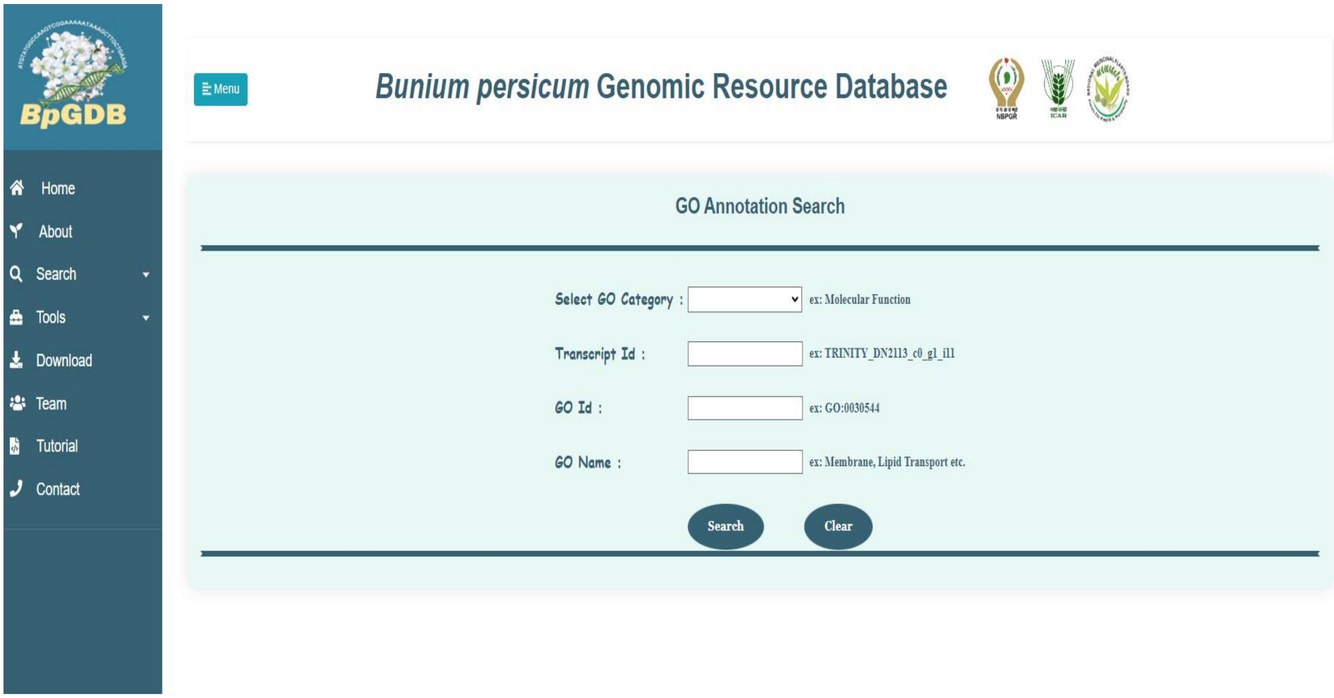
11. **GO-Annotation Search page** through which the user can search database based on different parameters like GO-Category, Transcript Id, GO Id, GO Name.



Bunium persicum Genomic Resource Database

GO Annotation Search

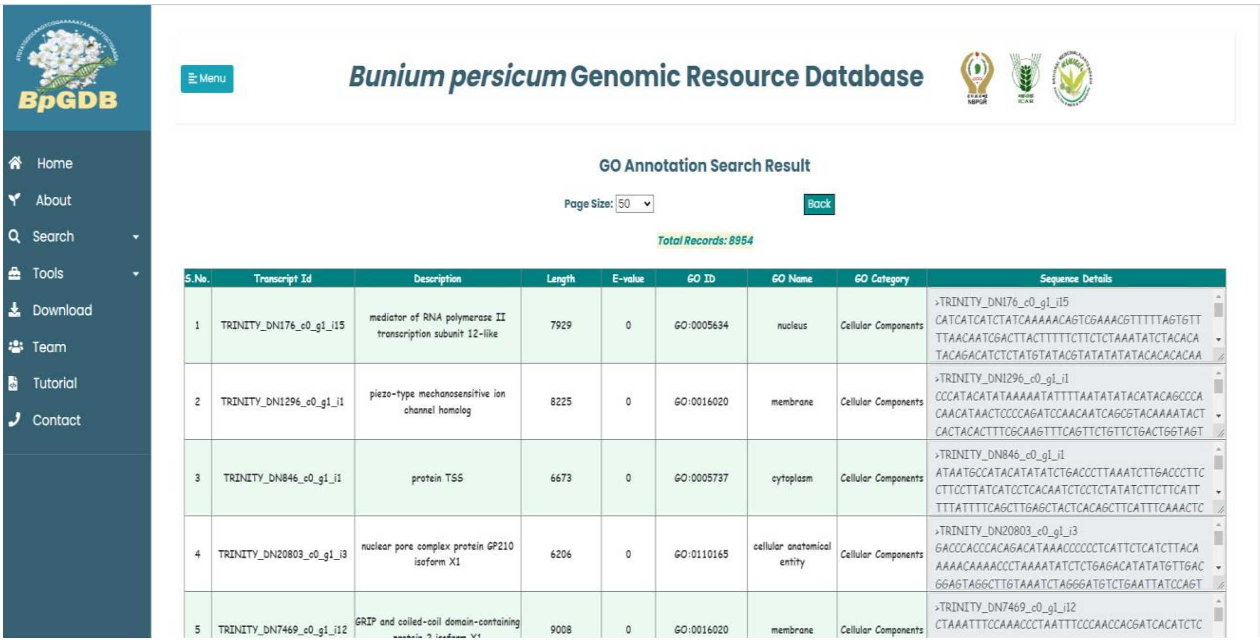
Select GO Category : ex: Molecular Function

Transcript Id : ex: TRINITY_DN2113_c0_g1_i11

GO Id : ex: GO:0030544

GO Name : ex: Membrane, Lipid Transport etc.

11.(a). GO Annotation Search Result page consists details like Transcript Id, Description, Length, E-value, GO Id, GO Name, Go Category with Sequence details.



Bunium persicum Genomic Resource Database

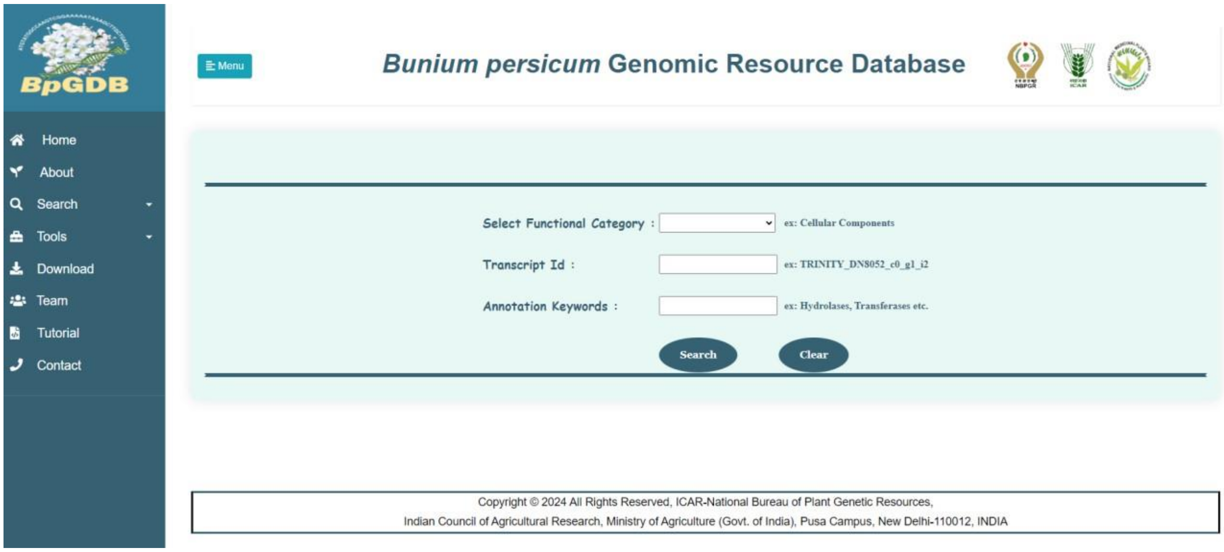
GO Annotation Search Result

Page Size: 50

Total Records: 8954

S.No.	Transcript Id	Description	Length	E-value	GO ID	GO Name	GO Category	Sequence Details
1	TRINITY_DN176_c0_g1_i15	mediator of RNA polymerase II transcription subunit 12-like	7929	0	GO:0005634	nucleus	Cellular Components	>TRINITY_DN176_c0_g1_i15 CATCATCATCTATCAAAAACAGTCGAAACGTTTTTAGTGTT TTAACAATCGACTTACTTTTTCTTCTCTAAATATCTACACA TACAGACATCTCTATGTATACGTATATATATACACACACAA
2	TRINITY_DN1296_c0_g1_i1	piezo-type mechanosensitive ion channel homolog	8225	0	GO:0016020	membrane	Cellular Components	>TRINITY_DN1296_c0_g1_i1 CCCATACATATAAAAATATTTTAATATATACATACAGCCCA CAACATAACTCCCCAGATCCAACAATCAGCGTACAAAATACT CACTACACTTTCGCAAGTTTCAGTTCTGTTCTGACTGGTAGT
3	TRINITY_DN846_c0_g1_i1	protein TSS	6673	0	GO:0005737	cytoplasm	Cellular Components	>TRINITY_DN846_c0_g1_i1 ATAATGCCATACATATATCTGACCCTTAAATCTTGACCCTTC CTTCCTTATCATCCTCACAATCTCCTCTATATCTTCTTCATT TTTATTTTCAGCTTGAGCTACTCACAGCTTCATTTCAAACTC
4	TRINITY_DN20803_c0_g1_i3	nuclear pore complex protein GP210 isoform X1	6206	0	GO:0110165	cellular anatomical entity	Cellular Components	>TRINITY_DN20803_c0_g1_i3 GACCCACCCACAGACATAAACCCCCCTCATTCTCATCTTACA AAAACAAAACCCTAAAATATCTCTGAGACATATATGTTGAC GGAGTAGGCTTGTAAATCTAGGGATGTCTGAATTATCCAGT
5	TRINITY_DN7469_c0_g1_i12	GRIP and coiled-coil domain-containing	9008	0	GO:0016020	membrane	Cellular Components	>TRINITY_DN7469_c0_g1_i12 CTAAATTTCCAAACCCTAATTTCCCAACCACGATCACATCTC

12. **NR Annotation Search page** through which the user can search database based on different parameters like Functional Category, Transcript Id, Annotation Keywords.



Bunium persicum Genomic Resource Database

Select Functional Category : ex: Cellular Components

Transcript Id : ex: TRINITY_DN8052_c0_g1_i2

Annotation Keywords : ex: Hydrolases, Transferases etc.

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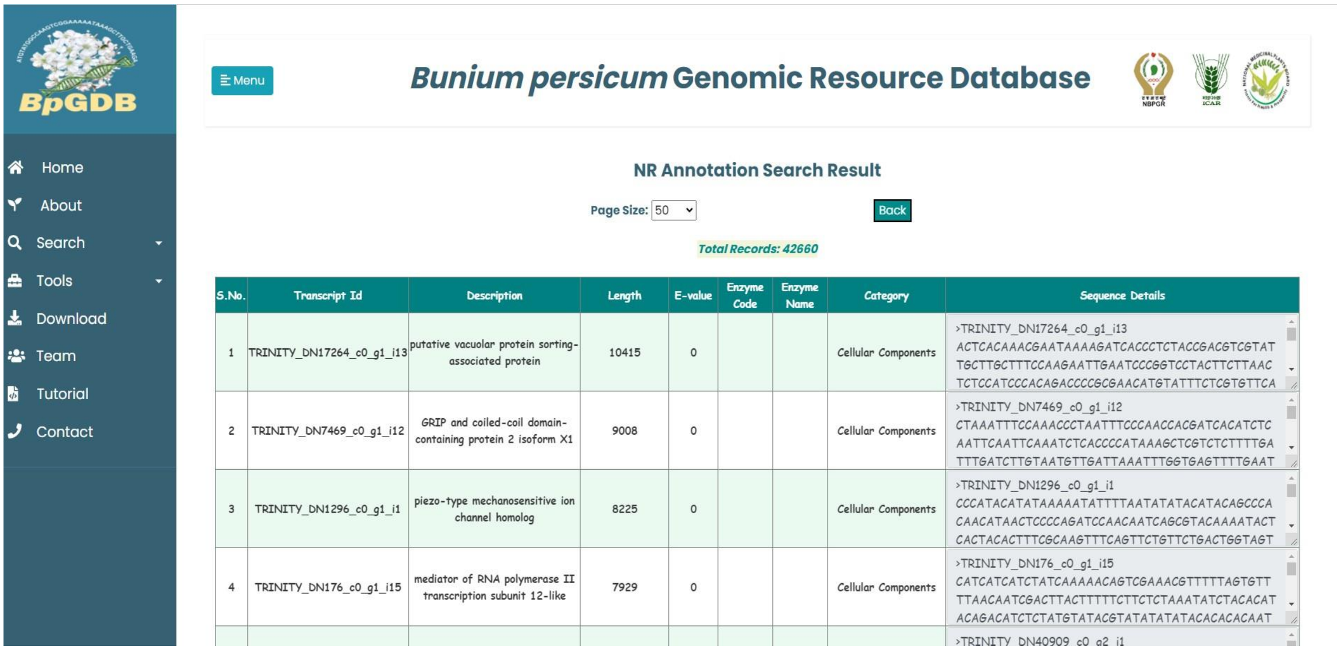
12.(a). NR Annotation Search Result page consists details like Transcript Id, Description, Length, E-value, Category, Enzyme Code, Enzyme Name with Sequence details.



Bunium persicum Genomic Resource Database

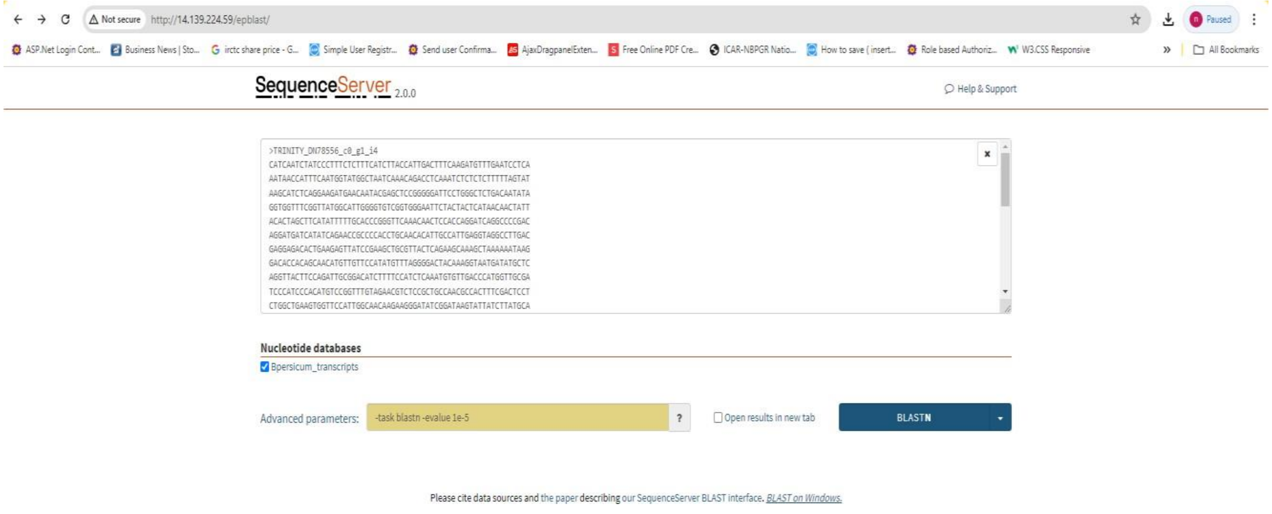
NR Annotation Search Result

Page Size: 50

Total Records: 42660

S.No.	Transcript Id	Description	Length	E-value	Enzyme Code	Enzyme Name	Category	Sequence Details
1	TRINITY_DN17264_c0_g1_i13	putative vacuolar protein sorting-associated protein	10415	0			Cellular Components	>TRINITY_DN17264_c0_g1_i13 ACTCACAAACGAATAAAAGATCACCCTCTACCGACGTCGTAT TGCTTGCTTTCCAAGAATTGAATCCCGGTCCTACTTCTTAAC TCTCCATCCCACAGACCCCGCGAACATGTATTTCTCGTGTTCA
2	TRINITY_DN7469_c0_g1_i12	GRIP and coiled-coil domain-containing protein 2 isoform X1	9008	0			Cellular Components	>TRINITY_DN7469_c0_g1_i12 CTAAATTTCCAAACCCTAATTTCCCAACCACGATCACATCTC AATTCAATTCAAATCTCACCCCATAAAGCTCGTCTCTTTTGA TTTGATCTTGTAATGTTGATTAAATTTGGTGAGTTTTGAAT
3	TRINITY_DN1296_c0_g1_i1	piezo-type mechanosensitive ion channel homolog	8225	0			Cellular Components	>TRINITY_DN1296_c0_g1_i1 CCCATACATATAAAAATATTTTAATATATACATACAGCCCA CAACATAACTCCCCAGATCCAACAATCAGCGTACAAAATACT CACTACACTTTCGCAAGTTTCAGTTCTGTTCTGACTGGTAGT
4	TRINITY_DN176_c0_g1_i15	mediator of RNA polymerase II transcription subunit 12-like	7929	0			Cellular Components	>TRINITY_DN176_c0_g1_i15 CATCATCATCTATCAAAAACAGTCGAAACGTTTTTAGTGTT TTAACAATCGACTTACTTTTTCTTCTCTAAATATCTACACAT ACAGACATCTCTATGTATACGTATATATATACACACACAAT
								>TRINITY_DN40909_c0_g2_i1

13. User can use Blast Search tool by clicking on Tools > Blast Search sub-menu to perform “Nucleotide Sequence search”



```
>TRINITY_DN78556_c0_g1_i4
CATCAATCTATCCCTTTCTCTTTCATCTTACCATTGACTTTCAAGATGTTTGAATCCTCA
AATAACCATTTCAATGGTATGGCTAATCAAACAGACCTCAAATCTCTCTCTTTTTAGTAT
AAGCATCTCAGGAAGATGAACAATACGAGCTCCGGGGGATTCCTGGGCTCTGACAATATA
GGTGGTTTCGGTTATGGCATTGGGGTGTCGGTGGGAATTCTACTACTCATAACAACTATT
ACACTAGCTTCATATTTTTGCACCCGGGTTCAAACAACTCCACCAGGATCAGGCCCCGAC
AGGATGATCATATCAGAACCGCCCCACCTGCAACACATTGCCATTGAGGTAGGCCTTGAC
GAGGAGACACTGAAGAGTTATCCGAAGCTGCGTTACTCAGAAGCAAAGCTAAAAAATAAG
GACACCACAGCAACATGTTGTTCCATATGTTTAGGGGACTACAAAGGTAATGATATGCTC
AGGTTACTTCCAGATTGCGGACATCTTTTCCATCTCAAATGTGTTGACCCATGGTTGCGA
TCCCATCCCACATGTCCGGTTTGTAGAACGTCTCCGCTGCCAACGCCACTTTCGACTCCT
CTGGCTGAAGTGGTTCCATTGGCAACAAGAAGGGATATCGGATAAGTATTATCTTATGCA
```

Nucleotide databases

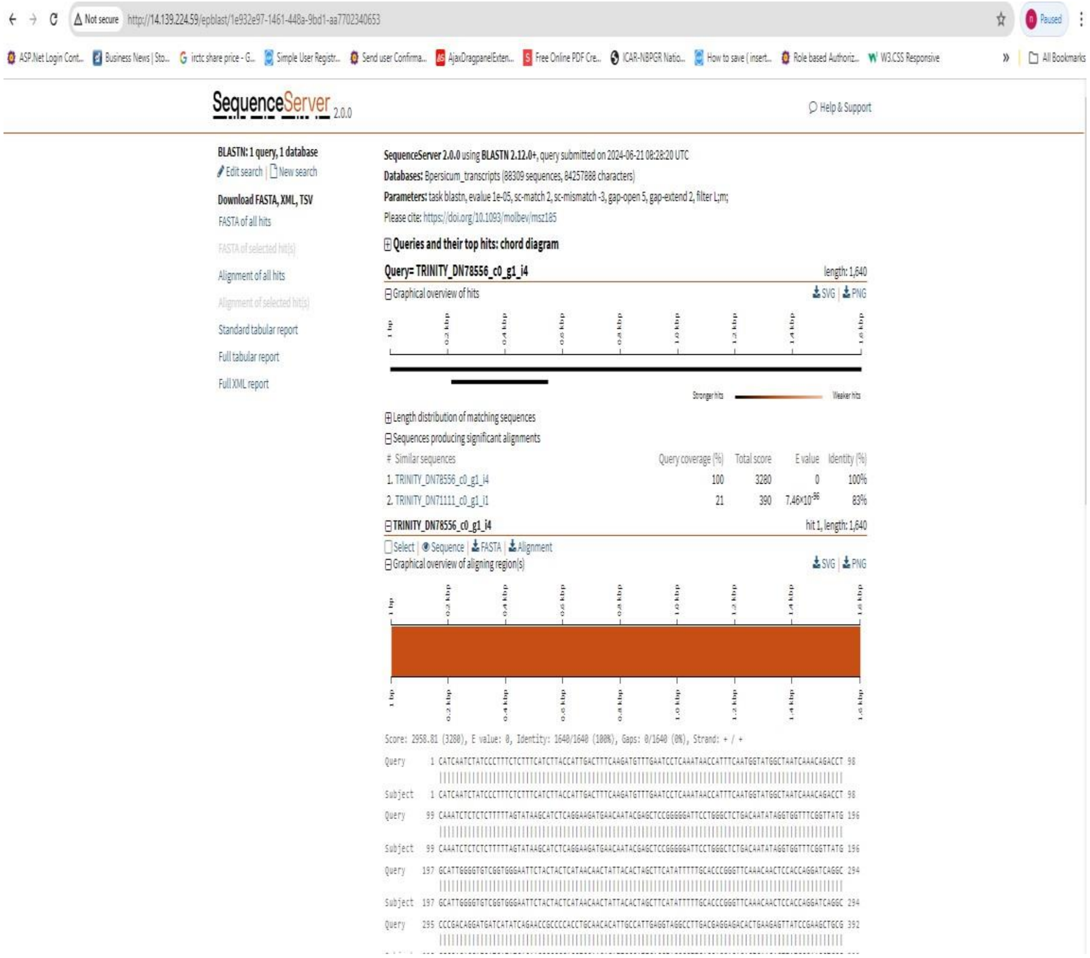
☑ Bpersicum_transcripts

Advanced parameters: -task blastn -evalue 1e-5 ?

☐ Open results in new tab

Please cite data sources and the paper describing our SequenceServer BLAST interface. BLAST on Windows.

13.(a). Search Parameters Results as follows.



BLASTN: 1 query, 1 database

Download FASTA, XML, TSV

SequenceServer 2.0.0 using **BLASTN 2.12.0+**, query submitted on 2024-06-21 08:28:20 UTC

Databases: Bpersicum_transcripts (88309 sequences, 84257888 characters)

Parameters: task blastn, evalue 1e-05, sc-match 2, sc-mismatch -3, gap-open 5, gap-extend 2, filter L;m;

Please cite: https://doi.org/10.1093/molbev/msz185

⊞ **Queries and their top hits: chord diagram**

Query= TRINITY_DN78556_c0_g1_i4 length: 1,640

⊟ Graphical overview of hits

⊞ Length distribution of matching sequences

⊟ Sequences producing significant alignments

# Similar sequences	Query coverage (%)	Total score	E value	Identity (%)
1. TRINITY_DN78556_c0_g1_i4	100	3280	0	100%
2. TRINITY_DN71111_c0_g1_i1	21	390	7.46×10^{-96}	83%

⊟ **TRINITY_DN78556_c0_g1_i4** hit 1, length: 1,640

⊟ Graphical overview of aligning region(s)

```
Score: 2958.81 (3280), E value: 0, Identity: 1640/1640 (100%), Gaps: 0/1640 (0%), Strand: + / +

Query     1 CATCAATCTATCCCTTTCTCTTTCATCTTACCATTGACTTTCAAGATGTTTGAATCCTCAAATAACCATTTCAATGGTATGGCTAATCAAACAGACCT 98
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Subject   1 CATCAATCTATCCCTTTCTCTTTCATCTTACCATTGACTTTCAAGATGTTTGAATCCTCAAATAACCATTTCAATGGTATGGCTAATCAAACAGACCT 98

Query    99 CAAATCTCTCTCTTTTTAGTATAAGCATCTCAGGAAGATGAACAATACGAGCTCCGGGGGATTCCTGGGCTCTGACAATATAGGTGGTTTCGGTTATG 196
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Subject  99 CAAATCTCTCTCTTTTTAGTATAAGCATCTCAGGAAGATGAACAATACGAGCTCCGGGGGATTCCTGGGCTCTGACAATATAGGTGGTTTCGGTTATG 196

Query   197 GCATTGGGGTGTCGGTGGGAATTCTACTACTCATAACAACTATTACACTAGCTTCATATTTTTGCACCCGGGTTCAAACAACTCCACCAGGATCAGGC 294
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Subject 197 GCATTGGGGTGTCGGTGGGAATTCTACTACTCATAACAACTATTACACTAGCTTCATATTTTTGCACCCGGGTTCAAACAACTCCACCAGGATCAGGC 294

Query   295 CCCGACAGGATGATCATATCAGAACCGCCCCACCTGCAACACATTGCCATTGAGGTAGGCCTTGACGAGGAGACACTGAAGAGTTATCCGAAGCTGCG 392
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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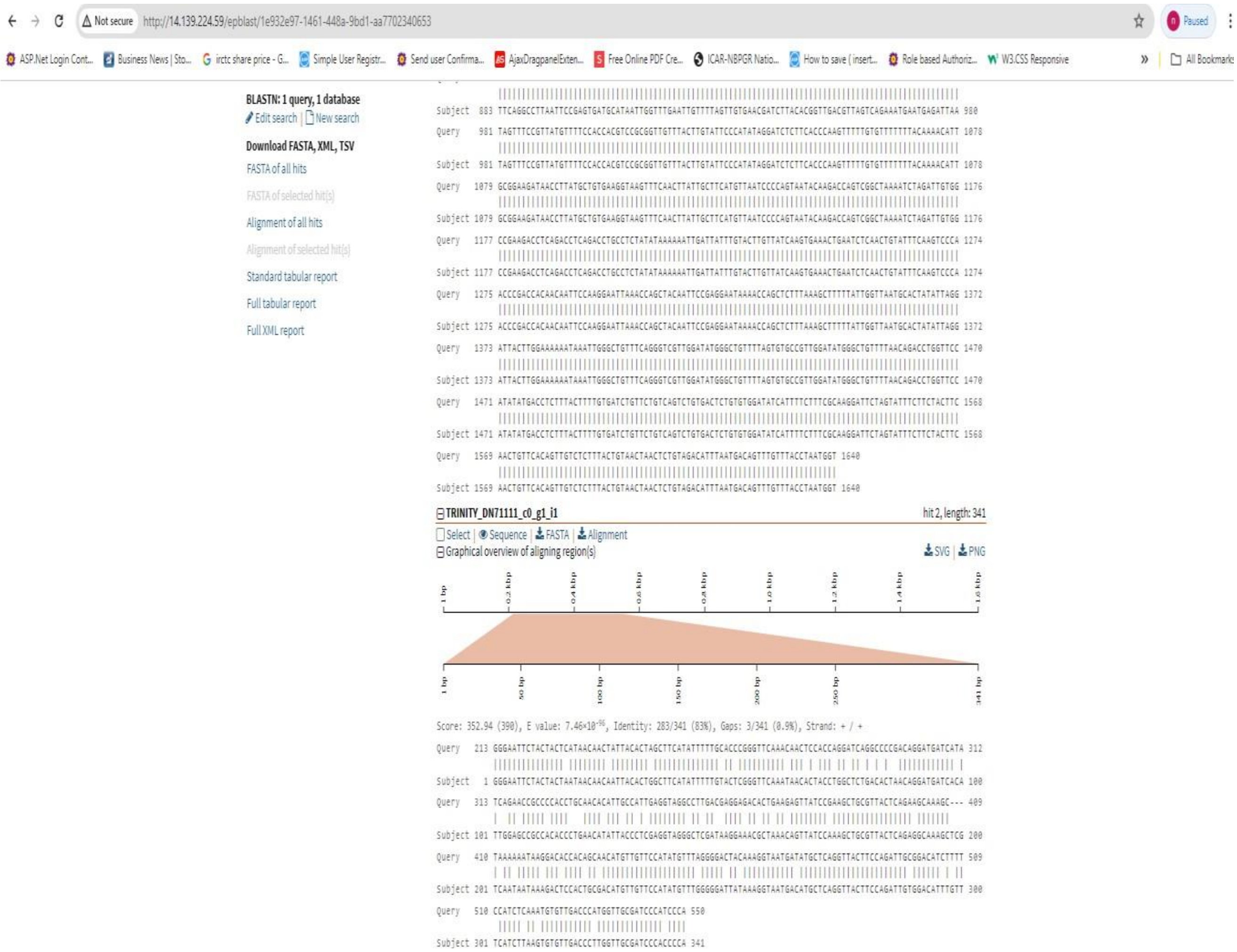
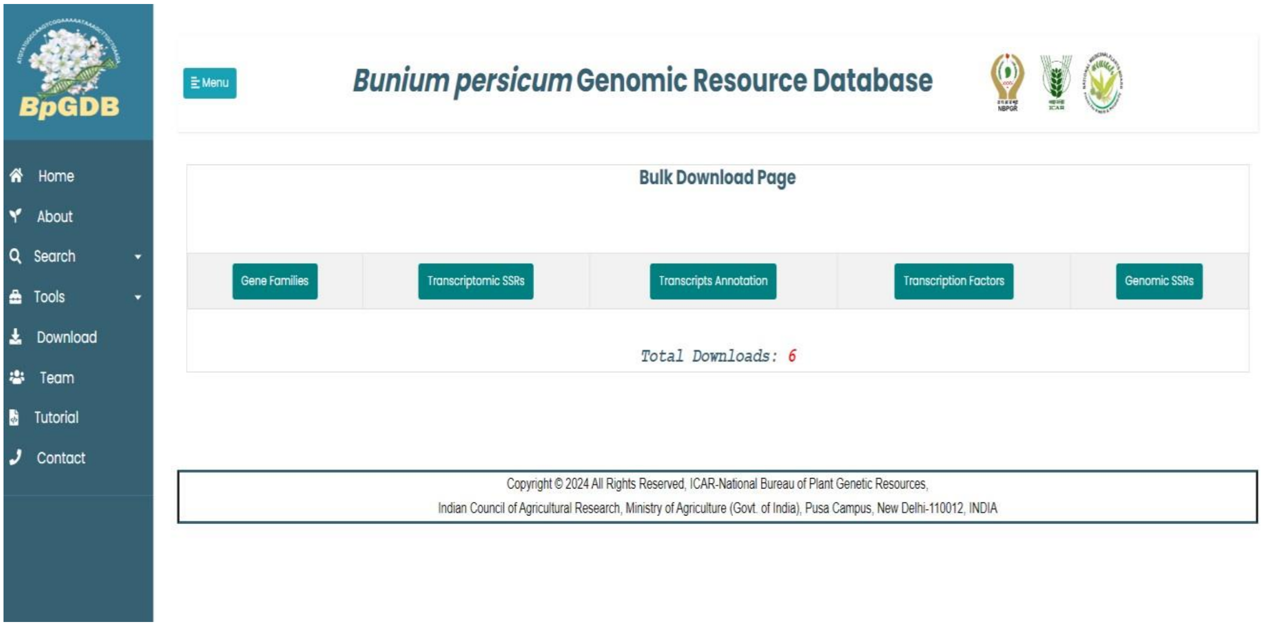


```
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Subject  883 TTCAGGCCTTAATTCCGAGTGATGCATAATTGGTTTGAATTGTTTTAGTTGTGAACGATCTTACACGGTTGACGTTAGTCAGAAATGAATGAGATTAA 980
Query    981 TAGTTTCCGTTATGTTTTCCACCACGTCCGCGGTTGTTTACTTGTATTCCCATATAGGATCTCTTCACCCAAGTTTTTGTGTTTTTTTACAAAACATT 1078
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Subject  981 TAGTTTCCGTTATGTTTTCCACCACGTCCGCGGTTGTTTACTTGTATTCCCATATAGGATCTCTTCACCCAAGTTTTTGTGTTTTTTTACAAAACATT 1078
Query   1079 GCGGAAGATAACCTTATGCTGTGAAGGTAAGTTTCAACTTATTGCTTCATGTTAATCCCCAGTAATACAAGACCAGTCGGCTAAAATCTAGATTGTGG 1176
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Subject 1079 GCGGAAGATAACCTTATGCTGTGAAGGTAAGTTTCAACTTATTGCTTCATGTTAATCCCCAGTAATACAAGACCAGTCGGCTAAAATCTAGATTGTGG 1176
Query   1177 CCGAAGACCTCAGACCTCAGACCTGCCTCTATATAAAAAATTGATTATTTGTACTTGTTATCAAGTGAAACTGAATCTCAACTGTATTTCAAGTCCCA 1274
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Subject 1177 CCGAAGACCTCAGACCTCAGACCTGCCTCTATATAAAAAATTGATTATTTGTACTTGTTATCAAGTGAAACTGAATCTCAACTGTATTTCAAGTCCCA 1274
Query   1275 ACCCGACCACAACAATTCCAAGGAATTAAACCAGCTACAATTCCGAGGAATAAAACCAGCTCTTTAAAGCTTTTTATTGGTTAATGCACTATATTAGG 1372
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Subject 1275 ACCCGACCACAACAATTCCAAGGAATTAAACCAGCTACAATTCCGAGGAATAAAACCAGCTCTTTAAAGCTTTTTATTGGTTAATGCACTATATTAGG 1372
Query   1373 ATTACTTGGAAAAAATAAATTGGGCTGTTTCAGGGTCGTTGGATATGGGCTGTTTTAGTGTGCCGTTGGATATGGGCTGTTTTAACAGACCTGGTTCC 1470
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Subject 1373 ATTACTTGGAAAAAATAAATTGGGCTGTTTCAGGGTCGTTGGATATGGGCTGTTTTAGTGTGCCGTTGGATATGGGCTGTTTTAACAGACCTGGTTCC 1470
Query   1471 ATATATGACCTCTTTACTTTTGTGATCTGTTCTGTCAGTCTGTGACTCTGTGTGGATATCATTTTCTTTCGCAAGGATTCTAGTATTTCTTCTACTTC 1568
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Subject 1471 ATATATGACCTCTTTACTTTTGTGATCTGTTCTGTCAGTCTGTGACTCTGTGTGGATATCATTTTCTTTCGCAAGGATTCTAGTATTTCTTCTACTTC 1568
Query   1569 AACTGTTCACAGTTGTCTCTTTACTGTAACTAACTCTGTAGACATTTAATGACAGTTTGTTTACCTAATGGT 1640
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Subject 1569 AACTGTTCACAGTTGTCTCTTTACTGTAACTAACTCTGTAGACATTTAATGACAGTTTGTTTACCTAATGGT 1640
```

```
Score: 352.94 (390), E value: 7.46×10⁻⁹⁶, Identity: 283/341 (83%), Gaps: 3/341 (0.9%), Strand: + / +

Query    213 GGGAATTCTACTACTCATAACAACTATTACACTAGCTTCATATTTTTGCACCCGGGTTCAAACAACTCCACCAGGATCAGGCCCCGACAGGATGATCATA 312
             ||||||||||||||| |||||||| |||||||| |||||||||||||| || |||||||||| || | |||| || || | | |  |||||||||||| |
Subject    1 GGGAATTCTACTACTAATAACAACAATTACACTGGCTTCATATTTTTGTACTCGGGTTCAAATAACACTACCTGGCTCTGACACTAACAGGATGATCACA 100
Query    313 TCAGAACCGCCCCACCTGCAACACATTGCCATTGAGGTAGGCCTTGACGAGGAGACACTGAAGAGTTATCCGAAGCTGCGTTACTCAGAAGCAAAGC--- 409
             |  || ||||| ||||   |||| ||| || | |||||||| || ||  |||| || || || |||||||| ||||||||||||||||| |||||||
Subject  101 TTGGAGCCGCCACACCCTGAACATATTACCCTCGAGGTAGGGCTCGATAAGGAAACGCTAAACAGTTATCCAAAGCTGCGTTACTCAGAGGCAAAGCTCG 200
Query    410 TAAAAAATAAGGACACCACAGCAACATGTTGTTCCATATGTTTAGGGGACTACAAAGGTAATGATATGCTCAGGTTACTTCCAGATTGCGGACATCTTTT 509
             | || ||||| ||| |||| || |||||||||||||||||||| ||||| || ||||||||||| ||||||||||||||||||||||| |||||| | ||
Subject  201 TCAATAATAAAGACTCCACTGCGACATGTTGTTCCATATGTTTGGGGGATTATAAAGGTAATGACATGCTCAGGTTACTTCCAGATTGTGGACATTTGTT 300
Query    510 CCATCTCAAATGTGTTGACCCATGGTTGCGATCCCATCCCA 550
              ||||| || ||||||||||| |||||||||||||| ||||
Subject  301 TCATCTTAAGTGTGTTGACCCTTGGTTGCGATCCCACCCCA 341
```

14. **Download Page** from where the user can download Bulk Data which also keep record of total number of downloads done by the user.



Total Downloads: 6

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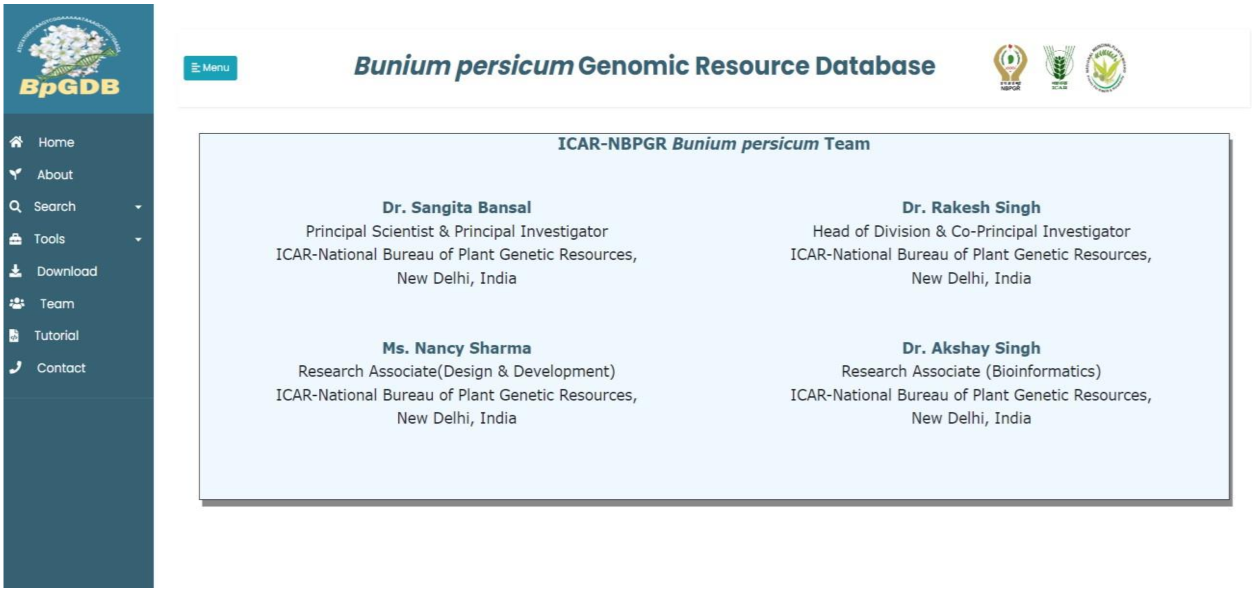
Indian Council of Agricultural Research, Ministry of Agriculture (Govt. of India), Pusa Campus, New Delhi-110012, INDIA

15. **Team Page** which consists the detail of persons who are involved in this project.



***Bunium persicum* Genomic Resource Database**

ICAR-NBPGR *Bunium persicum* Team

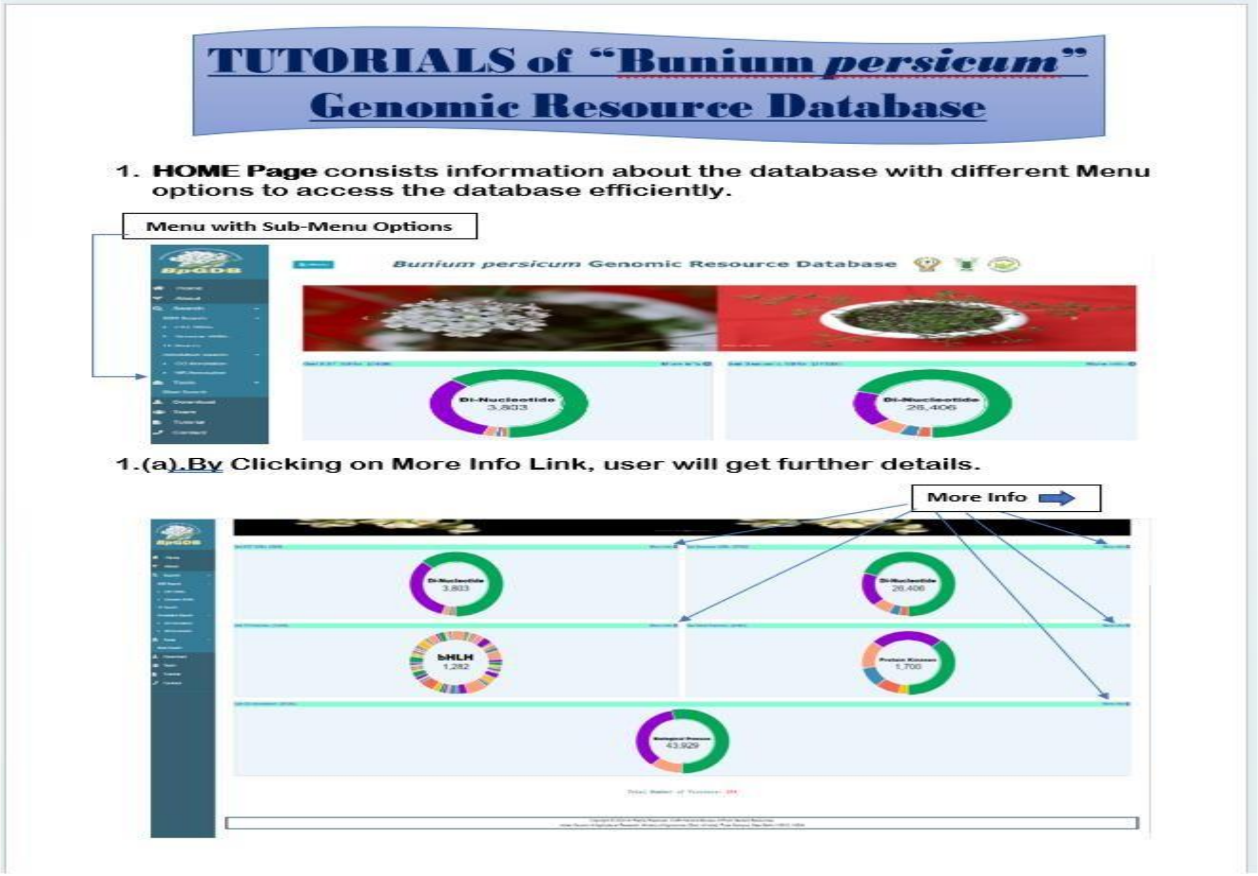
Dr. Sangita Bansal
Principal Scientist & Principal Investigator
ICAR-National Bureau of Plant Genetic Resources,
New Delhi, India

Dr. Rakesh Singh
Head of Division & Co-Principal Investigator
ICAR-National Bureau of Plant Genetic Resources,
New Delhi, India

Ms. Nancy Sharma
Research Associate(Design & Development)
ICAR-National Bureau of Plant Genetic Resources,
New Delhi, India

Dr. Akshay Singh
Research Associate (Bioinformatics)
ICAR-National Bureau of Plant Genetic Resources,
New Delhi, India

16. **Tutorial/Manual Page** which helps the user to access the database easily & efficiently.

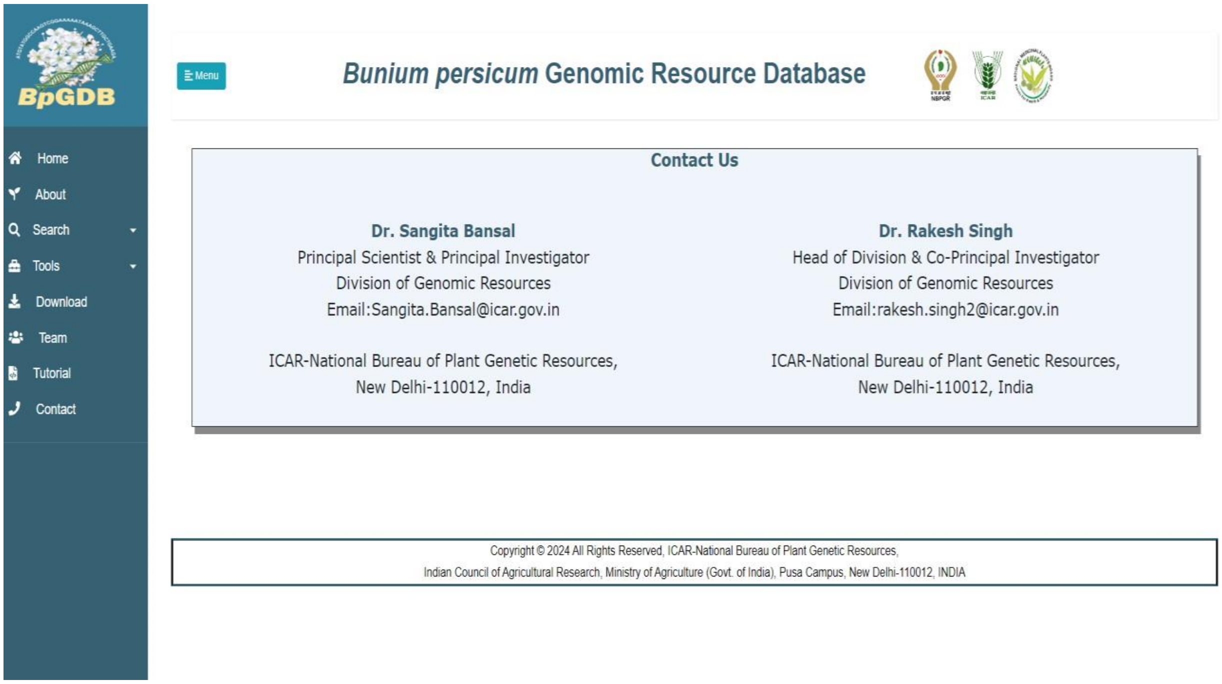


TUTORIALS of "Bunium *persicum*" Genomic Resource Database

1. **HOME Page** consists information about the database with different Menu options to access the database efficiently.

1.(a).By Clicking on More Info Link, user will get further details.

17. **Contact Us Page** consists the detail of the persons with whom the user can send their queries or suggestions.



Bunium persicum Genomic Resource Database

Contact Us

Dr. Sangita Bansal
Principal Scientist & Principal Investigator
Division of Genomic Resources
Email:Sangita.Bansal@icar.gov.in

ICAR-National Bureau of Plant Genetic Resources,
New Delhi-110012, India

Dr. Rakesh Singh
Head of Division & Co-Principal Investigator
Division of Genomic Resources
Email:rakesh.singh2@icar.gov.in

ICAR-National Bureau of Plant Genetic Resources,
New Delhi-110012, India

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