



GDR GBrowse

The generic Genome Browser (GBrowse)

- A combination database and interactive web page for manipulating and displaying annotations on genomes
- Developed by GMOD (*Generic Model Organism Database*)
- GDR GBrowse : a customized GBrowse for the genomes in GDR

GDR GBrowse Overview

Description menus

Search

Bird's eye view

Details

Tracks

The screenshot displays the GDR GBrowse web interface. At the top, the logo for GDR (Genome Database for Rosaceae) is visible, along with a navigation menu containing Home, Species, Projects, Maps, Search, Tools, Community, and Contact. Below the navigation is a search bar with the text "Prunus Persica: 600 bp from scaffold_1:14,389,558..14,390,157". The interface includes a "Search" section with a "Landmark or Region" input field containing "scaffold_1:14389558..14390157" and a "Search" button. There are also buttons for "Download Decorated FASTA File", "Configure...", and "Go". The "Data Source" is listed as "Prunus Persica". The "Overview" section shows a genomic map of scaffold_1 with a red vertical line indicating the current region. The "Region" section shows a zoomed-in view of the region from 14389500 to 14390100. The "Details" section shows a "Transcript Model" for ppa014948n and "Arabidopsis Peptide Alignment" for AT5G28950.1_GX150P, AT1G43722.1_GX107P, and AT5G41980.1_GX153P. The "Tracks" section is at the bottom. A "Clear highlighting" link is located in the bottom right corner.

Generic Genome Browser version 2.0. For questions about the data at this site, please contact its webmaster. For support of the browser software only, send email to gmod-gbrowse@lists.sourceforge.net or visit the [GMOD Project](#) web pages.

GDR GBrowse Search

The screenshot shows the GDR GBrowse search interface. At the top, the logo for GDR (Genome Database for Rosaceae) is displayed. Below the logo is a navigation menu with links for Home, Species, Projects, Maps, Search, Tools, Community, and Contact. The search bar contains the text "from scaffold_1:14,387,358..14,392,357". Below the search bar, there are several callouts and annotations:

- Search by annotation ID, name, or comment:** A callout box pointing to the search input field.
- Scroll/zoom:** A callout box pointing to the navigation controls (left and right arrows) on the right side of the interface.
- Region displayed:** A callout box pointing to the genomic region being displayed on the scaffold.
- Dropdown list:** A callout box pointing to the dropdown menu on the right side of the interface, which lists various view options (Show 5 kbp, Show 125 kbp, Show 100 kbp, Show 50 kbp, Show 20 kbp, Show 10 kbp, Show 5 kbp, Show 2 kbp, Show 1 kbp).
- Hide Details (minus-sign):** A callout box pointing to the minus sign icon in the left sidebar.
- Open Details (plus-sign):** A callout box pointing to the plus sign icon in the left sidebar.

The interface also shows a sidebar on the left with sections for Search, Overview, Region, Details, and Tracks. The main content area displays a genomic track for scaffold_1, with a red vertical line indicating the region of interest. Below the scaffold track, there are tracks for Marker and Transcript Model, with a green arrow pointing to the ppa014948m transcript.

GDR GBrowse Search

GDR | Genome Database for Rosaceae

Home Species Projects Maps Search Tools Community Contact

File Help

Prunus Persica: 5 kbp from scaffold_1:14,387,358..14,392,357

Browser [Upload and Share Tracks](#) [Preferences](#)

I Search

Landmark or Region:
 Search [Download](#) [Decorate](#)

Examples: [scaffold_1:12360000..12479999](#), [ppa014948m](#), [BU045951](#), [CPPCT016](#), [AG25A](#).

Data Source: Prunus Persica

Scroll/Zoom: << >>

I Overview

I Region

I Details

Transcript Model [ppa014948m](#) [scaffold_1:14389558..14390157]

AT5627260..1_Gx13P AT5635695..1_Gx150P
 AT1630140..1_Gx15P
 AT2629880..1_Gx22P
 AT5628950..1_Gx67P

click

ppa014948m Details

Name: ppa014948m
 Type: mRNA
 Description: JGI
 Source: scaffold_1:14389558..14390157 (+ strand)
 Position: scaffold_1:14389558..14390157 (+ strand)
 Length: 600
 Alias: PROT:ppa014948m
 LOC:ppa014948m.g
 PACid: 17640688
 load_id: 21064748
 primary_id: 21886438
 gbrowse_dbid: scaffolds:database

Parts:

Part	Type	Description
1	CDS	
2	CDS	

ppa014948m class=Sequence position=scaffold_1:14389558..14390157 (+ strand)
 ATGGACGCG ACSTAAAGCAG CTATCGTAAT CGTCACGGTG CAATACCACA AAGTGTATTA GCACTGTGTA
 GGAATTCATA TAGTTCCTTA GTTGGTGGGA GGGCTCAGCT CAGGATCCAA GAATACTACA AGAAGCTTGA
 ATGGACTTAA AGTGCCACAA GGATATTTTA AATTITAAAT TTTTTCCTAT TGTTTACATG AGCTCATACA
 ACTACATATG GTTTCATTA GCTCATACAT TGGATATATA CTAACATATG TGTAACTAT TATCAAGGAAA

GDR GBrowse Tracks

Browser [Upload and Share Tracks](#) [Preferences](#)

Search

Landmark or Region:
scaffold_1:14387358..1439235 Search

Download Decorated FASTA File

Examples: [scaffold_1:12360000..12479999](#), [ppa014948m](#), [BU045951](#), [CPPCT016](#), [AG25A](#)

Data Source
Prunus Persica

Scroll/Zoom: Show 5 kbp Flip

Overview

Region

Details

remove track
(cross-sign)

Tracks

The screenshot displays the GDR GBrowse interface for scaffold_1. The top section shows search and navigation options. The main area is divided into Overview, Region, and Details. The Region track shows a zoomed-in view of scaffold_1: 5 kbp, with a 1 kbp scale bar. Below this, several tracks are visible: Transcript Model, Alternate Transcript Model, Arabidopsis Peptide Alignment, and Soybean Peptide Alignment. The Soybean Peptide Alignment track is highlighted with a callout box indicating the 'remove track (cross-sign)' icon. The bottom of the interface shows a 'Tracks' section with a green circle around the 'Tracks' label.


GDR GBrowse Tracks

■ Tracks


<input checked="" type="checkbox"/> Overview	<input type="checkbox"/> All on	<input type="checkbox"/> All off
<input checked="" type="checkbox"/> Genetic Mapped Markers		
■ Region	<input type="checkbox"/> All on	<input type="checkbox"/> All off
<input type="checkbox"/> Genetic Mapped Markers		
■ Alignments	<input type="checkbox"/> All on	<input type="checkbox"/> All off
<input type="checkbox"/> Blat Aligned Prunus persica EST assembly V1	<input type="checkbox"/> Genetic Marker Alignment	<input type="checkbox"/> PASA Aligned ESTs
■ Genome Sequence	<input type="checkbox"/> All on	<input type="checkbox"/> All off
<input type="checkbox"/> DNA/GC Content		
■ Model Plant Gene Alignments	<input type="checkbox"/> All on	<input type="checkbox"/> All off
<input checked="" type="checkbox"/> Arabidopsis Peptide Alignment	<input type="checkbox"/> Poplar Peptide Alignment	<input checked="" type="checkbox"/> Soybean Peptide Alignment
<input type="checkbox"/> Grape Peptide Alignment	<input type="checkbox"/> Rice Peptide Alignment	
■ RNA-seq Illumina profiles (log 10 scale)	<input type="checkbox"/> All on	<input type="checkbox"/> All off
<input type="checkbox"/> Cotyledon+Embryo, unique alignments	<input type="checkbox"/> Fruit, all alignments	<input type="checkbox"/> Root, unique alignments
<input type="checkbox"/> Cotyledon+Embryo, all alignments	<input type="checkbox"/> Leaf, unique alignments	<input type="checkbox"/> Root, all alignments
<input type="checkbox"/> Fruit, unique alignments	<input type="checkbox"/> Leaf, all alignments	
■ Repeats	<input type="checkbox"/> All on	<input type="checkbox"/> All off
<input type="checkbox"/> 20mers aligning with 0 errors (log 10 scale)	<input type="checkbox"/> ReAS	
<input type="checkbox"/> LTRs	<input checked="" type="checkbox"/> Consensus Repeats	
■ Transcripts	<input type="checkbox"/> All on	<input type="checkbox"/> All off

choose tracks
you want to see

GDR GBrowse Tracks



Genome Database for Rosaceae



Home Species Projects Maps Search Tools

File ▾ Help ▾

Prunus Persica: 61 kbp from scaffold_1:3,426,000..3,487,000

Browser [Upload and Share Tracks](#) [Preferences](#)

Search

Landmark or Region:

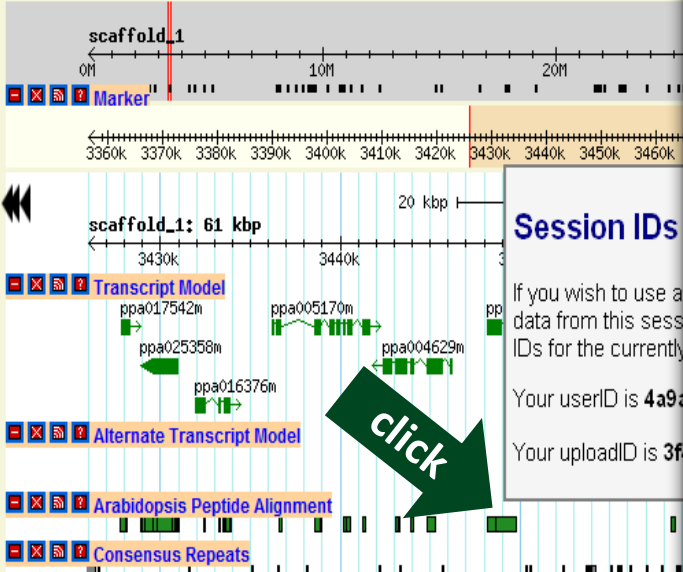
Examples: [scaffold_1:1236000..1247999](#), [ppa014948m](#), [BU045951](#), [CPPCT016](#), [AG25A](#).

[Data Source](#)
Prunus Persica

Overview

Region

Details



Session IDs

If you wish to use a data from this session IDs for the currently selected tracks:

Your userID is **4a9a**

Your uploadID is **3f**

click

AT2G33320.1_GX3P Details

Name: AT2G33320.1_GX3P
[Link To TAIR](#)

Type: match

Description:

Source: arabi_peptide

Position: scaffold_1:3448184..3449791 (+ strand)

Length: 1608

Score: 0

Alias: AT2G33320.1
 AT2G33320.1
 AT2G33320

Description: C2 domain-containing protein AT2G33320

load_id: 7688856

primary_id: 398091

gbrowse_dbid: scaffolds:database

Parts:

Type:	HSP
Description:	
Source:	arabi_peptide
Position:	scaffold_1:3448184..3449791
Length:	1608
Score:	0
Identities:	264
Query:	SILAPFQLELNVISAG GMRFVALQVRRPSPGF GSMVNGSEVSIKKNK EDRPRRKPAHKPSF SVEGLQSKLERWRTE
Score:	402
Start:	2
Stop:	602
Subject:	SIFPSFQLELNIIASQI GMRFVALQVRRPSPGF ASALMSAESETVPTT RPPRDYDRTSSRASP AKERSQAYETESSILS GRLPRLGSADDLSYL

load_id: 7688857

parent_id: 7688856

Done

GDR GBrowse Tracks

File Help

Prunus Persica: 20 kbp from scaffold_1:14,384,158..14,404,158

Browser Upload and Share Tracks Preferences

Search

Landmark or Region:

scaffold_1:14393900..14398099 Search

Download Decorated FASTA File Configure...

Examples: scaffold_1:12360000..12479999, ppa014948m, BU045951, CPPCT016, AG25A.

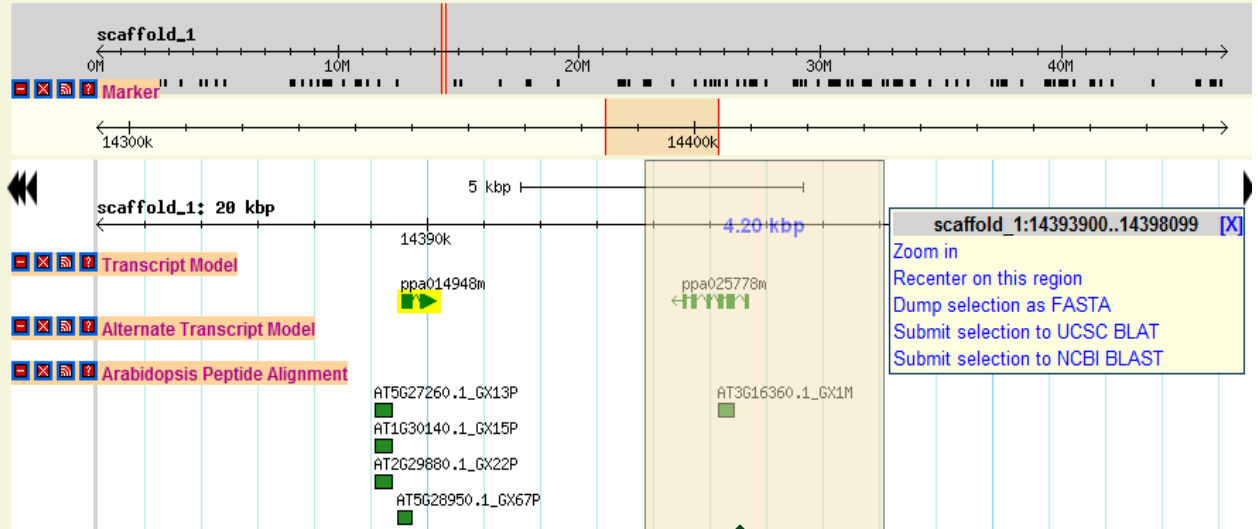
Data Source
Prunus Persica

Scroll/Zoom: << < - Show 20 kbp + >

Overview

Region

Details



Selecting regions
with mouse

GDR GBrowse Tracks

GDR Genome Database for Rosaceae

Home Species Projects Maps Search Tools Community Contact

File Help

Prunus Persica: 20 kbp from scaffold_1:14,384,158..14,404,158

Browser Upload and Share Tracks Preferences

Search

Landmark or Region: scaffold_1:14393900..14398099 Search Download Decorated FASTA File Configure...

Examples: scaffold_1:12360000..12479999, ppa014948m, BU045951, CPPCT016, AG25A.

Data Source Prunus Persica

Scroll/Zoom: Show 20 kbp

Overview

Region

Details

scaffold_1:14393900..14398099

Transcript Model

Alternate Transcript Model

Arabidopsis Peptide Alignment

AT5G27260..1_GX13P

AT1G30140..1_GX15P

AT2G29880..1_GX22P

AT5G28950..1_GX67P

ppa014948m

ppa025778m

AT3G16360..1_GX11M

Click

Zoom in

Recenter on this region

Copy selection as FASTA

Submit selection to NCBI BLAT

Submit selection to NCBI BLAST

```
>scaffold_1:14393900..14398099
atccttaccattgctaccaccacattgctaccacaaatgcataattttgtttttccattt
tcaaatcgggtatcaaaaacgttttggatgttttggtagaaaattgtctctgtt
taactaccaaacacattctcaaatcttgaaaattgtaagacgttatgagacaagcctta
aatactctctctctgcttttgcctctctctctctctctctctctcaagcaaaatt
agaaaagactagttatctggttaagggtgaattgatttaatttagcgggcatgtatt
gggctcaagacaaagggtgtgtgtagccaaccccaagaaatttgaagcatctcattgt
atataaaaagccatttcatattctagcaaggaacatgataatcatgaagaaaaaac
ttaatgcatagttacagggaaaaatttttttttttttttttttttttttttttttttt
tacagggatattagaatccaaaagcactaattaaagtctcctaatacaaatctaacagag
ttggaacacatacatagtaaaaaacccaacacactcaaatattgtgacctctgct
ctctctctgctgctcaataatttctctcacttggggcagctgctctcaataggtc
cagcttgccttgcaactgaaagacaaaaaaatacaaaaaataaaaaatacaaaa
cacattttaatatataatacacacacacacacacacacacacacacacacacacac
tgaaaaagcctcaagcctctctctcagtggtgcatgtctctctcaatgctggaaa
gtccatgcatctggttaccctgcaaaaacttgaagtgaactaccaacttattaca
catttttcccttttaaatattctctatattatcattttattatgttttgaaga
ttgtaaaaaggaagactcaaatcgagtttaagagaataaataatgatgagagttttt
agagattgatgctgaattcgctgaagtaacctctccattctctgcttgcattatccc
taaacctgtggcactcagcttttacccttttggctccgatgctggcaccacaaataga
aatgttagttgggataaaattctgcatctcaaaagccaatagataataacttacaga
tctctgtaaatattcttaaaataaaacaaatgaggacgttttatttttttaccct
gagctactccttgaactgatgcatgtagcctccaattatataaatcatgaggggtc
ctctctgcatatacactatacatattatattgctcctgacataaaatattgctatta
aaaagtgaaaaattataattgaccacagcgcagctctatggtttggagtgatcta
gatgaatctgtgtagtagtagtagcaatttctccacacaaaattgggttagcatcatc
tgcagctcctccaactgaataaaactgctcgcacagaaatccctgaaattcccaaaagt
tgaaaatgaagagtgctaaaatagctacaagtgocattagttttcttttttgaatta
ctgtctgggattattgtgttgtctatacttttggagaactattgtccaatgatgttg
cacgtatgataaacaagggaaagggaaaggttaaaaagagatgaaaaagaaaagaa
cctgatcaaaagagggaactgacctagagacgaacctgacctggttctgtccattgaa
agcaaaagatataaagaagatataatggggagagagagagagaagaacagtggaaga
agaaagtgtgatgagataaataattgttaaggagcaagaggggtttatataactttg
ggggtgtgacggaggagggaaactgaggttagaacatgaaaagaaagagagatggag
tगतtgggggttttgggggcaaatctgattctggttactaagtgaataaataaataagt
gattggtattgtttatgaattatgttaaatctggaatgatctgctctcatgtagatag
ataccttattcctaataagtaaaatccccctcatttagatattatcatttttttaaaat
gaattgggttaaatataatgcttaagcactcaaatccatcccatattctccacctaaa
gggtgattagatagcaacataaatgattcaaaaaaatactatgacatataccagttcacg
ttttatgtgtaaaagttttggtgacttgcatttatataatataatataatata
```

GDR GBrowse Configuring Tracks

File ▾ Help ▾

Prunus Persica: 61 kbp from scaffold_1:3,426,000..3,487,000

Browser [Upload and Share Tracks](#) [Preferences](#)

Search

Landmark or Region:
scaffold_1:3426000..3487000 Search

Examples: scaffold_1:12360000..12479999, ppa014948m, BU045951, CPPCT016, AG25A.

Data Source
Prunus Persica

Download Decorated FASTA File

Scroll/Zoom: << < - Show 61 kbp + > >> Flip

Configure... Decorated FASTA File

The marked-up FASTA dumper plugin dumps out the currently displayed genomic segment in FASTA format.

This plugin was written by Lincoln Stein and Jason Stajich.

Output text html

Orientation Flip

Transcript Model	<input checked="" type="radio"/> None	<input type="radio"/> CAPS	<input type="radio"/> Bold	<input type="radio"/> Underline	<input type="radio"/> Italics	<input type="radio"/> Font	red	<input type="radio"/>	red	<input type="radio"/>
Alternate Transcript Model	<input checked="" type="radio"/> None	<input type="radio"/> CAPS	<input type="radio"/> Bold	<input type="radio"/> Underline	<input type="radio"/> Italics	<input type="radio"/> Font	red	<input type="radio"/>	red	<input type="radio"/>
PASA Aligned ESTs	<input checked="" type="radio"/> None	<input type="radio"/> CAPS	<input type="radio"/> Bold	<input type="radio"/> Underline	<input type="radio"/> Italics	<input type="radio"/> Font	red	<input type="radio"/>	red	<input type="radio"/>
Blat Aligned Prunus persica EST assembly V1	<input checked="" type="radio"/> None	<input type="radio"/> CAPS	<input type="radio"/> Bold	<input type="radio"/> Underline	<input type="radio"/> Italics	<input type="radio"/> Font	red	<input type="radio"/>	red	<input type="radio"/>
Genetic Marker Alignment	<input checked="" type="radio"/> None	<input type="radio"/> CAPS	<input type="radio"/> Bold	<input type="radio"/> Underline	<input type="radio"/> Italics	<input type="radio"/> Font	red	<input type="radio"/>	red	<input type="radio"/>
Genetic Mapped Markers	<input checked="" type="radio"/> None	<input type="radio"/> CAPS	<input type="radio"/> Bold	<input type="radio"/> Underline	<input type="radio"/> Italics	<input type="radio"/> Font	red	<input type="radio"/>	red	<input type="radio"/>
Genetic Mapped Markers	<input checked="" type="radio"/> None	<input type="radio"/> CAPS	<input type="radio"/> Bold	<input type="radio"/> Underline	<input type="radio"/> Italics	<input type="radio"/> Font	red	<input type="radio"/>	red	<input type="radio"/>
Arabidopsis Peptide Alignment	<input checked="" type="radio"/> None	<input type="radio"/> CAPS	<input type="radio"/> Bold	<input type="radio"/> Underline	<input type="radio"/> Italics	<input type="radio"/> Font	red	<input type="radio"/>	red	<input type="radio"/>
Grape Peptide Alignment	<input checked="" type="radio"/> None	<input type="radio"/> CAPS	<input type="radio"/> Bold	<input type="radio"/> Underline	<input type="radio"/> Italics	<input type="radio"/> Font	red	<input type="radio"/>	red	<input type="radio"/>
Poplar Peptide Alignment	<input checked="" type="radio"/> None	<input type="radio"/> CAPS	<input type="radio"/> Bold	<input type="radio"/> Underline	<input type="radio"/> Italics	<input type="radio"/> Font	red	<input type="radio"/>	red	<input type="radio"/>
Soybean Peptide Alignment	<input checked="" type="radio"/> None	<input type="radio"/> CAPS	<input type="radio"/> Bold	<input type="radio"/> Underline	<input type="radio"/> Italics	<input type="radio"/> Font	red	<input type="radio"/>	red	<input type="radio"/>
Rice Peptide Alignment	<input checked="" type="radio"/> None	<input type="radio"/> CAPS	<input type="radio"/> Bold	<input type="radio"/> Underline	<input type="radio"/> Italics	<input type="radio"/> Font	red	<input type="radio"/>	red	<input type="radio"/>
Consensus Repeats	<input checked="" type="radio"/> None	<input type="radio"/> CAPS	<input type="radio"/> Bold	<input type="radio"/> Underline	<input type="radio"/> Italics	<input type="radio"/> Font	red	<input type="radio"/>	red	<input type="radio"/>

click

Customize your track views

GDR Gbrowse Preferences

Prunus Persica: 61 kbp from scaffold_1:3,426,000..3,487,000

Browser Upload and Share

Preferences

- Show grid
- Cache tracks
- Show tooltips



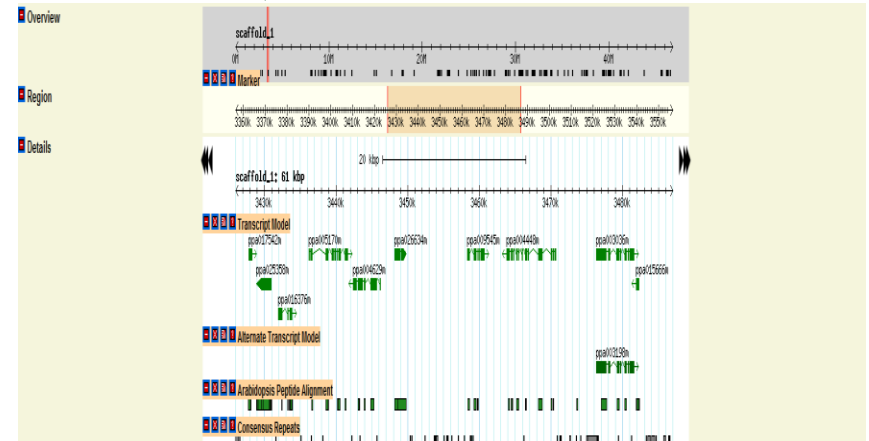
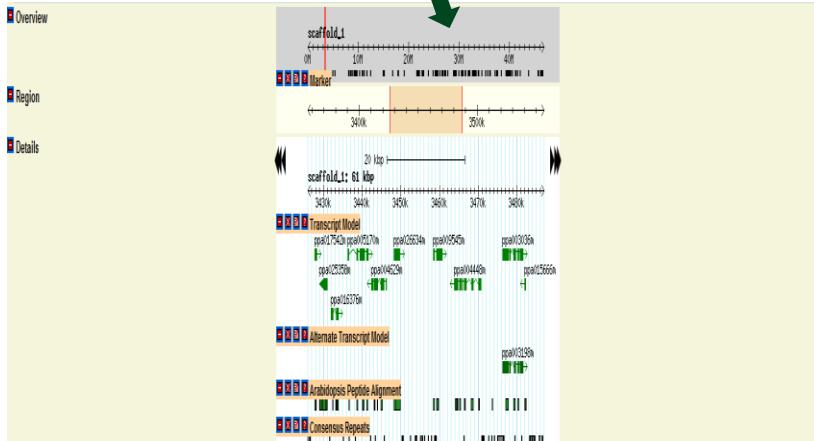
click

Image Width
 450 640 800 1024

Highlight feature(s) (feature1 feature2...) [Clear highlighting](#)

Highlight regions (region1:start..end region2:start..end) [Clear highlighting](#)

Region Size (bp)
200000



“Image Width”

GDR GBrowse Preferences

The image shows the GDR GBrowse Preferences interface. The top navigation bar includes Home, Species, Projects, Maps, Search, Tools, Community, and Contact. The main content area is titled "Prunus Persica: 5 kbp from scaffold_1:14,387,358..14,392,357". The "Preferences" tab is active, showing options for "Show grid", "Cache tracks", and "Show tooltips". The "Highlight feature(s)" dialog box is open, with "ppa014946m@yellow" selected in the "Highlight feature(s)" field. A green arrow labeled "click" points to the "Update Appearance" button. Another green arrow labeled "edit" points to the "Highlight feature(s)" field. The main browser view shows a genomic track for "scaffold_1" with a 5 kbp region highlighted in blue. A feature "ppa014946m" is highlighted in yellow within this region. Other tracks include "Transcript Model", "Alternate Transcript Model", and "Arabidopsis Peptide Alignment".

edit

click

Highlights the specified region and feature

GDR GBrowse Reports

GDR | Genome Database for Rosaceae

Home Species Projects Maps Search Tools Community

Download sequences or track data

Prunus Persica: 5 kbp from scaffold_1:14,387,358..14,392,357

Browser Upload and Share Tracks Preferences

Search

Landmark or Region:

Download Decorated FASTA File | Configure... Go

Display settings

click

click

click

```
>scaffold_1:14387358..14392357
aattgccagctaaacaatcgaacctggcttaagtccaagttagaatactcagactata
atctgattaatttggattattgtgtagcggagctcaggtaagaagaaacagagagag
agcttggagagaaatgagaaaattgacttattctctcaacttagtcacgcaacagctg
tacagcaaaatatactgttggaaatagaatattcccattacatcaatcaaatctagcc
atcaatttctactctcattgagatagctacacctggcgaattcattactacaataagg
gtacattttgtagtccattggactgtgacccatggttcacaaatatacaatacaaat
acttagctaacacacttactacttacaaggaagggttagagcttagctcagctactctg
acagacctcaactttctctgttttggactcctctgactagtcagctcagctcaagctaatg
tgatgggtagtgcgaattctggctggagctctggctgggaaatataatccogtgatga
tagagagagattggactgtgattttgtgactaatctgggagtggtgacatctcagagct
gaatatgggggtttctctgtggtttaaacttgcattccaaggggctctcaaatctg
cgtataaaatggactcgcagctgcagctcactctcacaataatctctctctgtt
ctcagctcagctcctctctgttctcagctgctacactctctcacaataatctctctctgtt
tgtgtagtaaccaactctataatggcaaaaacagggctcaattggttagcgaagggt
agctataatttggattggagctgtagatctcagctaggttaggagctacctctgtag
gatgattttagaagtctcctaagaactcgtactgtccocctcaatttagaggggtgattc
aattaggattataaaaagcttataaaaagcttataaaaagcttataaaaagcttataaaa
tatacaacttataaaaagcttataaaaagcttataaaaagcttataaaaagcttataaaa
ctttataaaaagcttataaaaagcttataaaaagcttataaaaagcttataaaaagctt
aaactagggtgattcgaatggctcattatattggaaggattccttaaggctgataaaatt
cgtagggtttagcgaagggttataaaaagcttataaaaagcttataaaaagcttataaaa
ccccaaatatttctcagcagcttttctctctcgaacagagacacaacagctctctctc
ctctcctctcgaagggtgctcctctctctctctctctctctctctctctctctctctct
ttttctcaattttctcactcagcttctctctctctctctctctctctctctctctctctct
gtttctctctctctctctctctctctctctctctctctctctctctctctctctctctct
ttttctctcgaactatgatgagactatgaaatgaaatgaaatgaaatgaaatgaaatgaa
ctataatcgtcaaaaaattgagcaaatatagtagaacattataaaaagcttataaaa
```

Configure... Decorated FASTA File

he marked-up FASTA dumper plugin dumps out the currently displayed genomic segment in FASTA format.
his plugin was written by Lincoln Stein and Jason Stajich.

Cancel Configure Go

Output text html

Orientation Flip

Transcript Model None CAPS Bold Underline Italic Font

Alternate Transcript Model None CAPS Bold Underline Italic Font

PASA Aligned ESTs None CAPS Bold Underline Italic Font

Blat Aligned Prunus persica EST assembly V1 None CAPS Bold Underline Italic Font

Genetic Marker Alignment None CAPS Bold Underline Italic Font

Genetic Mapped Markers None CAPS Bold Underline Italic Font

Genetic Mapped Markers None CAPS Bold Underline Italic Font

Arabidopsis Peptide Alignment None CAPS Bold Underline Italic Font

Grape Peptide Alignment None CAPS Bold Underline Italic Font

Poplar Peptide Alignment None CAPS Bold Underline Italic Font

Soybean Peptide Alignment None CAPS Bold Underline Italic Font

Rice Peptide Alignment None CAPS Bold Underline Italic Font

```
[Transcripts]
box_subparts = 0
visible = show
key = Transcript Model
feature = mRNA:JGI
fgcolor = green
bgcolor = green
category = Transcripts
glyph = transcript2

[Alternative Transcripts]
box_subparts = 0
visible = show
key = Alternate Transcript Model
feature = mRNA:alt
fgcolor = darkgreen
bgcolor = darkgreen
category = Transcripts
glyph = transcript2

[Marker:overview]
feature = sequence_variant
visible = show
bgcolor = black
label = 1
height = 5
key = Genetic Mapped Markers
glyph = generic

[Arabidopsis Peptide Alignment]
feature = match:arabi_peptide
visible = show
```

GDR GBrowse Reports

The screenshot displays the GDR (Genome Database for Rosaceae) GBrowse interface. At the top, the GDR logo and the text "Genome Database for Rosaceae" are visible. Below the logo, there are navigation tabs for "Home", "Species", and "Projects". The main content area shows a genomic track for "scaffold_1" with a "Transcript Model" for "ppa014948m". A file download dialog box is open in the foreground, titled "File Download". The dialog asks, "Do you want to save this file, or find a program online to open it?". The file details are: Name: scaffold_1_14387358..14392357.gff3, Type: Unknown File Type, and From: www.rosaceae.org. The dialog has buttons for "Find", "Save", and "Cancel". A warning message at the bottom of the dialog states: "While files from the Internet can be useful, some files can potentially harm your computer. If you do not trust the source, do not find a program to open this file or save this file. [What's the risk?](#)".

GDR Gbrowse – Adding your annotations



GDR | Genome Database
for Rosaceae

Home Species Projects Maps Search Tools Community Contact

File Help

Prunus Persica: 61 kbp from scaffold_1:3,426,000..3,487,000

Browser Upload and Share Tracks Preferences

Uploaded Tracks

[\[Help with the file format\]](#)
Upload a track

Browse Upload Remove

Add custom track(s): [\[From text\]](#) [\[From a file\]](#)

Imported Tracks

[\[Help with the file format\]](#)
Enter remote track URL

Upload Remove

[\[Import a track\]](#)

**Upload or import your
own annotation files**

GDR GBrowse Tutorial

References

- <http://www.openhelix.com/gbrowse>
- <http://gmod.org/wiki/Gbrowse>

Acknowledgements

- This tutorial was based on the Open Helix Gbrowse 1.6 tutorial which was modified for the peach genome sequence and annotations implemented in GBrowse 2.0