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Last update: 3 March 2025

PapayNetBase Tutorial

Sitemap of ***PapayaNetBase.*** There are nine menus for users to explore in the ***PapayaNetBase.***

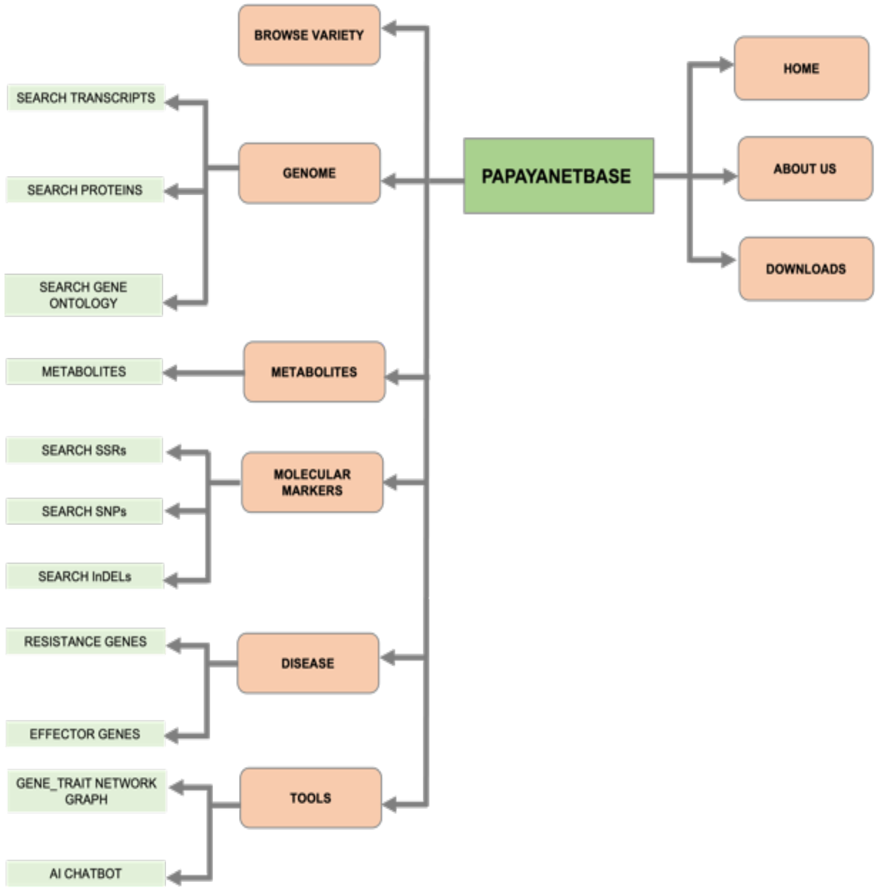
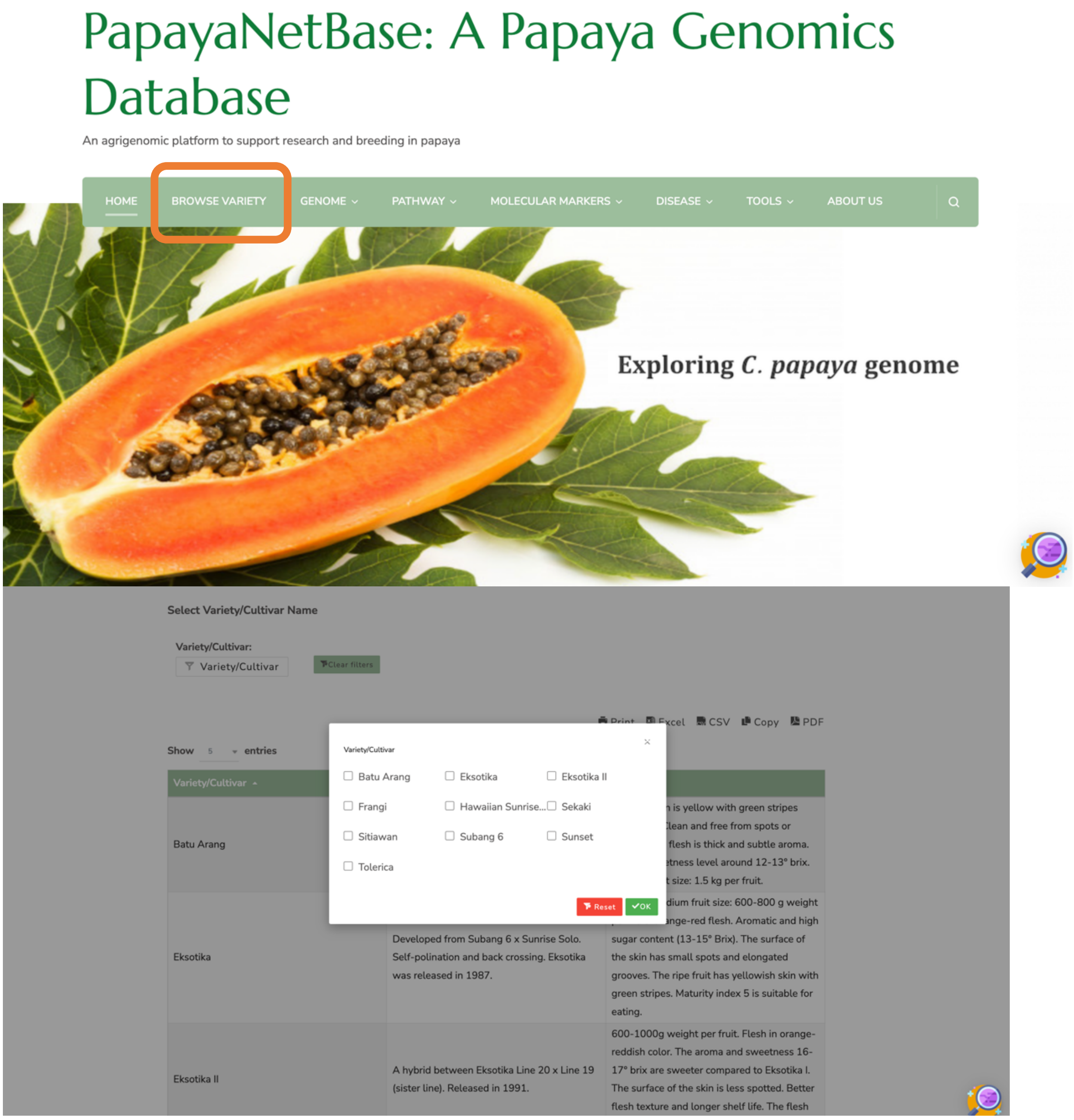


Figure 1. Sitemap of ***PapayaNetBase.***

From the 'Home' menu or main page, users can select any of these menus to search, browse, or filter the available data. The 'Browse Variety' menu provides information on local papaya varieties using the search and filter function.

Search for information on papaya varieties



PapayaNetBase: A Papaya Genomics Database

An agrigenomic platform to support research and breeding in papaya

Select Variety/Cultivar Name

Variety/Cultivar:

Variety/Cultivar

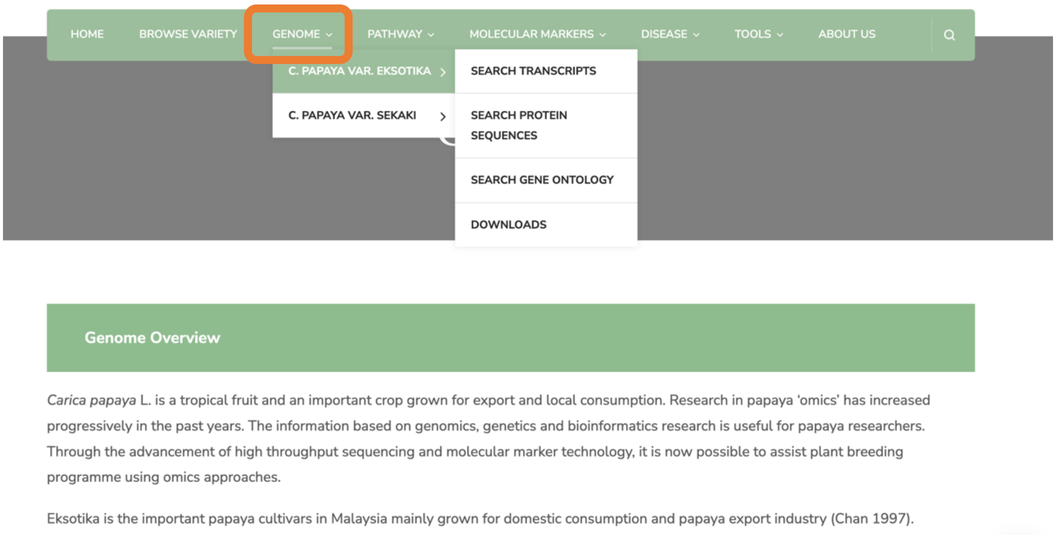
☐ Batu Arang ☐ Eksotika ☐ Eksotika II
☐ Frangi ☐ Hawaiian Sunrise... ☐ Sekaki
☐ Sitiawan ☐ Subang 6 ☐ Sunset
☐ Tolerica

Variety/Cultivar		
Batu Arang		n is yellow with green stripes lean and free from spots or flesh is thick and subtle aroma. tness level around 12-13° brix. t size: 1.5 kg per fruit.
Eksotika	Developed from Subang 6 x Sunrise Solo. Self-polination and back crossing. Eksotika was released in 1987.	dium fruit size: 600-800 g weight nge-red flesh. Aromatic and high sugar content (13-15° Brix). The surface of the skin has small spots and elongated grooves. The ripe fruit has yellowish skin with green stripes. Maturity index 5 is suitable for eating.
Eksotika II	A hybrid between Eksotika Line 20 x Line 19 (sister line). Released in 1991.	600-1000g weight per fruit. Flesh in orange-reddish color. The aroma and sweetness 16-17° brix are sweeter compared to Eksotika I. The surface of the skin is less spotted. Better flesh texture and longer shelf life. The flesh

Figure 2. Filter variety/cultivar using multi check-box. The results will display in table format.

Search for papaya genome information

The 'Genome' menu allows users to query transcripts, protein, and gene ontology from C. papaya var. Eksotika and C. papaya var. Sekaki. The Eksotika and Sekaki genome overview are displayed in 'Genome' page.
There are three sub-menus under each variety menu where user can: i) search for predicted transcripts annotation, ii) search for protein sequences, and iii) search for gene ontology.

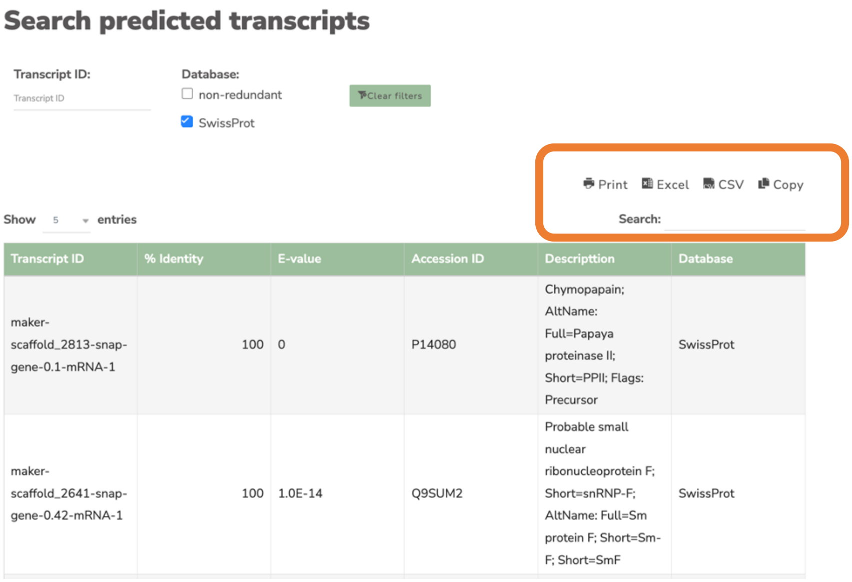


Carica papaya L. is a tropical fruit and an important crop grown for export and local consumption. Research in papaya 'omics' has increased progressively in the past years. The information based on genomics, genetics and bioinformatics research is useful for papaya researchers. Through the advancement of high throughput sequencing and molecular marker technology, it is now possible to assist plant breeding programme using omics approaches.

Eksotika is the important papaya cultivars in Malaysia mainly grown for domestic consumption and papaya export industry (Chan 1997).

Search for Eksotika/Sekaki transcripts

Select 'database' OR type 'transcript ID'. Click 'Excel' OR 'CSV' to download the results. Use 'Search' to search any keyword of interest.



Search predicted transcripts

Transcript ID: Transcript ID

Database:
☐ non-redundant
☑ SwissProt

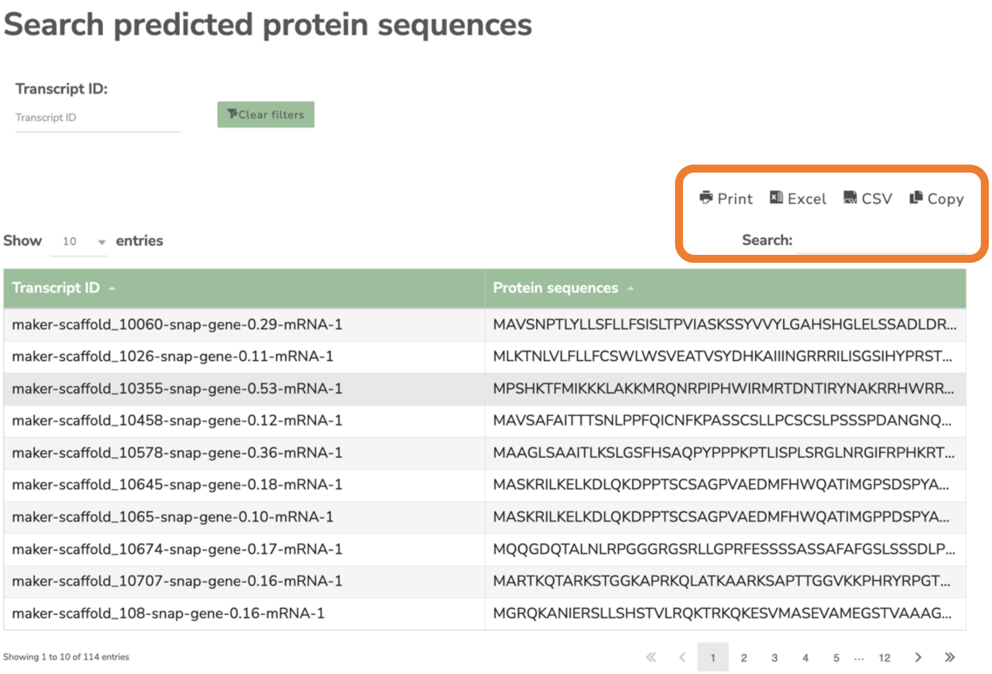
Show 5 entries

Search:

Transcript ID	% Identity	E-value	Accession ID	Descripttion	Database
maker-scaffold_2813-snap-gene-0.1-mRNA-1	100	0	P14080	Chymopapain; AltName: Full=Papaya proteinase II; Short=PPII; Flags: Precursor	SwissProt
maker-scaffold_2641-snap-gene-0.42-mRNA-1	100	1.0E-14	Q9SUM2	Probable small nuclear ribonucleoprotein F; Short=snRNP-F; AltName: Full=Sm protein F; Short=Sm-F; Short=SmF	SwissProt

Search for Eksotika/Sekaki protein sequences

Type 'transcript ID'. Click 'Excel' OR 'CSV' to download the results. Use 'Search' to search any keyword of interest.



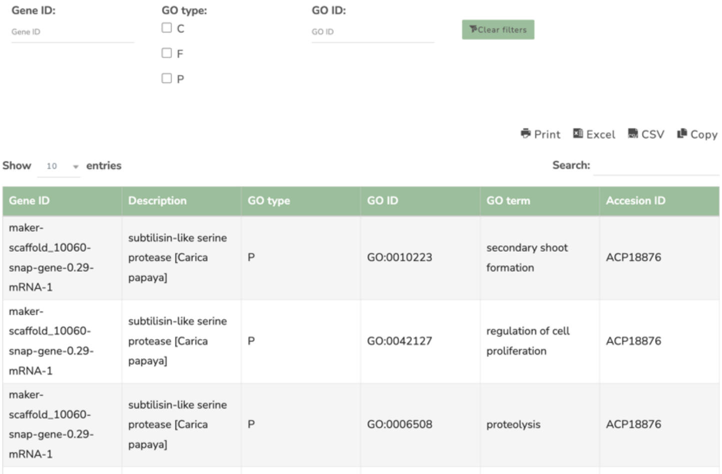
Search predicted protein sequences

Transcript ID	Protein sequences
maker-scaffold_10060-snap-gene-0.29-mRNA-1	MAVSNPTLYLLSFLLFSISLTPVIASKSSYVVYLGAHSHGLELSSADLDR...
maker-scaffold_1026-snap-gene-0.11-mRNA-1	MLKTNLVLFLLFCSWLWSVEATVSYDHKAIIINGRRRILISGSIHYPRST...
maker-scaffold_10355-snap-gene-0.53-mRNA-1	MPSHKTFMIKKKLAKKMRQNRPIPHWIRMRTDNTIRYNAKRRHWRR...
maker-scaffold_10458-snap-gene-0.12-mRNA-1	MAVSAFAITTTSNLPPFQICNFKPASSCSLLPCSCSLPSSSPDANGNQ...
maker-scaffold_10578-snap-gene-0.36-mRNA-1	MAAGLSAAITLKSLGSFHSAQPYPPPKPTLISPLSRGLNRGIFRPHKRT...
maker-scaffold_10645-snap-gene-0.18-mRNA-1	MASKRILKELKDLQKDPPTSCSAGPVAEDMFHWQATIMGPSDSPYA...
maker-scaffold_1065-snap-gene-0.10-mRNA-1	MASKRILKELKDLQKDPPTSCSAGPVAEDMFHWQATIMGPPDSPYA...
maker-scaffold_10674-snap-gene-0.17-mRNA-1	MQQGDQTALNLRPGGGRGSRLLGPRFESSSSASSAFAFGSLSSSDLP...
maker-scaffold_10707-snap-gene-0.16-mRNA-1	MARTKQTARKSTGGKAPRKQLATKAARKSAPTTGGVKKPHRYRPGT...
maker-scaffold_108-snap-gene-0.16-mRNA-1	MGRQKANIERSLLSHSTVLRQKTRKQKESVMASEVAMEGSTVAAAG...

Showing 1 to 10 of 114 entries

Search for Eksotika/Sekaki gene ontology

Type ‘Transcript ID’. Click check-box to select ‘GO category’. Click ‘Excel’ OR ‘CSV’ to download the results. Use ‘Search’ to search any keyword of interest.



Gene ID	Description	GO type	GO ID	GO term	Accesion ID
maker-scaffold_10060-snap-gene-0.29-mRNA-1	subtilisin-like serine protease [Carica papaya]	P	GO:0010223	secondary shoot formation	ACP18876
maker-scaffold_10060-snap-gene-0.29-mRNA-1	subtilisin-like serine protease [Carica papaya]	P	GO:0042127	regulation of cell proliferation	ACP18876
maker-scaffold_10060-snap-gene-0.29-mRNA-1	subtilisin-like serine protease [Carica papaya]	P	GO:0006508	proteolysis	ACP18876

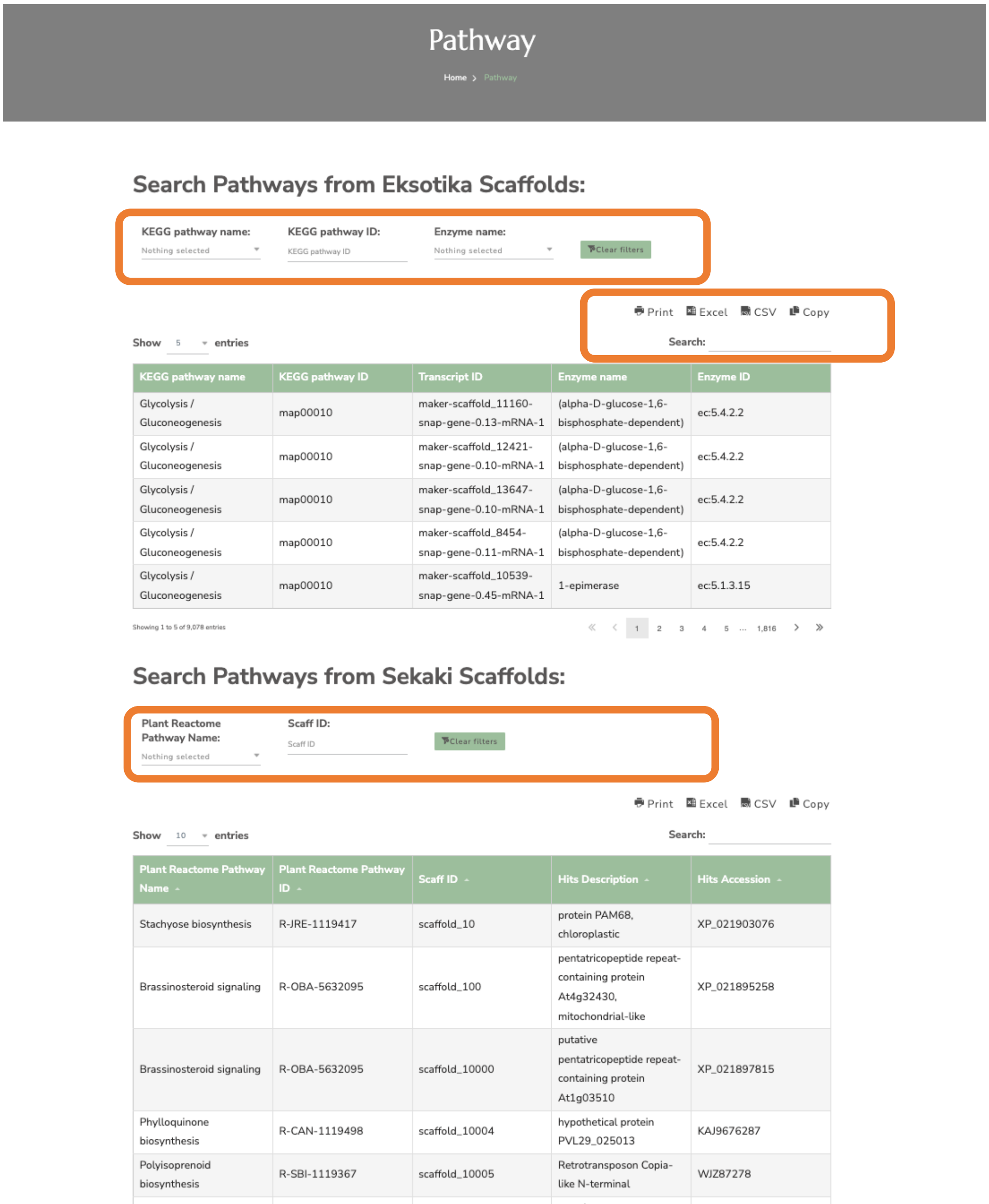
Search for pathways from Eksotika and Sekaki genome

Use drop-down list to search 'KEGG pathway name' and 'Enzyme name'.

If you have KEGG ID, then type in 'KEGG pathway ID'. For Eksotika, pathway annotation was performed against KEGG database, while pathway annotation in Sekaki was conducted against Plant Reactome database.

To download the result, click 'Excel' OR 'CSV' button.

Use 'Search' box to search anything using keyword of interest.



Search Pathways from Eksotika Scaffolds:

KEGG pathway name	KEGG pathway ID	Transcript ID	Enzyme name	Enzyme ID
Glycolysis / Gluconeogenesis	map00010	maker-scaffold_11160-snap-gene-0.13-mRNA-1	(alpha-D-glucose-1,6-bisphosphate-dependent)	ec:5.4.2.2
Glycolysis / Gluconeogenesis	map00010	maker-scaffold_12421-snap-gene-0.10-mRNA-1	(alpha-D-glucose-1,6-bisphosphate-dependent)	ec:5.4.2.2
Glycolysis / Gluconeogenesis	map00010	maker-scaffold_13647-snap-gene-0.10-mRNA-1	(alpha-D-glucose-1,6-bisphosphate-dependent)	ec:5.4.2.2
Glycolysis / Gluconeogenesis	map00010	maker-scaffold_8454-snap-gene-0.11-mRNA-1	(alpha-D-glucose-1,6-bisphosphate-dependent)	ec:5.4.2.2
Glycolysis / Gluconeogenesis	map00010	maker-scaffold_10539-snap-gene-0.45-mRNA-1	1-epimerase	ec:5.1.3.15

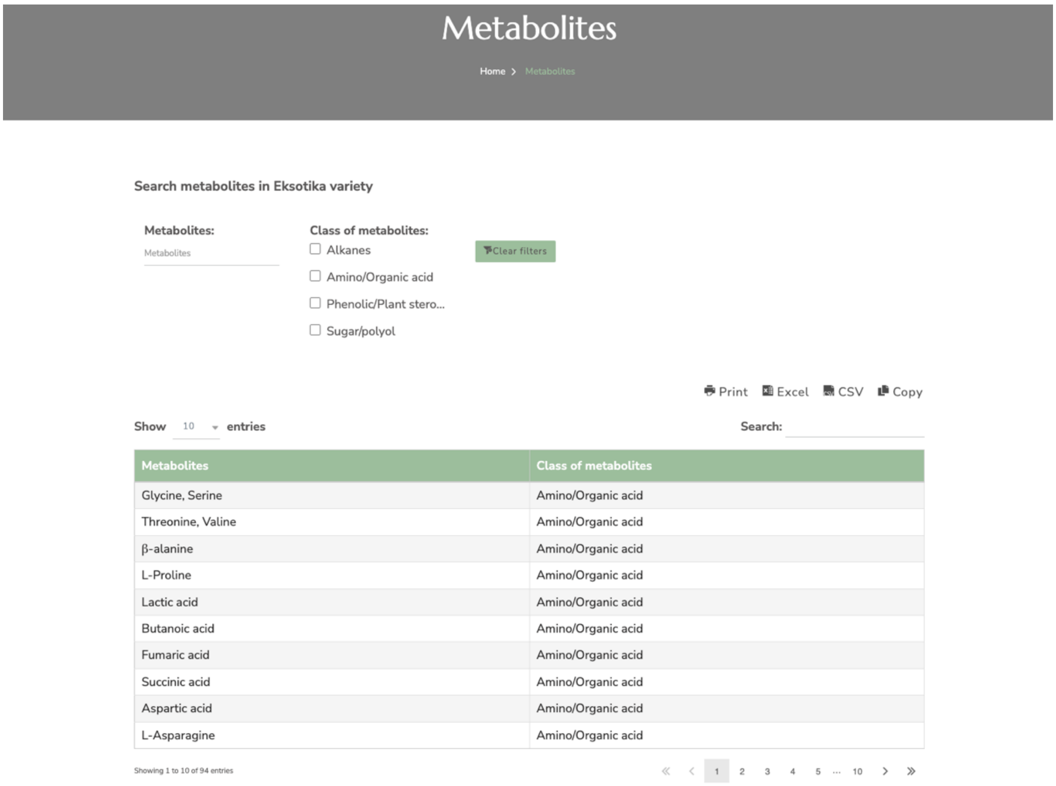
Showing 1 to 5 of 9,078 entries

Search Pathways from Sekaki Scaffolds:

Plant Reactome Pathway Name	Plant Reactome Pathway ID	Scaff ID	Hits Description	Hits Accession
Stachyose biosynthesis	R-JRE-1119417	scaffold_10	protein PAM68, chloroplastic	XP_021903076
Brassinosteroid signaling	R-OBA-5632095	scaffold_100	pentatricopeptide repeat-containing protein At4g32430, mitochondrial-like	XP_021895258
Brassinosteroid signaling	R-OBA-5632095	scaffold_10000	putative pentatricopeptide repeat-containing protein At1g03510	XP_021897815
Phylloquinone biosynthesis	R-CAN-1119498	scaffold_10004	hypothetical protein PVL29_025013	KAJ9676287
Polyisoprenoid biosynthesis	R-SBI-1119367	scaffold_10005	Retrotransposon Copia-like N-terminal	WJZ87278

Search for metabolites from Eksotika

Type any metabolite of interest using ‘Metabolites’ OR ‘Search’ functions.
Select ‘Class of Metabolites’ check-box to search metabolite classes.



Search metabolites in Eksotika variety

Metabolites: Metabolites

Class of metabolites:
☐ Alkanes
☐ Amino/Organic acid
☐ Phenolic/Plant stero...
☐ Sugar/polyol

Show 10 entries

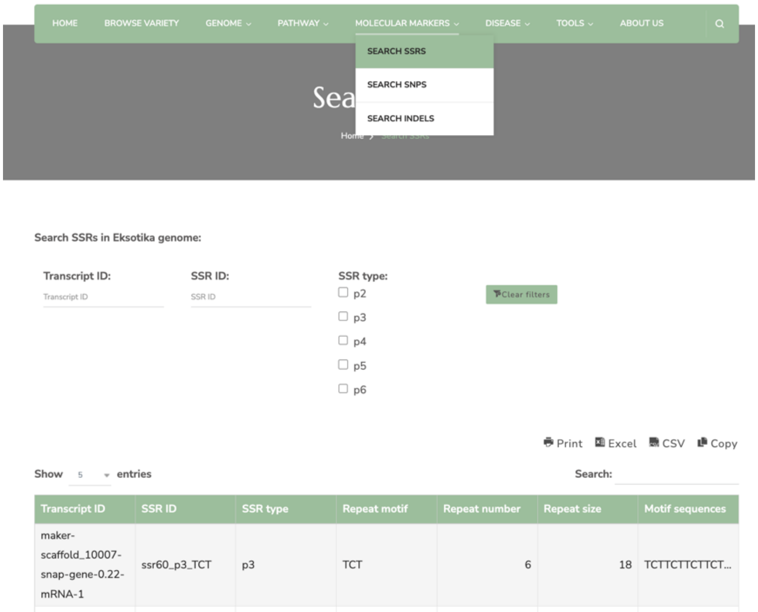
Search:

Metabolites	Class of metabolites
Glycine, Serine	Amino/Organic acid
Threonine, Valine	Amino/Organic acid
β-alanine	Amino/Organic acid
L-Proline	Amino/Organic acid
Lactic acid	Amino/Organic acid
Butanoic acid	Amino/Organic acid
Fumaric acid	Amino/Organic acid
Succinic acid	Amino/Organic acid
Aspartic acid	Amino/Organic acid
L-Asparagine	Amino/Organic acid

Showing 1 to 10 of 94 entries

Search for molecular markers in Eksotika and Sekaki genome

In the 'Molecular Markers' menu, user can query the SSRs, SNPs and InDels in Eksotika and Sekaki genome.



Search SSRs in Eksotika genome:

Transcript ID: Transcript ID

SSR ID: SSR ID

SSR type:

☐ p2

☐ p3

☐ p4

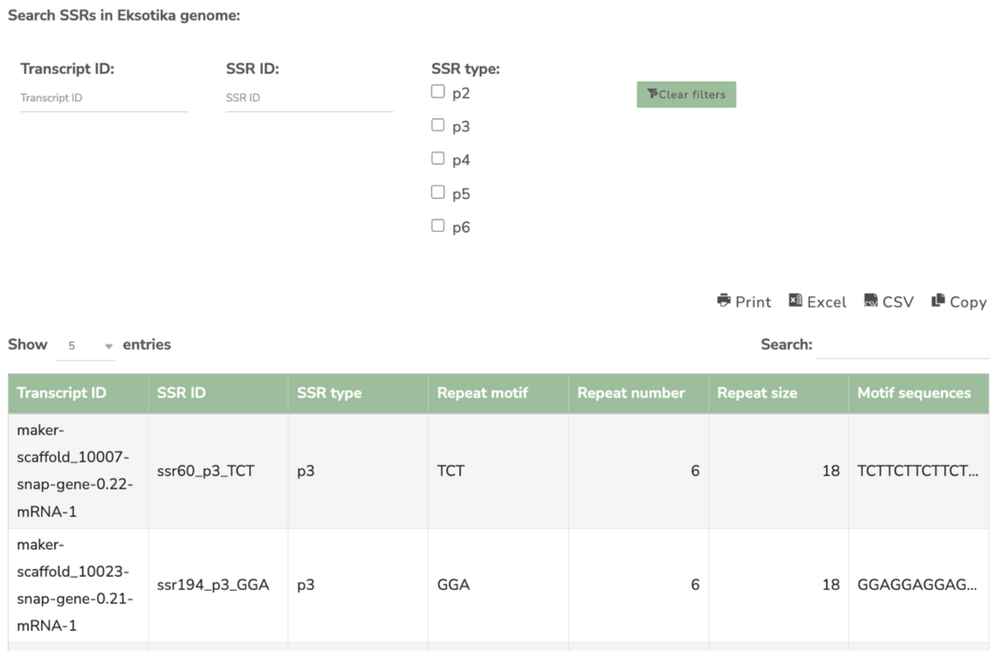
☐ p5

☐ p6

Transcript ID	SSR ID	SSR type	Repeat motif	Repeat number	Repeat size	Motif sequences
maker-scaffold_10007-snap-gene-0.22-mRNA-1	ssr60_p3_TCT	p3	TCT	6	18	TCTTCTTCTTCT...

Search for SSRs in Eksotika genome

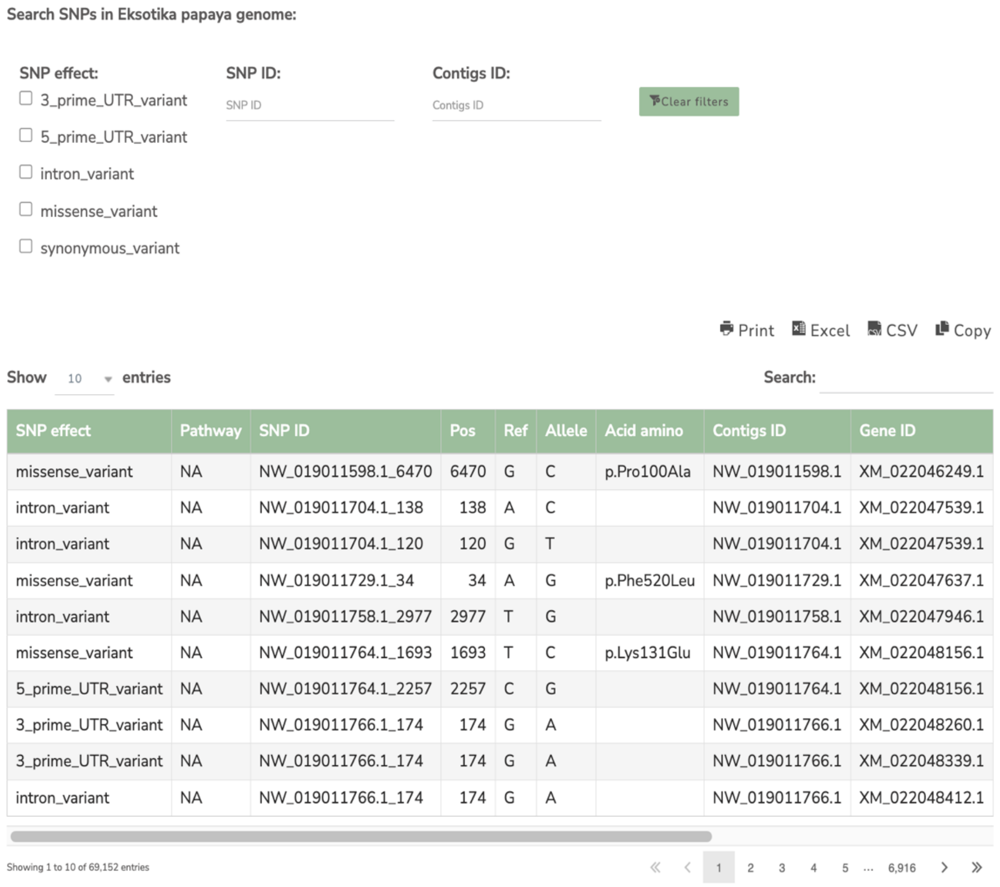
Type transcript ID in ‘Transcript ID’ box to search SSR in the transcript region. Select ‘SSR type’ if you have specific SSR type, such as di-tri-tetra-nucleotide.



Transcript ID	SSR ID	SSR type	Repeat motif	Repeat number	Repeat size	Motif sequences
maker-scaffold_10007-snap-gene-0.22-mRNA-1	ssr60_p3_TCT	p3	TCT	6	18	TCTTCTTCTTCT...
maker-scaffold_10023-snap-gene-0.21-mRNA-1	ssr194_p3_GGA	p3	GGA	6	18	GGAGGAGGAG...

Search for SNPs in Eksotika OR Sekaki genome

User can query the SNPs by providing the 'SNP ID' OR 'Contig ID' or select by 'SNP effect'. User can download the results in Excel or CSV format.



Search SNPs in Eksotika papaya genome:

SNP effect:

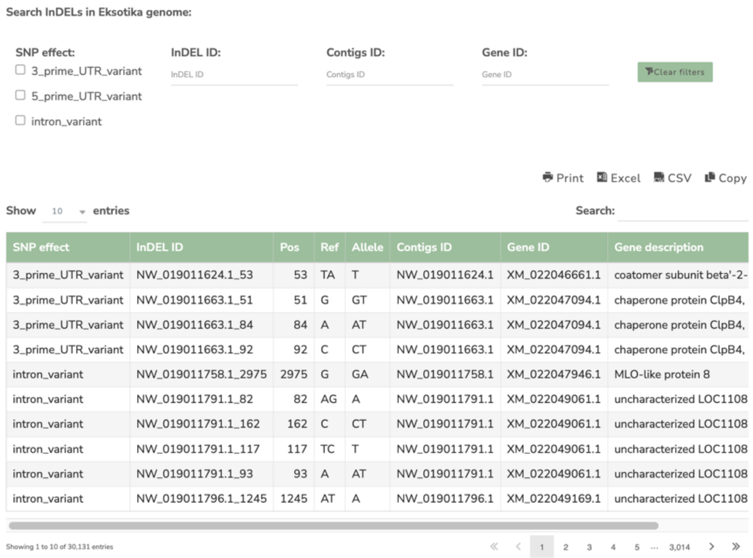
☐ 3_prime_UTR_variant
☐ 5_prime_UTR_variant
☐ intron_variant
☐ missense_variant
☐ synonymous_variant

SNP effect	Pathway	SNP ID	Pos	Ref	Allele	Acid amino	Contigs ID	Gene ID
missense_variant	NA	NW_019011598.1_6470	6470	G	C	p.Pro100Ala	NW_019011598.1	XM_022046249.1
intron_variant	NA	NW_019011704.1_138	138	A	C		NW_019011704.1	XM_022047539.1
intron_variant	NA	NW_019011704.1_120	120	G	T		NW_019011704.1	XM_022047539.1
missense_variant	NA	NW_019011729.1_34	34	A	G	p.Phe520Leu	NW_019011729.1	XM_022047637.1
intron_variant	NA	NW_019011758.1_2977	2977	T	G		NW_019011758.1	XM_022047946.1
missense_variant	NA	NW_019011764.1_1693	1693	T	C	p.Lys131Glu	NW_019011764.1	XM_022048156.1
5_prime_UTR_variant	NA	NW_019011764.1_2257	2257	C	G		NW_019011764.1	XM_022048156.1
3_prime_UTR_variant	NA	NW_019011766.1_174	174	G	A		NW_019011766.1	XM_022048260.1
3_prime_UTR_variant	NA	NW_019011766.1_174	174	G	A		NW_019011766.1	XM_022048339.1
intron_variant	NA	NW_019011766.1_174	174	G	A		NW_019011766.1	XM_022048412.1

Showing 1 to 10 of 69,152 entries

Search for InDels in Eksotika OR Sekaki genome

Enter the 'SNP ID' OR 'Contig ID' or select by 'SNP effect'. User can download the results in Excel or CSV format.

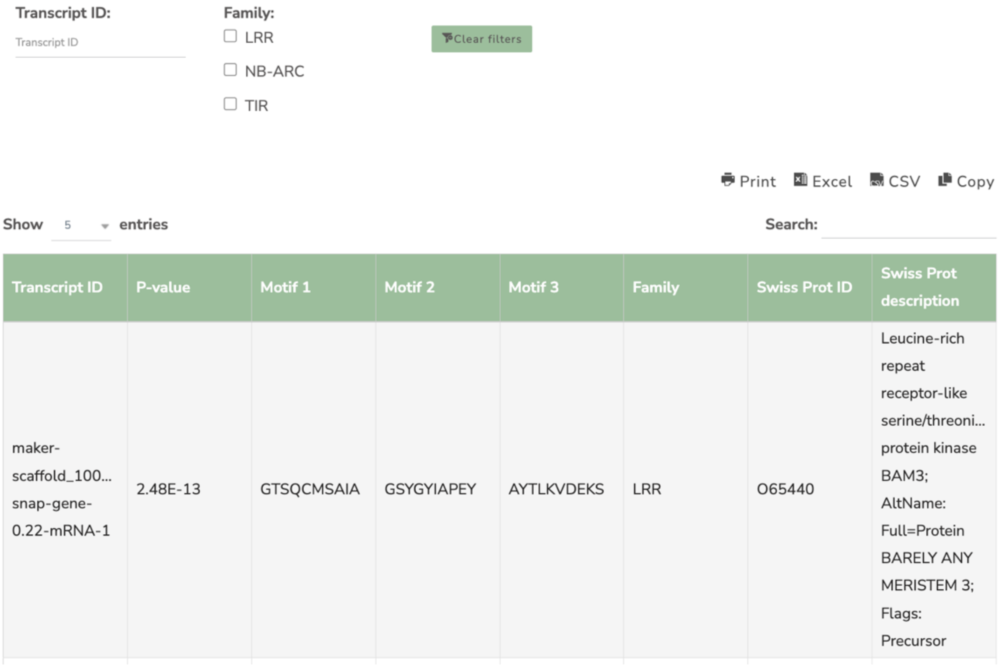


SNP effect	InDEL ID	Pos	Ref	Allele	Contigs ID	Gene ID	Gene description
3_prime_UTR_variant	NW_019011624.1_53	53	TA	T	NW_019011624.1	XM_022046661.1	coatomer subunit beta'-2-
3_prime_UTR_variant	NW_019011663.1_51	51	G	GT	NW_019011663.1	XM_022047094.1	chaperone protein ClpB4,
3_prime_UTR_variant	NW_019011663.1_84	84	A	AT	NW_019011663.1	XM_022047094.1	chaperone protein ClpB4,
3_prime_UTR_variant	NW_019011663.1_92	92	C	CT	NW_019011663.1	XM_022047094.1	chaperone protein ClpB4,
intron_variant	NW_019011758.1_2975	2975	G	GA	NW_019011758.1	XM_022047946.1	MLO-like protein 8
intron_variant	NW_019011791.1_82	82	AG	A	NW_019011791.1	XM_022049061.1	uncharacterized LOC1108
intron_variant	NW_019011791.1_162	162	C	CT	NW_019011791.1	XM_022049061.1	uncharacterized LOC1108
intron_variant	NW_019011791.1_117	117	TC	T	NW_019011791.1	XM_022049061.1	uncharacterized LOC1108
intron_variant	NW_019011791.1_93	93	A	AT	NW_019011791.1	XM_022049061.1	uncharacterized LOC1108
intron_variant	NW_019011796.1_1245	1245	AT	A	NW_019011796.1	XM_022049169.1	uncharacterized LOC1108

Showing 1 to 10 of 30,131 entries

Search for resistance genes in Eksotika genome

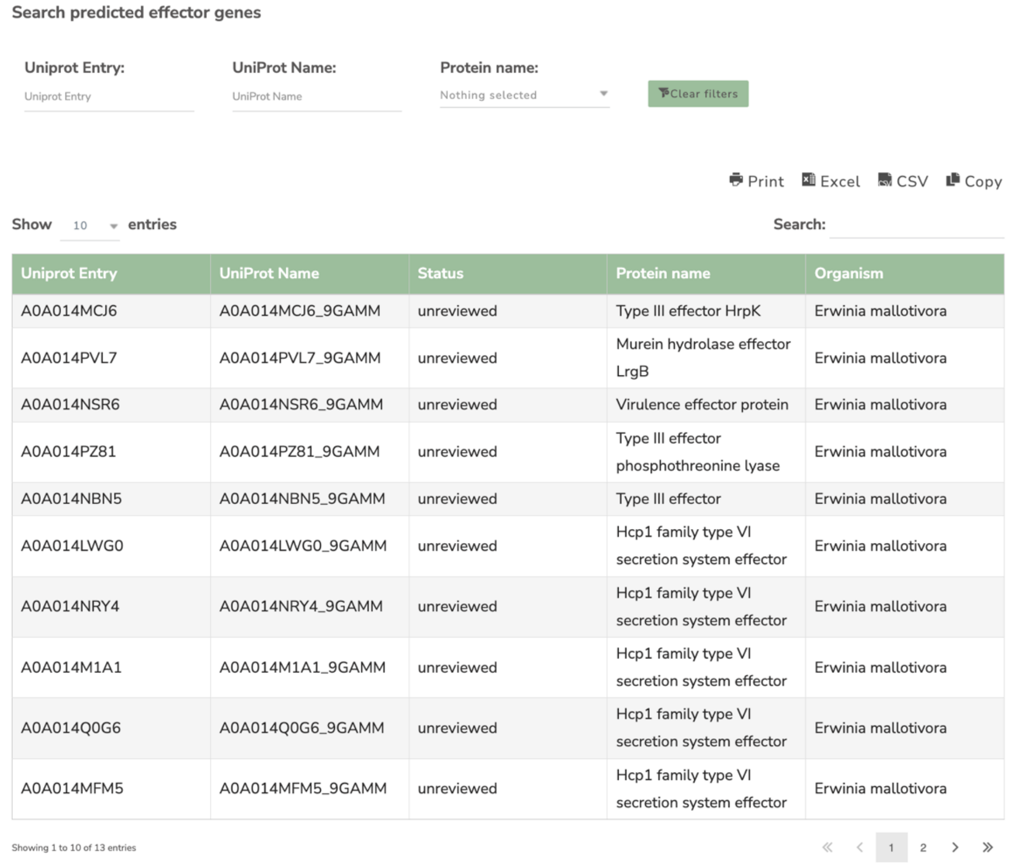
Enter ‘Transcript ID’ OR select resistance genes in check-box.



Transcript ID	P-value	Motif 1	Motif 2	Motif 3	Family	Swiss Prot ID	Swiss Prot description
maker-scaffold_100... snap-gene-0.22-mRNA-1	2.48E-13	GTSQCMSAIA	GSYGYIAPEY	AYTLKVDEKS	LRR	O65440	Leucine-rich repeat receptor-like serine/threoni... protein kinase BAM3; AltName: Full=Protein BARELY ANY MERISTEM 3; Flags: Precursor

Search for effector genes in Eksotika genome

Enter ‘UniProt Entry’ OR ‘UniProt Name’ OR select predicted effector genes in ‘Protein Name’ multi check-box.



Uniprot Entry	UniProt Name	Status	Protein name	Organism
A0A014MCJ6	A0A014MCJ6_9GAMM	unreviewed	Type III effector HrpK	Erwinia mallotivora
A0A014PVL7	A0A014PVL7_9GAMM	unreviewed	Murein hydrolase effector LrgB	Erwinia mallotivora
A0A014NSR6	A0A014NSR6_9GAMM	unreviewed	Virulence effector protein	Erwinia mallotivora
A0A014PZ81	A0A014PZ81_9GAMM	unreviewed	Type III effector phosphothreonine lyase	Erwinia mallotivora
A0A014NBN5	A0A014NBN5_9GAMM	unreviewed	Type III effector	Erwinia mallotivora
A0A014LWG0	A0A014LWG0_9GAMM	unreviewed	Hcp1 family type VI secretion system effector	Erwinia mallotivora
A0A014NRY4	A0A014NRY4_9GAMM	unreviewed	Hcp1 family type VI secretion system effector	Erwinia mallotivora
A0A014M1A1	A0A014M1A1_9GAMM	unreviewed	Hcp1 family type VI secretion system effector	Erwinia mallotivora
A0A014Q0G6	A0A014Q0G6_9GAMM	unreviewed	Hcp1 family type VI secretion system effector	Erwinia mallotivora
A0A014MFM5	A0A014MFM5_9GAMM	unreviewed	Hcp1 family type VI secretion system effector	Erwinia mallotivora

Showing 1 to 10 of 13 entries

Using Tools in PapayaNetBase

1. How to use PapayaNetBase: A knowledge graph database in papaya traits

PapayaNetBase provides 'Genes-Traits Network in Papaya' where user can select traits of interest and explore genes relationships with other omics information in knowledge graph visualisation. Click 'Tools' and will be redirected to the page.

PapayaNetBase: A Papaya Genomics Database

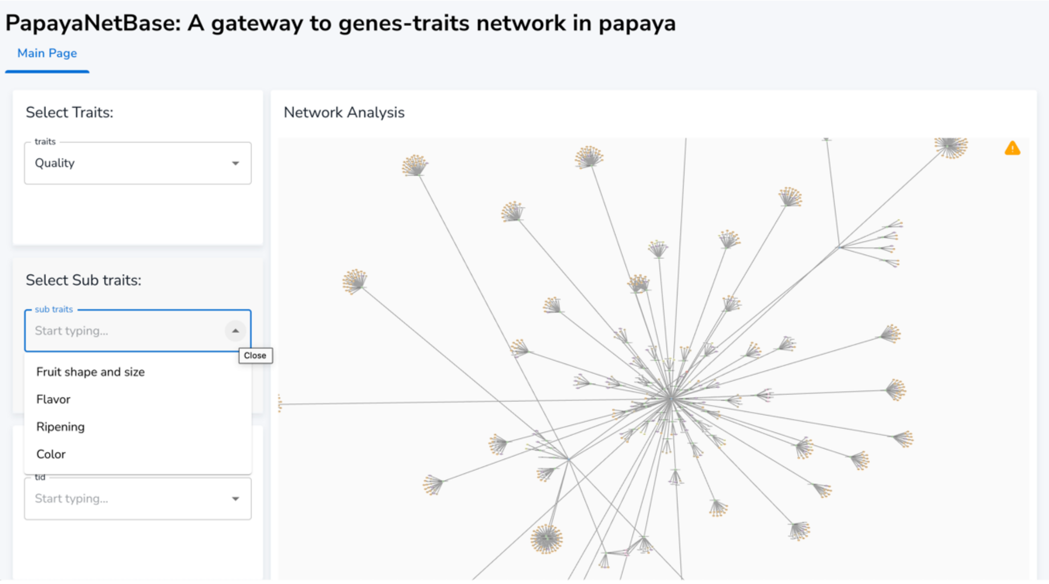
An agrigenomic platform to support research and breeding in papaya

Exploring *C. papaya* genome

1.1 Search using Traits and Sub-traits

i. Choose 'Select Traits' to select traits of interest.

ii. Then, select sub-traits. A knowledge graph database will be displayed.



PapayaNetBase: A gateway to genes-traits network in papaya

Select Traits:

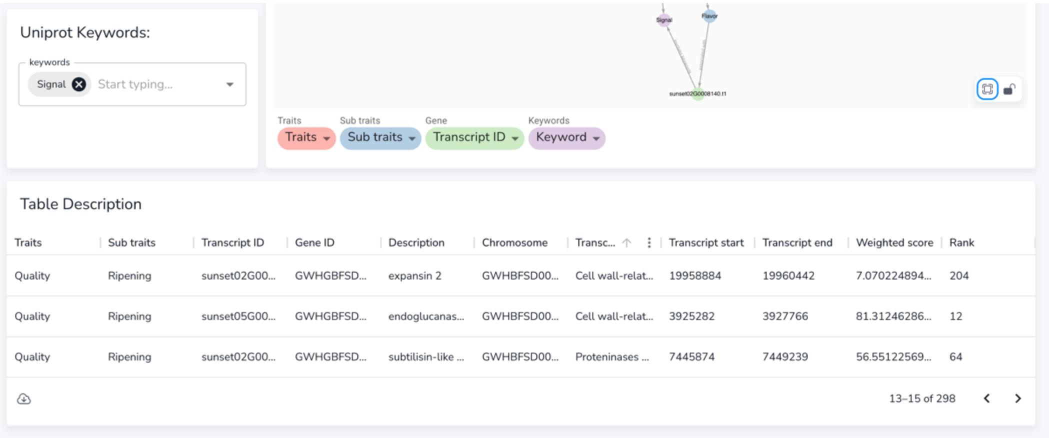
traits: Quality

Select Sub traits:

sub traits: Start typing...

iii. A table with gene descriptions and rank is displayed at the bottom page.

iv. To download, click the 'Download' button.



Uniprot Keywords:

keywords: Signal

Table Description

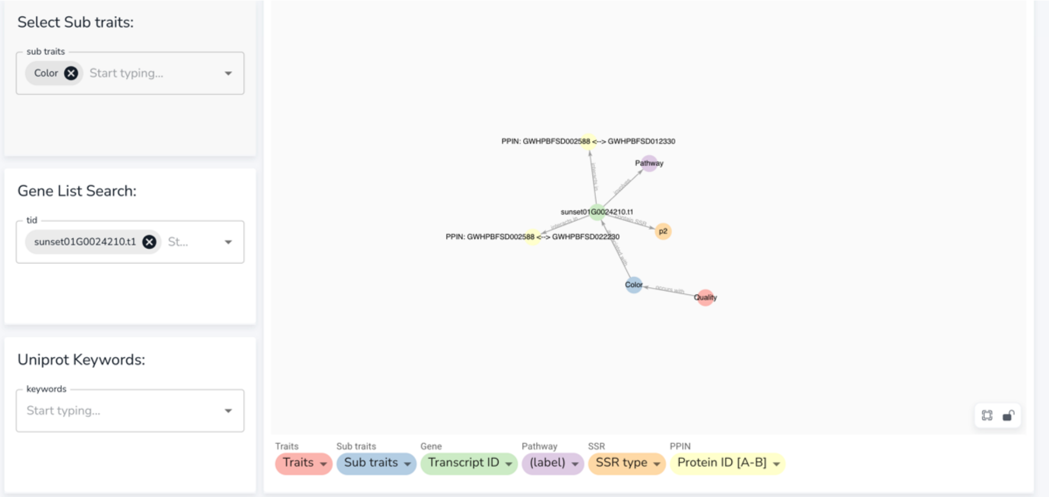
Traits	Sub traits	Transcript ID	Gene ID	Description	Chromosome	Transc...	Transcript start	Transcript end	Weighted score	Rank
Quality	Ripening	sunset02G00...	GWHGBFSD...	expansin 2	GWHBFSD00...	Cell wall-relat...	19958884	19960442	7.070224894...	204
Quality	Ripening	sunset05G00...	GWHGBFSD...	endoglucanas...	GWHBFSD00...	Cell wall-relat...	3925282	3927766	81.31246286...	12
Quality	Ripening	sunset02G00...	GWHGBFSD...	subtilisin-like ...	GWHBFSD00...	Proteninases ...	7445874	7449239	56.55122569...	64

13–15 of 298

1.2 Search using Gene ID

i. Type 'sunset' in the 'Gene List Search' to display Gene ID.

ii. OR Enter Gene ID in 'Gene List Search' if you have one.



Select Sub traits:

sub traits: Color

Gene List Search:

tid: sunset01G0024210.t1

Uniprot Keywords:

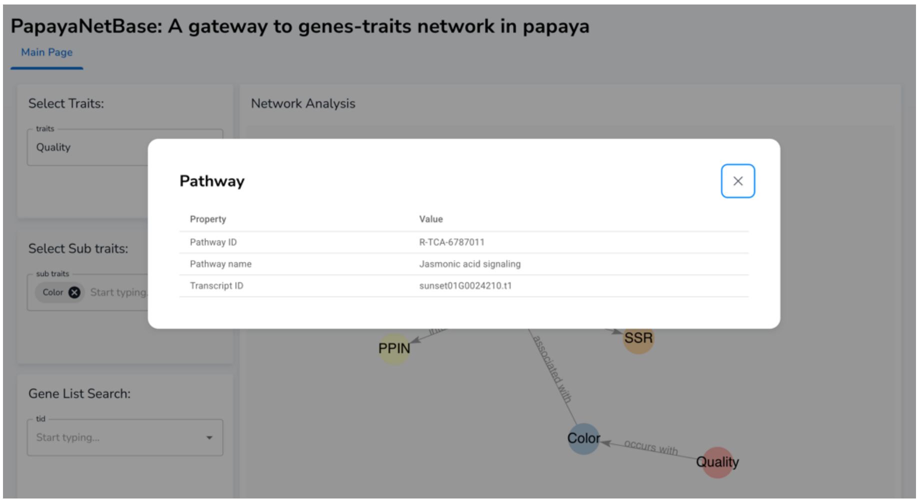
keywords: Start typing...

1.3 Search using UniProt keyword

Type any keywords of interest in 'Uniprot Keywords'.

1.4 Exploring nodes and edges

To explore each node, you can click in the node and a box will be floating to display the details on the nodes information.



PapayaNetBase: A gateway to genes-traits network in papaya

Select Traits:

traits: Quality

Select Sub traits:

sub traits: Color

Gene List Search:

tid: Start typing...

Network Analysis

Pathway

Property	Value
Pathway ID	R-TCA-6787011
Pathway name	Jasmonic acid signaling
Transcript ID	sunset01G0024210.t1

You can change node and edge descriptions by clicking the rectangular box in the bottom page.

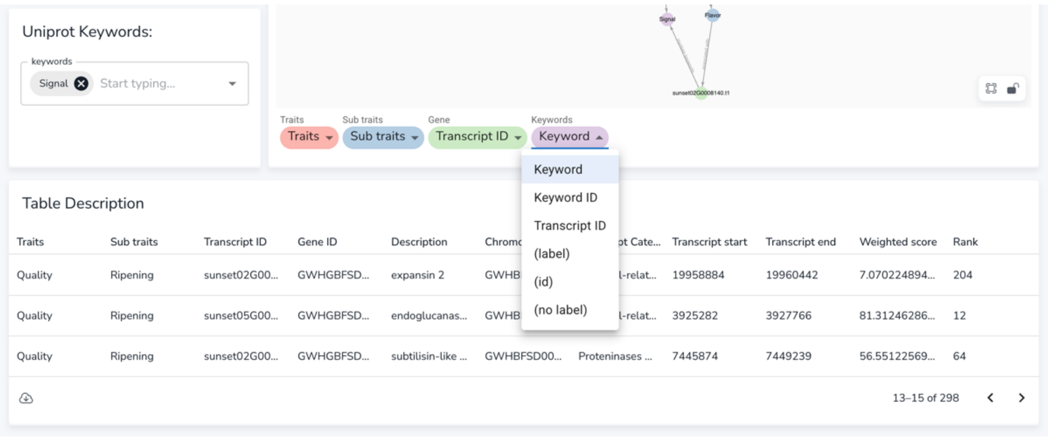


Table Description

Traits	Sub traits	Transcript ID	Gene ID	Description	Chromo	ot Cate...	Transcript start	Transcript end	Weighted score	Rank
Quality	Ripening	sunset02G00...	GWHGBFSD...	expansin 2	GWHB	l-relat...	19958884	19960442	7.070224894...	204
Quality	Ripening	sunset05G00...	GWHGBFSD...	endoglucanas...	GWHB	l-relat...	3925282	3927766	81.31246286...	12
Quality	Ripening	sunset02G00...	GWHGBFSD...	subtilisin-like ...	GWHBFSD00...	Proteninases ...	7445874	7449239	56.55122569...	64

2. How to use PapayaNetBase AI chatbot

This tutorial will guide users on how to interact with the PapayaNetBase Chatbot, access its features, and utilize it for papaya-related queries, research, and information.

Step 1: Accessing the Chatbot

Chatbot icon can be found in the bottom right corner of the Homepage.

PapayaNetBase: A Papaya Genomics Database

An agrigenomic platform to support research and breeding in papaya

Exploring *C. papaya* genome

<u>Step 2: Starting a Conversation</u>

Click on the chat icon, and the chatbot will greet you with a welcome message.

Sample use case:

- "Inquire about common papaya diseases and their management."
- 'What are the best papaya varieties for drought tolerance?'"
- What are the molecular markers for disease resistance in papaya?'"

Use keywords like 'genomics,' 'traits,' 'market potential,' or 'pest management' for specific information."

FAQ on Chatbot

What can the Papaya Chatbot do?

The chatbot can provide information on papaya cultivation, genomics, traits, market potential, and more.

How do I get the best results from the chatbot?

Use clear and specific questions or keywords related to your query.

Can the chatbot access data from the CPEDB?

Yes, the chatbot can retrieve and display data from the CPEDB upon request.

Is the chatbot available 24/7?

Yes, the chatbot is available round the clock to assist you.