# GDR in Drupal

## facilitating community building and efficient maintenance

WASHINGTON STATE
UNIVERSITY

# GDR (Genome Database for Rosaceae)

is a web-based community database of Rosaceae genetics and genomics data and analysis tools facilitating utilization of the data among member species

www.rosaceae.org

# Topics

- GDR News
- Major objectives for the next grant period
  - Content
  - Infrastructure using Chado/Drupal (Demo)
- Data/tools currently available from GDR
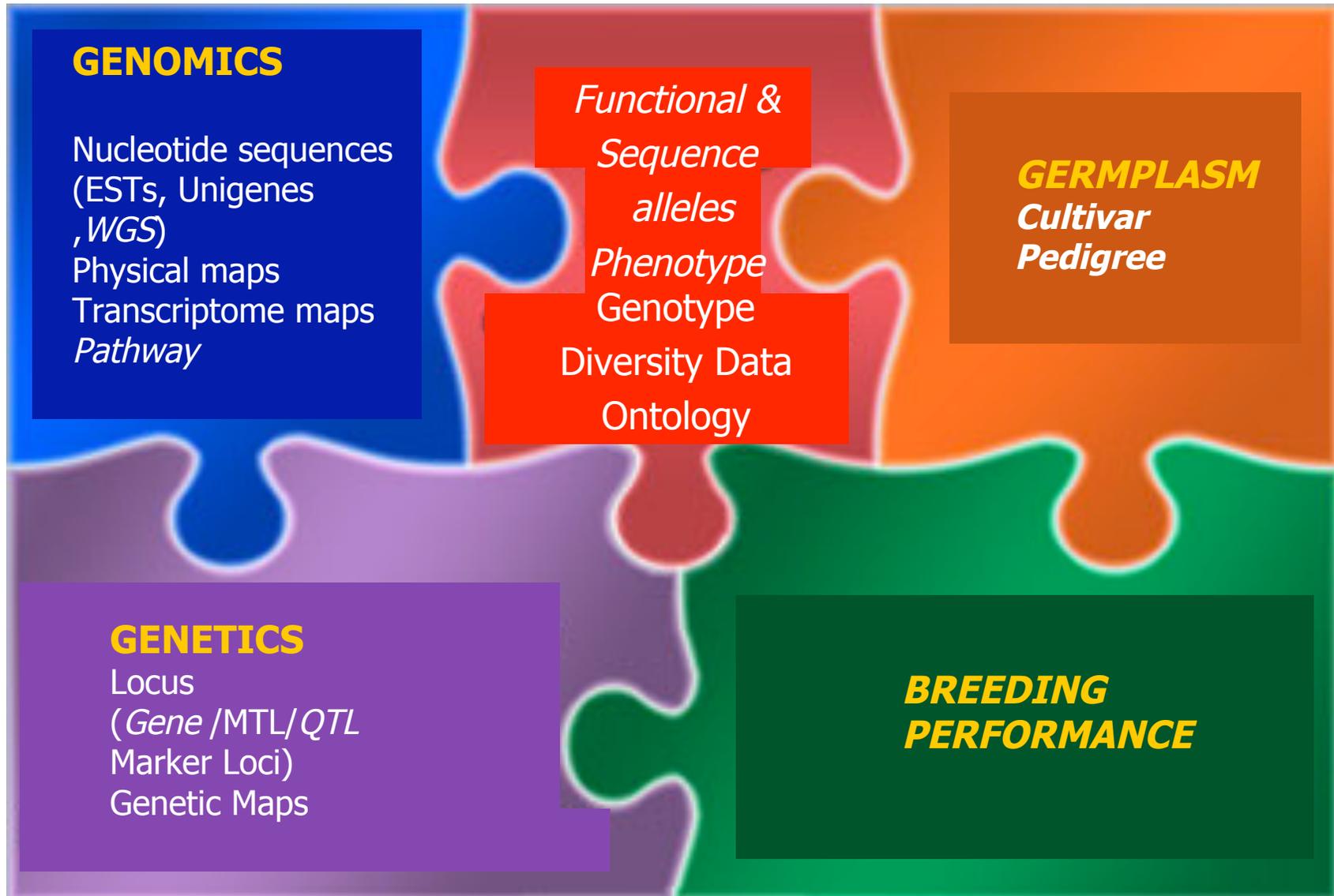- How to access the data and tools (Demo)

# GDR News

- GDR receives funding from Sept 2009 to Aug 2013 from the USDA Specialty Crop Research Initiative program ☺

- Tree fruit Genome Database Resources (tfGDR) will expand GDR to include Citrus.

- Whole genome sequence of peach in GBrowse (will go public in Apr 1)
    - apple and strawberry data to follow

- GDR is implemented in Drupal.

- Project site developed for RosBreed.

# Major goals for the next 4 years

- To integrate whole genome sequences, large-scale phenotyping/genotyping data, and breeding data with the current GDR data

- To develop an infrastructure using chado and drupal (tripal) that is easy to develop, implement and maintain

# Data to be integrated..

**GENOMICS**

Nucleotide sequences
(ESTs, Unigenes
,*WGS*)
Physical maps
Transcriptome maps
*Pathway*

*Functional &*
*Sequence*
*alleles*
*Phenotype*
Genotype
Diversity Data
Ontology

**GERMPLASM**
**Cultivar**
**Pedigree**

**GENETICS**
Locus
(*Gene* /MTL/*QTL*
Marker Loci)
Genetic Maps

**BREEDING**
**PERFORMANCE**

# Plan for Building an Efficient Database

**Drupal**

**Content Management System**

**Tripal**

Demo by Stephen Ficklin
Jan 13th  (Tue) 2:30 pm

**Drupal modules as web front-end for Chado**

**Chado**

**Generic Database schema**

# Advantages of using Drupal

**For Database Developers**

- Easy to use and update
    - Provides functionality for community building – forums, calendars, project pages etc
- **Open Source,** popular, robust, secure and modular
- Users/Roles/Access Control

**For Users – control your own page/site!**

- You can create/edit pages and upload data
    - for meetings/conference/employment
    - for project/lab sites
    - as editors for gene, QTL, breeding data, etc
    - access private data securely before publication

GDR

# Editing a project page

# Creating a new page

# User Management

# Genomics Data

- Unigene for family Rosaceae and for genus of malus, prunus, fragaria, pyrus and rosa ESTs.

- EST annotation includes unigene set, homology, SSRs, ORF, SNPs, unique oligo sets for unigene microarray

- NCBI/Swiss-Prot/TremBL Rosaceae protein data

**Coming Soon – Whole Genome Sequence of Peach, Strawberry and Apple** ☺

# Genetics Data

- Locus (marker loci and MTL)
  - Over 1400 locus data available from marker/trait search site

- Maps and Genetic Diversity Data
  - 39 Rosaceae genetic maps in CMap
  - polymorphism/diversity search site
  - Genetically anchored peach physical and transcriptome map
  - Hybridization data between probes (ESTs and genetic markers) and peach BACs

- Publications
  - relevant to Rosaceae genetics and genomics

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# Access the data from
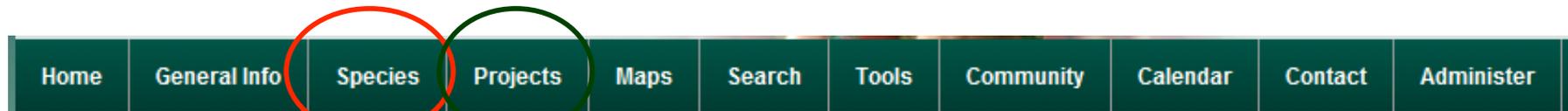


**species page**

| |
|---|
| Apple |
| Pear |
| Prunus ▶ |
| Raspberry   Prunus Data |
| Rose |
| Strawberry |

| |
|---|
| Almond |
| Cherry |
| Apricot |
| Peach |

**or**     **projects page**

| |
|---|
| Rosaceae EST Unigene |
| Individual EST Project |
| Peach Physical Map |
| Peach Transcriptome Map |
| NRI Projects |
| Organelle |
| Proteins |
| BACs |

Navigation bar: Home | General Info | Species | Projects | Maps | Search | Tools | Community | Calendar | Contact | Administer

# Or go directly to

| Home | General Info | Species | Projects | Maps | Search | Tools | Community | Calendar | Contact | Administer |

## maps

| CMap |
| --- |
| GDR MapViewer Peach |
| WebChrom Peach |
| WebFPC Peach |

## search

| Mapped BACs |
| --- |
| Markers |
| Traits |
| ESTs |
| Publications |
| Polymorphism |
| GO Terms |

## Tools
## to blast against
## or download

| NCBI BLAST |
| --- |
| Batch BLAST |
| FASTA |
| SSR |
| EST Assembly |
| Remote Analysis Tools |
| Download Data |

GDR

# Maps

| Home | General Info | Species | Projects | Maps | Search | Tools | Community | Calendar | Contact | Administer |

CMap

GDR MapViewer Peach

WebChrom Peach

WebFPC Peach

GDR

# CMap (comparative map viewer)

# Genetic, Physical, and Transcriptome Map
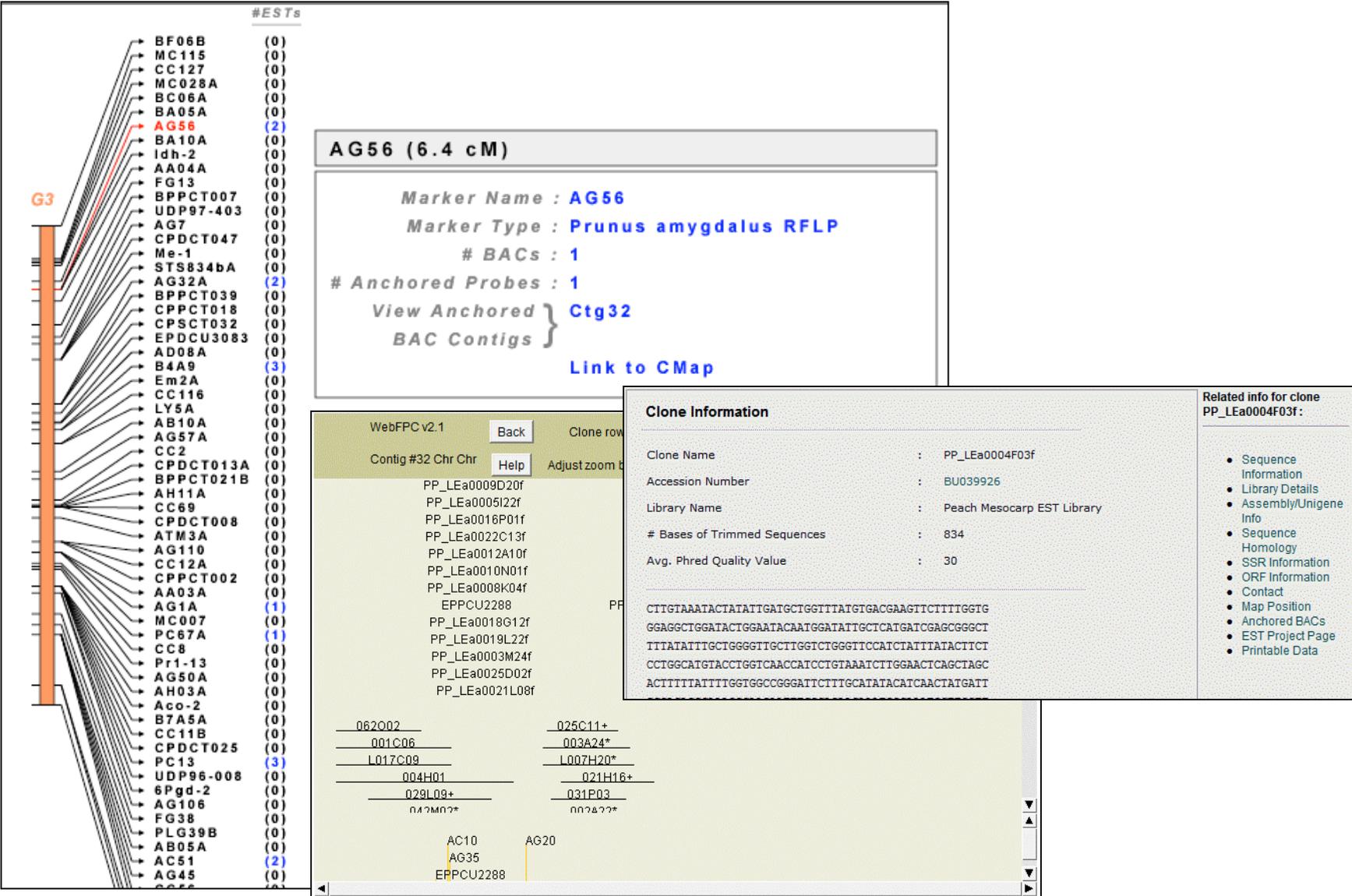
# search engine

| Home | General Info | Species | Projects | Maps | Search | Tools | Community | Calendar | Contact | Administer |
|------|--------------|---------|----------|------|--------|-------|-----------|----------|---------|------------|

NCBI BLAST

Batch BLAST

FASTA

SSR

EST Assembly

Remote Analysis Tools

Download Data

GDR

## Search EST

Click here to Search Unigene Contigs

Select database and search ESTs by clone name and other features. Visit project description page for more information on each EST database. More search options such as the unigene name, putative function and anchored ma...

| Prunus | Fragaria | Rosa | R |

### Search EST by Name

Accession No. ▼ Enter text

| All |
| Carpel |
| Flower |
| Friut Mesocarp |
| Fruit |
| Fruit En |
| Fruit Ep |
| Fruit Ep |
| Fruit M |
| Gynoec |
| Inflores |
| Leaf |
| Petal |
| Phloem |
| Recept |
| Recept |
| Root |
| Seed |
| Shoot |
| Unspec |
| Vegeta |
| Whole |
| Xylem |

### Search EST by Features

☐ Has SSRs

☐ Represents a Unigene From*

*This feature will return the unige
version 3 (Jun. 2006) and versio

### Search EST by Taxonomy

Taxonomy :

### Search EST by Tissue

Tissue (curated) :  All

### Search EST by Putative Function

---

### Contig Information

| Contig Name | : | Rosa_v4_Contig1008 |
| Length of Consensus Sequence | : | 591 |
| Assembly Name | : | Rosa Unigene Version 4 |
| Date Created | : | 02-MAY-08 |
| Number of Member Sequences | : | 8 |

```
ATAGCAAGCAAGCAAAGCAATTCCATTAATCAAAAGCAAAACCCATTTTC
AGTTACTCAAATCCAATCAGCACCATGTCTGGAAAGTGCGGCAACTGTGA
CTGCTCTGACGCTTCCCAGTGCACCAAGAAGGGAAACAGTTTGGTCATTG
TTGAGACTGAGAAGAGCTACGACACTGTTGTTATGGATGCACCAGCTGCC
GAGAACGGCGGAAAATGCAAATGCGGCACCACCTGCTCTTGCATCGACTG
CAAATGTGGAAATTAAGTCCCCTATTCACGACCAATGGCTGCCATATAAC
TATGTGGTGATAAAAATTGTGGAGTCTCGTCAATAAAGGATTTGTGAGAA
TCAAATAACTCCTCTGTTTATTTGTGATAGTAGTTTGATCGAGTCTGTGA
GTGAGTGGGTGAAAGATGTACTCTACTGTACGTATGTGTGTCAATCATAT
CTGTGTTCTTTAGTAGCTTGTAAGGTTCTTGATCTGGCCATTATCTGTGG
CCTTGTGATTATGTTTAATTAATGAAATTACTGTTCGTATACATGCTGAT
TTTNACCTCTTTAGCTGTNTCTAATATTTNTCAAAAAAAA
```

Related info for
**Rosa_v4_Contig1008**

- Sequence Information
- Comprising ESTs
- Sequence Homology
- Sequence GO Terms
- SSR/ORF Information
- View AutoSNP output

---

### Contig Search

Select database and search
Return to EST Search Page.

| Search Con |
| Unigene |
| Enter text |

### Search Contig by Features

☐ Has SSRs

☑ Has SNPs        (Only Genera Unigenes have SNPs available. The Rosaceae Unigene does not.)

### Search Contig by Putative Function

Match Description : [          ]

Match Organism : [          ]

GO Term (id number or name) : [          ]  *Please click here to browse available GO Terms.
(Only Version 3 Contigs have GO Terms.)

[ Submit ]  [ Clear ]

# Marker Search

Search molecular markers by name or b~~

marker is mapped, map position and the

simply-inherited traits. Some of the mark~~

probes in BAC hybridization, so some ES~~

associated BAC clones and EST clones as~~

positions. Template for data submission i~~

## Marker Information

| | |
|---|---|
| **Marker Name** | BPPCT028 |
| **Marker Alias** | *N/A* |
| **Genbank ID** | *N/A* |
| **Marker Type** | SSR |

### ⊟ Source

| | |
|---|---|
| **source organism** | Prunus persica |
| **source cultivar** | O Henry |
| **source description** | Genomic DNA |
| **source genbank id** | AF374944 |
| **source marker** | *N/A* |

### ⊟ Detection

| | |
|---|---|
| **PCR condition** | 94 C 1 min, 94 C 45 sec, 57 C 45 sec, 72 C 2 min. 35 cycles, 72 C |

**Search by Name**    A~~

Marker Ty~~

Marker de~~

Marker mapped in species

any

## Associated BACs

BACs are associated with some markers as the source of the marker, by hybridizing to the marker, and/or by hybridizing to the EST that is the source of the marker. Click the BAC name for more data.

**BPPCT028 is hybridized to the BACs**

| clone name |
|---|
| 024G18 |

Monomorphic Population

Polymorphism Data

### ⊟ Map Position

| map name | linkage group | bin | start | stop | locus name | view in CMap |
|---|---|---|---|---|---|---|
| TxE | G1 | *N/A* | 77.4 | *N/A* | BPPCT028 | CMap |
| JxF | G1 | *N/A* | 124.1 | *N/A* | BPPCT028 | CMap |
| P2175 x GN | P2175G1 | *N/A* | 119.9 | *N/A* | BPPCT028 | CMap |
| P2175 x GN | GN1 | *N/A* | 133.7 | *N/A* | BPPCT028 | CMap |

Click locus name or the CMap link to view markers in the GDR map viewer or CMap. Click map name for more information of the map.

## Map Position

Map Name

Linkage Group

Bin Name

**Trait**

| trait name | Root-knot nematode resistance |
|---|---|
| trait alias | RKN resistance |
| trait category | Biotic stress |
| published symbol | Mi |
| taxon | peach |
| trait description | The search for peach rootstocks resistant to root-knot nematodes has been a long and continuing project in the United States and other countries. Some rootstocks, such as Nemaguard, Nemared, Flordaguard, Guardian, Okinawa, and Higama, show various levels of resistance to root-knot nematodes. Lu et al. (1997) were the first to propose a two-gene model for |
| screening method | Bioassays were used to measure nematode resistance: each F2 genotype was scored for number of galls and egg masses. |

**Map Position**

| map name | linkage group | position | comments |
|---|---|---|---|
| TxE | G2 | 0 - 1 cM | tentatively anchored to the position from the position in other maps with common markers |

**References**

| author | title | year | citation |
|---|---|---|---|
| Lu, Z.X., Sosinski, B., Reighard, G.L. | Construction of a genetic linkage map and identification of AFLP markers for resistance | 1998 | Genome / Genome Apr 1998. v. 41 (2) p. 199-207. ISSN 0831-2796; GENOE3 |

## Search Peach BAC

Peach BACs that have been hybridized to a probe (genetic markers or peach ESTs) and those that have been used in fingerprinting can be searched in this site. Search options include BAC clone name and the marker probe specifications such as map name, linkage group, probe source organism and probe type. BAC data page provides data such as hybridized markers and ESTs, BAC library details and BAC contig assembly results.

Below are the prunus BAC clones of which sequences are publicly available.
082I18 (GenBank) | 028F08 (GenBank) | pPn31C7(GenBank) | PpN018G07(GenBank) 045O02 (GDR) | 058P04 (GDR) | 080O24 (GDR) | AprC27 (GDR)

### Search by BAC name

(eg. Select "Starts with" and type in "101C" to get all the BACs with name that begins with "101C".)

Starts with ▼ | 10 | Submit Query

(Select the four catego

**Map Name**
FVxFN
FxB

New BAC Search                                                      Page 1 of 19 | Next

| BAC Name | | |
|---|---|---|
| 108J24 | 106J18 | 101B06 |
| 108J12 | 106N10 | 101D04 |
| 104K22 | 106N19 | 101K07 |
| 108J15 | 107H19 | 102D05 |
| 109L12 | 107L19 | 102D13 |
| 103C03 | 107O02 | 102H12 |
| 104N01 | 108A10 | 102F06 |
| 105N07 | 108F09 | 109J03 |
| 106F04 | 100G24 | 102P08 |
| 106I20 | 100K08 | 105A12 |

## Hybridized Probes / ESTs

Data of probes/ESTs that hybridized to the BAC clone is provided below.

Marker or EST name is linked to a page with detailed information.

No genetically linked probes have been hybridized to this clone.

| Probe Name | Probe Type | Source Organism | Hybridization Date | Hybridization Done By |
|---|---|---|---|---|
| PP_LEa0035B0 | | | | |

### Related info for BAC clone 100A08 :

- Hybridized Probes/ESTs
- Library Details
- Contig Assembly

## BAC Contig Assembly

The BAC clone 100A08 belongs to a contig.

(For peach physical map development, BAC clones are being assembled into contigs using an approach that combines hybridization of mapped markers and BAC fingerprinting. We use Image for band-calling and FPC for the automatic assembly of the bands.)

**Contig Number**

**FPC file Name**

**Date of FPC assembly**

**FPC done by**

**View Contig in WebFPC**

**BAC Clones in Contig**

### Related info for BAC clone 100A08 :

- Hybridized Probes/ESTs
- Library Details
- Contig Assembly

---

WebFPC v2.1  Back  Clone rows 12  Show Clones No Buried  Marker Remarks / Clone Remarks 2

Contig #360 Chr Chr  Help  Adjust zoom by 2.0  Zoom  In  Out  Marker hiding

PP_LEa0016G14f
PP_LEa0018C02f
PP_LEa0005G18f
PP_LEa0012D19f
PP_LEa0026O16f
PP_LEa0014N03f

L009D06
L003I21*
009K13
098H02
074O18
020N17
100B08
L082K12
L006I16
048F17
L003J03
065L16

# Rosaceae Community Resources

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RosIGI

USRosExec

NRI Projects

Conferences

Employment

Mailing Lists

Message Boards

Links

GDR

# Acknowledgements

- GDR Team – Dorrie Main, Sook Jung, Meg Staton, Randall Svancara, Taein Lee, Ping Zheng, Albert Abbott

- Previous members: Anna Blenda, Stephen Ficklin, Christopher Jesudurai

- Rosaceae Community

- NSF Plant Genome Program

- USDA Specialty Crop Research Initiative

# Thank you!

## Visit us at

- Plant Database Booth
  - Sunday 8-8:30 pm
  - Monday 10-10:30 am, 4-4:30 pm

- Poster C915
  - Monday 10 -11:30