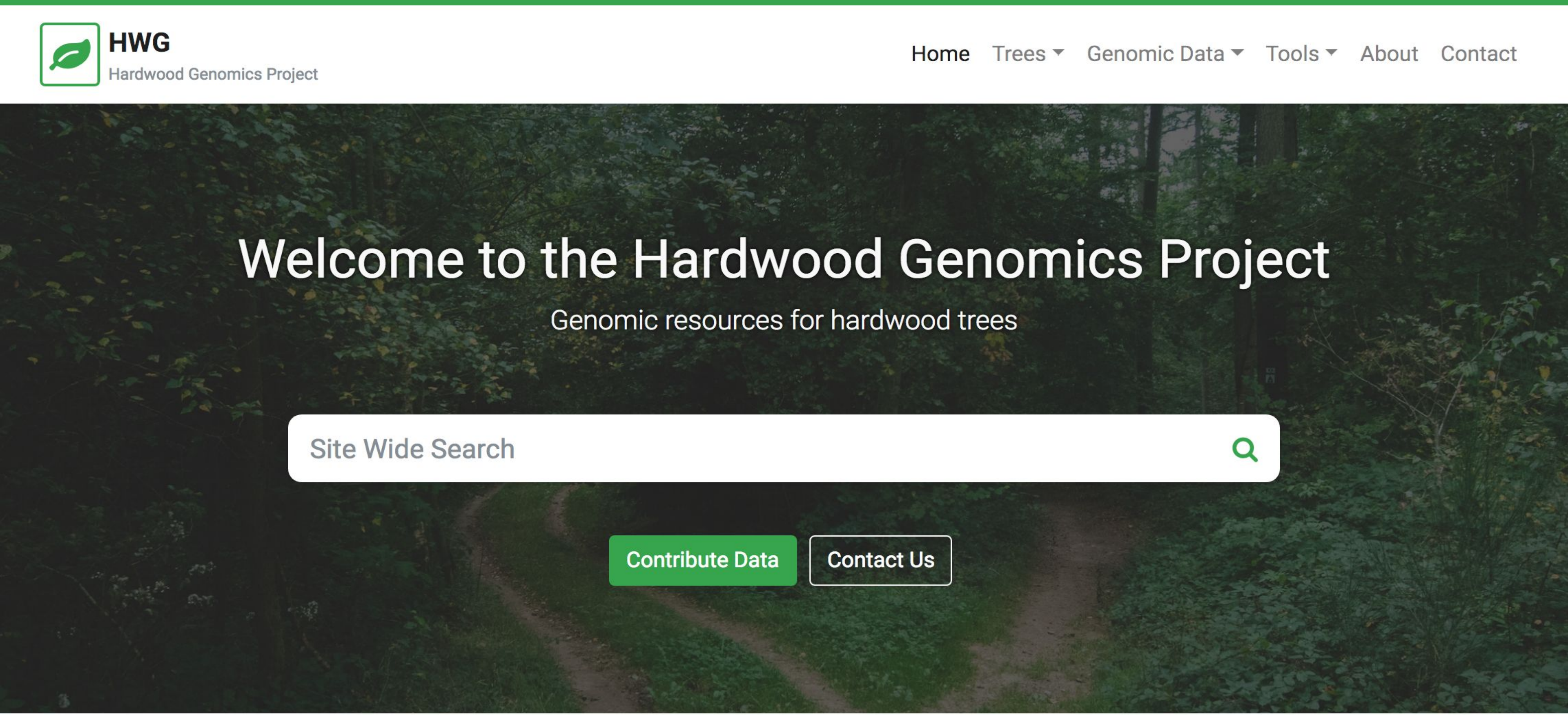

HWG
Hardwood Genomics Project
Home
Trees
Genomic Data
Tools
About
Contact
Site Wide Search
Contribute Data
Contact Us

Welcome to the Hardwood Genomics Project

Genomic resources for hardwood trees

https://beta.hardwoodgenomics.org/

# Comparative Genomics of Environmental Stress Responses in North American Hardwoods

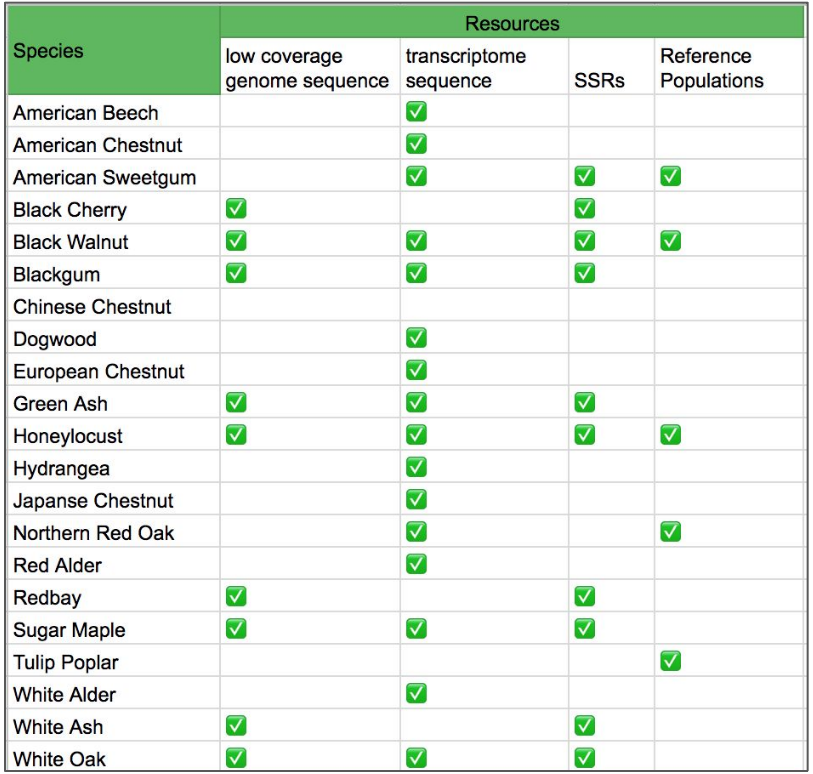
- Started in 2011
- Housing genetic and genomic resources for hardwood tree species
- Increasingly devastating forest threats: diseases, invasive pests and climate change

# Expanding HWG database

- New data and new interfaces
  - Controlled vocabularies
  - Genetic markers and maps, phenotype data
  - Search and expression visualization interfaces
- Tripal improvement
  - Tripal gateway
  - Cross site communication

Tripal

# Genetic and genomic resources in HWG

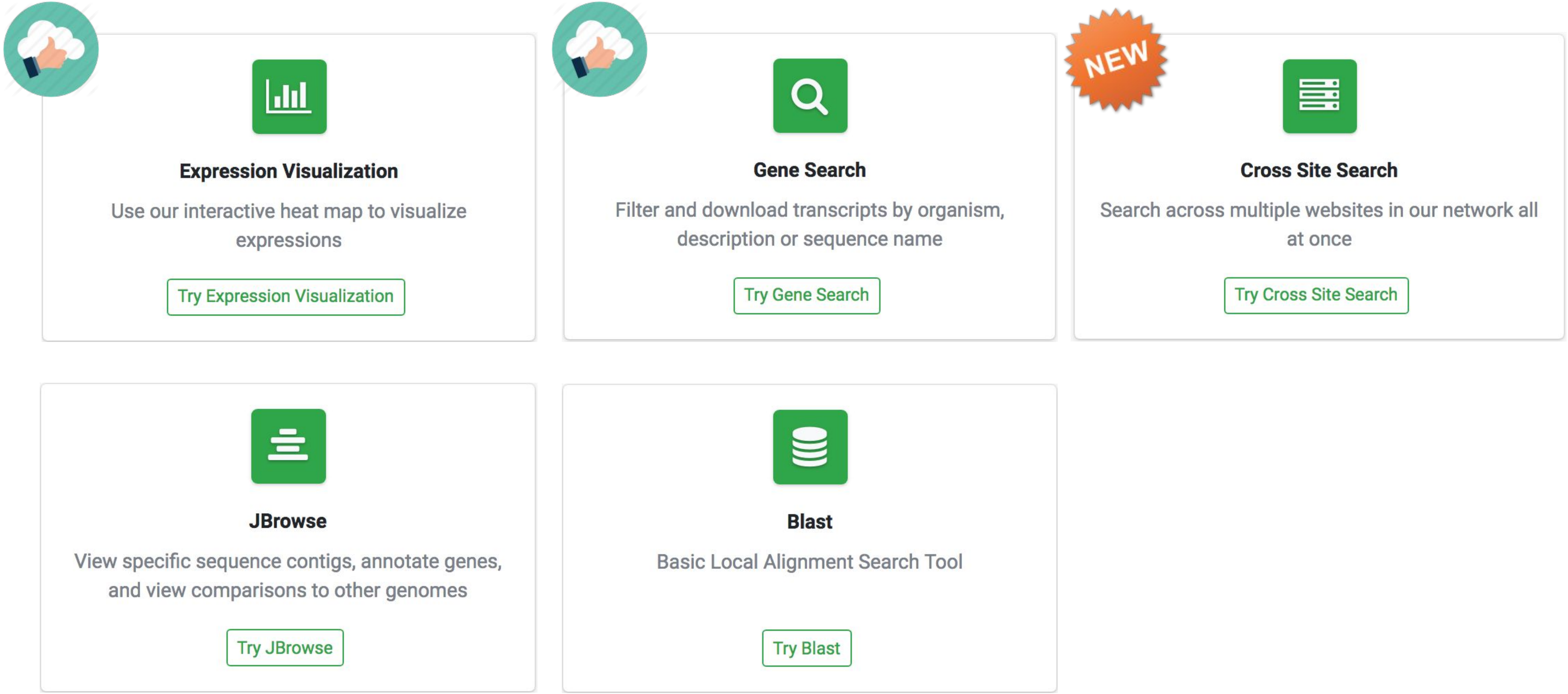


| Species | Resources | | | |
|---|---|---|---|---|
| | low coverage genome sequence | transcriptome sequence | SSRs | Reference Populations |
| American Beech | | ✅ | | |
| American Chestnut | | ✅ | | |
| American Sweetgum | | ✅ | ✅ | ✅ |
| Black Cherry | ✅ | | ✅ | |
| Black Walnut | ✅ | ✅ | ✅ | ✅ |
| Blackgum | ✅ | ✅ | ✅ | |
| Chinese Chestnut | | | | |
| Dogwood | | ✅ | | |
| European Chestnut | | ✅ | | |
| Green Ash | ✅ | ✅ | ✅ | |
| Honeylocust | ✅ | ✅ | ✅ | ✅ |
| Hydrangea | | ✅ | | |
| Japanse Chestnut | | ✅ | | |
| Northern Red Oak | | ✅ | | ✅ |
| Red Alder | | ✅ | | |
| Redbay | ✅ | | ✅ | |
| Sugar Maple | ✅ | ✅ | ✅ | |
| Tulip Poplar | | | | ✅ |
| White Alder | | ✅ | | |
| White Ash | ✅ | | ✅ | |
| White Oak | ✅ | ✅ | ✅ | |

# Reference Genomes

- Chinese Chestnut
- English Walnut
- European Ash
- Valley Oak

# Tools available for accessing and visualizing database resources


NEW

**Expression Visualization**

Use our interactive heat map to visualize expressions

Try Expression Visualization

**Gene Search**

Filter and download transcripts by organism, description or sequence name

Try Gene Search

**Cross Site Search**

Search across multiple websites in our network all at once

Try Cross Site Search

**JBrowse**

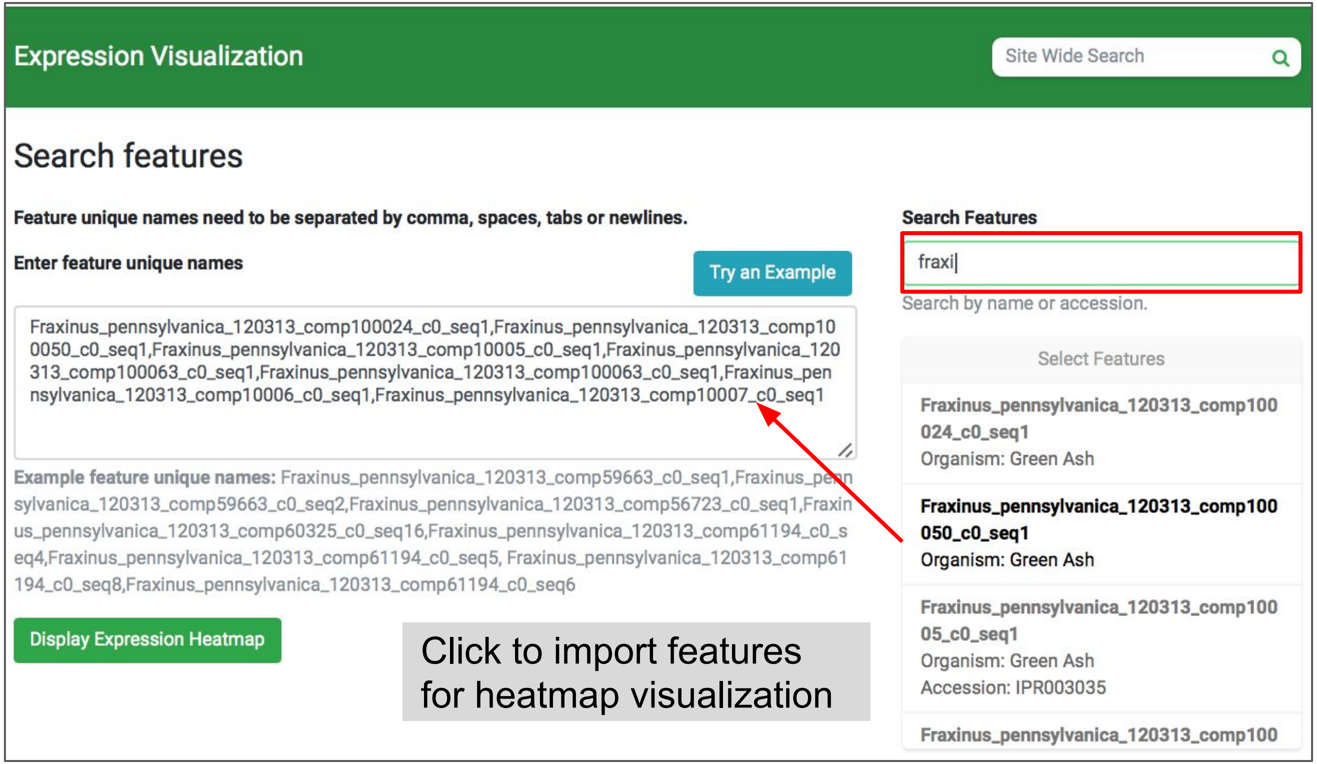
View specific sequence contigs, annotate genes, and view comparisons to other genomes

Try JBrowse

**Blast**

Basic Local Alignment Search Tool

# Expression visualization



## Search features

**Feature unique names need to be separated by comma, spaces, tabs or newlines.**

**Enter feature unique names**

Fraxinus_pennsylvanica_120313_comp100024_c0_seq1,Fraxinus_pennsylvanica_120313_comp100050_c0_seq1,Fraxinus_pennsylvanica_120313_comp10005_c0_seq1,Fraxinus_pennsylvanica_120313_comp100063_c0_seq1,Fraxinus_pennsylvanica_120313_comp100063_c0_seq1,Fraxinus_pennsylvanica_120313_comp10006_c0_seq1,Fraxinus_pennsylvanica_120313_comp10007_c0_seq1

**Example feature unique names:** Fraxinus_pennsylvanica_120313_comp59663_c0_seq1,Fraxinus_pennsylvanica_120313_comp59663_c0_seq2,Fraxinus_pennsylvanica_120313_comp56723_c0_seq1,Fraxinus_pennsylvanica_120313_comp60325_c0_seq16,Fraxinus_pennsylvanica_120313_comp61194_c0_seq4,Fraxinus_pennsylvanica_120313_comp61194_c0_seq5, Fraxinus_pennsylvanica_120313_comp61194_c0_seq8,Fraxinus_pennsylvanica_120313_comp61194_c0_seq6

**Search Features**

fraxi

Search by name or accession.

**Fraxinus_pennsylvanica_120313_comp100024_c0_seq1**
Organism: Green Ash

**Fraxinus_pennsylvanica_120313_comp100050_c0_seq1**
Organism: Green Ash

**Fraxinus_pennsylvanica_120313_comp10005_c0_seq1**
Organism: Green Ash
Accession: IPR003035

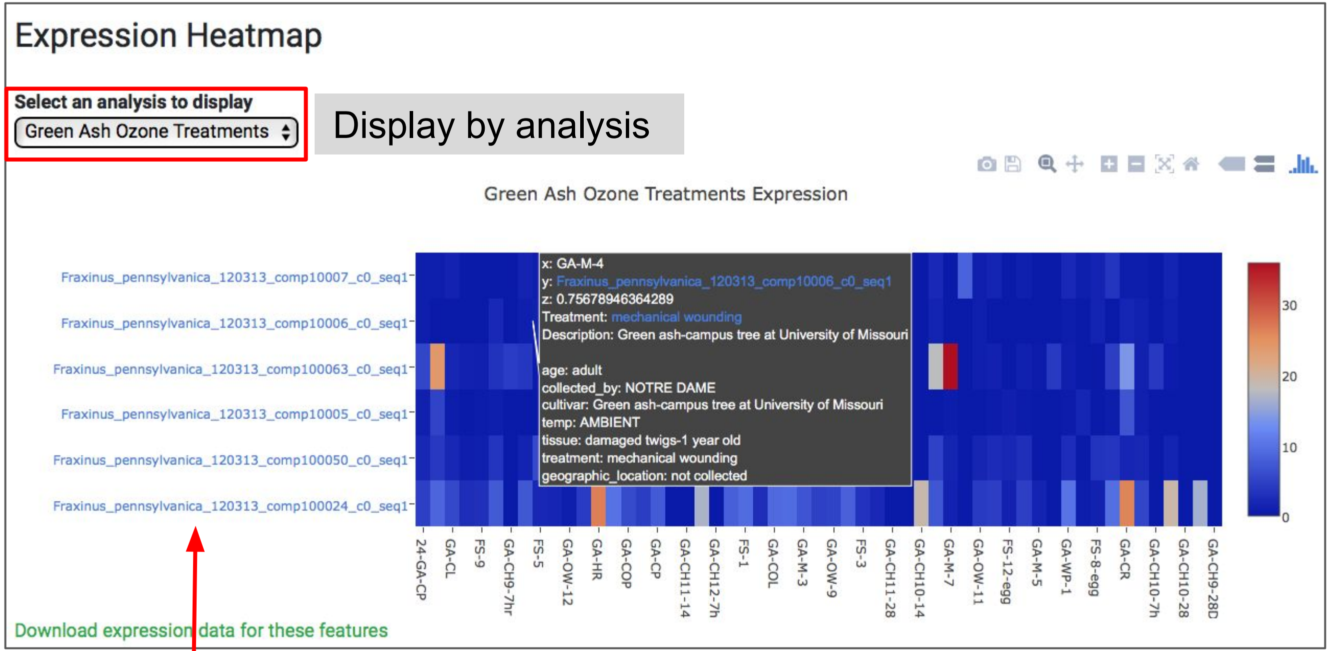
**Fraxinus_pennsylvanica_120313_comp100**

Click to import features for heatmap visualization

More powerful feature search

display search results as typing

# Expression visualization



## Expression Heatmap

**Select an analysis to display**

Green Ash Ozone Treatments

Display by analysis

Green Ash Ozone Treatments Expression

x: GA-M-4
y: Fraxinus_pennsylvanica_120313_comp10006_c0_seq1
z: 0.75678946364289
Treatment: mechanical wounding
Description: Green ash-campus tree at University of Missouri

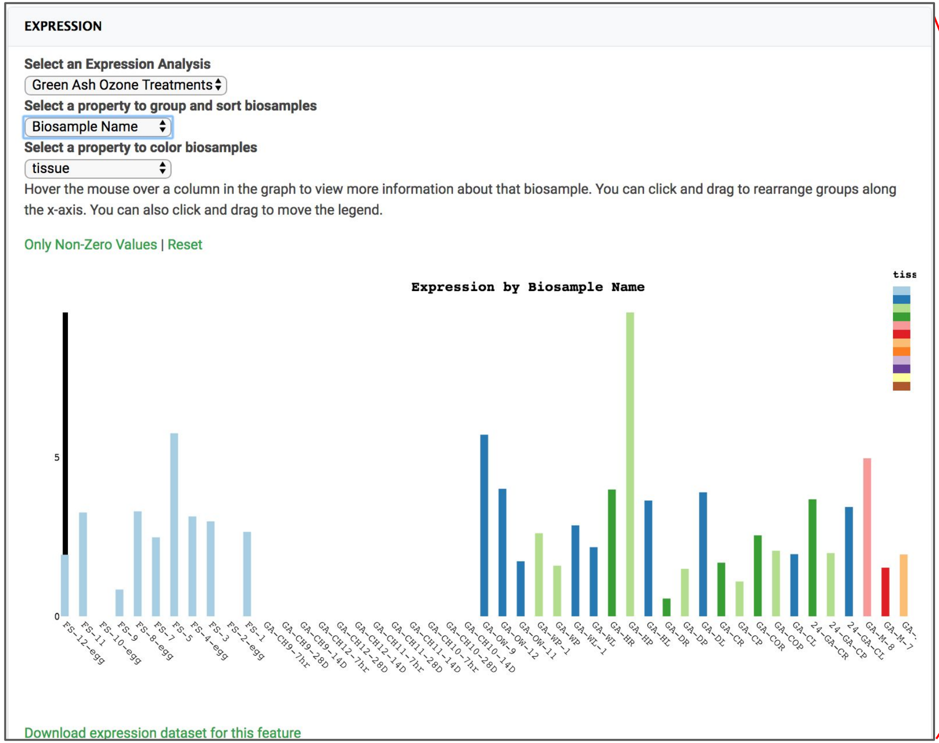
age: adult
collected_by: NOTRE DAME
cultivar: Green ash-campus tree at University of Missouri
temp: AMBIENT
tissue: damaged twigs-1 year old
treatment: mechanical wounding
geographic_location: not collected

Download expression data for these features

Fraxinus_pennsylvanica_120313_comp10007_c0_seq1
Fraxinus_pennsylvanica_120313_comp10006_c0_seq1
Fraxinus_pennsylvanica_120313_comp100063_c0_seq1
Fraxinus_pennsylvanica_120313_comp10005_c0_seq1
Fraxinus_pennsylvanica_120313_comp100050_c0_seq1
Fraxinus_pennsylvanica_120313_comp100024_c0_seq1
24-GA-CP
GA-CL
FS-9
GA-CH9-7hr
FS-5
GA-OW-12
GA-HR
GA-COP
GA-CP
GA-CH11-14
GA-CH12-7h
FS-1
GA-COL
GA-M-3
GA-OW-9
FS-3
GA-CH11-28
GA-CH10-14
GA-M-7
GA-OW-11
FS-12-egg
GA-M-5
GA-WP-1
FS-8-egg
GA-CR
GA-CH10-7h
GA-CH10-28
GA-CH9-28D
30
20
10
0

Link to individual feature visualization

# Expression visualization



**EXPRESSION**

Select an Expression Analysis: Green Ash Ozone Treatments

Select a property to group and sort biosamples: Biosample Name

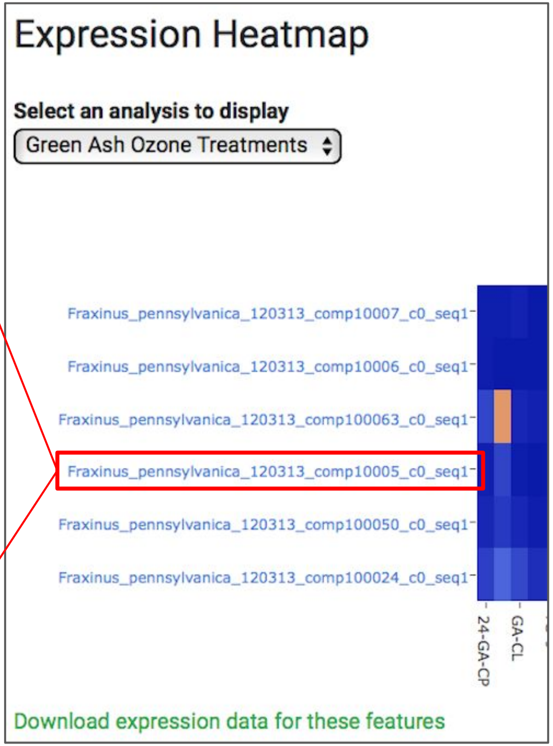
Select a property to color biosamples: tissue

Hover the mouse over a column in the graph to view more information about that biosample. You can click and drag to rearrange groups along the x-axis. You can also click and drag to move the legend.

Only Non-Zero Values | Reset

Expression by Biosample Name
tiss
5
0
FS-12-egg
FS-11
FS-10-egg
FS-9
FS-8-egg
FS-7
FS-5
FS-4-egg
FS-3
FS-2-egg
FS-1
GA-CH9-7hr
GA-CH9-28D
GA-CH9-14D
GA-CH12-7hr
GA-CH12-28D
GA-CH11-14D
GA-CH11-7hr
GA-CH11-28D
GA-CH11-14D
GA-CH10-7hr
GA-CH10-28D
GA-CH10-14D
GA-OW-9
GA-OW-12
GA-OW-11
GA-WP-1
GA-WP
GA-WL-1
GA-WL
GA-HR
GA-HP
GA-HL
GA-DR
GA-DP
GA-DL
GA-CR
GA-CP
GA-COR
GA-COP
GA-CL
24-GA-CR
24-GA-CP
24-GA-CL
GA-M-8
GA-M-7
GA-

Download expression dataset for this feature



## Expression Heatmap

Select an analysis to display: Green Ash Ozone Treatments

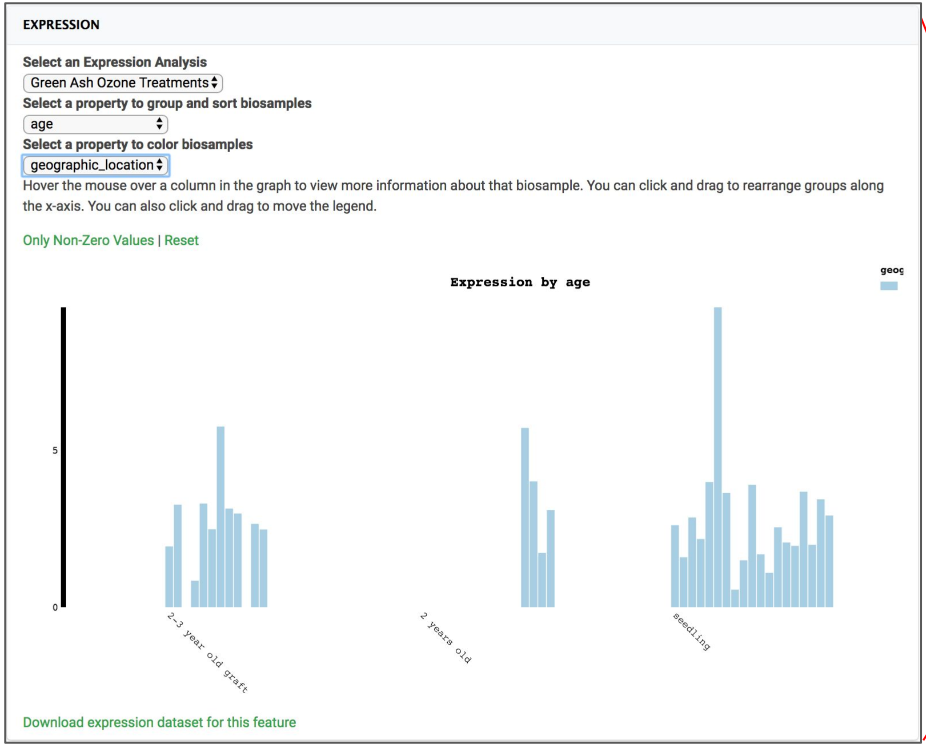
Fraxinus_pennsylvanica_120313_comp10007_c0_seq1
Fraxinus_pennsylvanica_120313_comp10006_c0_seq1
Fraxinus_pennsylvanica_120313_comp100063_c0_seq1
Fraxinus_pennsylvanica_120313_comp10005_c0_seq1
Fraxinus_pennsylvanica_120313_comp100050_c0_seq1
Fraxinus_pennsylvanica_120313_comp100024_c0_seq1
24-GA-CP
GA-CL

Download expression data for these features

**HWG**
Hardwood Genomics Project

https://beta.hardwoodgenomics.org/

# Expression visualization



**EXPRESSION**

**Select an Expression Analysis**

Green Ash Ozone Treatments

**Select a property to group and sort biosamples**

age

**Select a property to color biosamples**

geographic_location

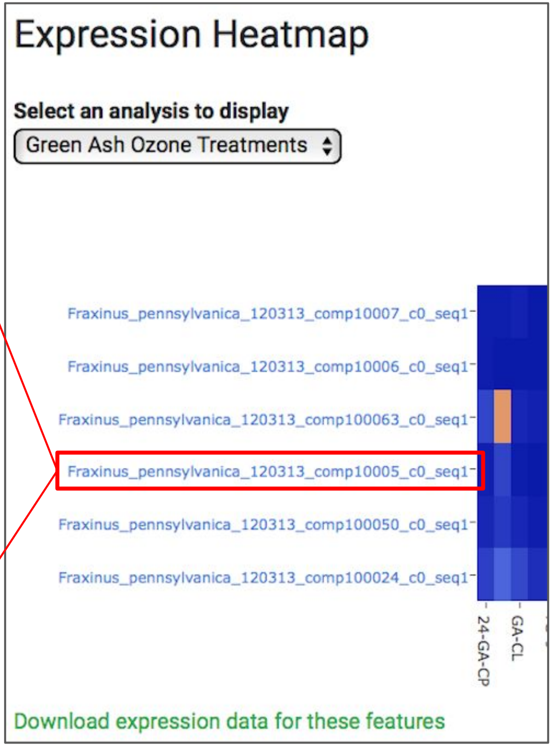
Hover the mouse over a column in the graph to view more information about that biosample. You can click and drag to rearrange groups along the x-axis. You can also click and drag to move the legend.

Only Non-Zero Values | Reset

**Expression by age**

geog
5
0
2-3 year old graft
2 years old
seedling

Download expression dataset for this feature



## Expression Heatmap

**Select an analysis to display**

Green Ash Ozone Treatments

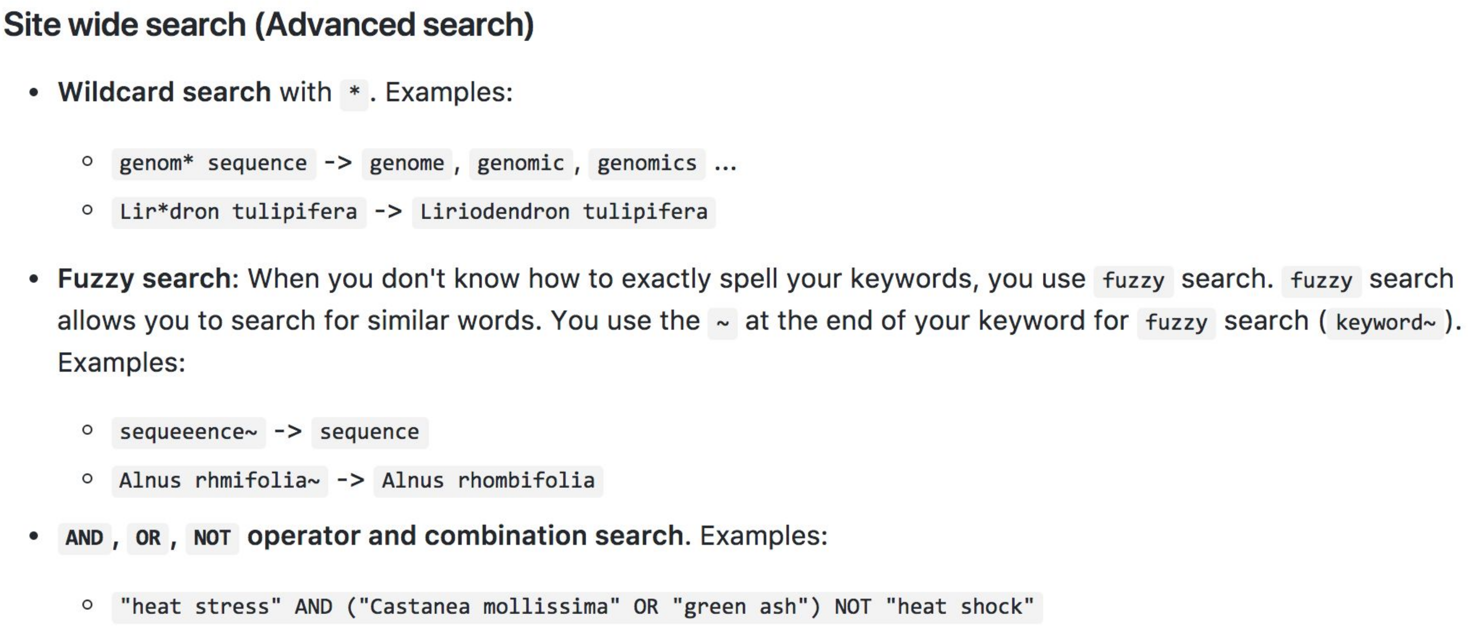
Fraxinus_pennsylvanica_120313_comp10007_c0_seq1
Fraxinus_pennsylvanica_120313_comp10006_c0_seq1
Fraxinus_pennsylvanica_120313_comp100063_c0_seq1
Fraxinus_pennsylvanica_120313_comp10005_c0_seq1
Fraxinus_pennsylvanica_120313_comp100050_c0_seq1
Fraxinus_pennsylvanica_120313_comp100024_c0_seq1
24-GA-CP
GA-CL

Download expression data for these features

# Tripal Elasticsearch: quick and easy access to data

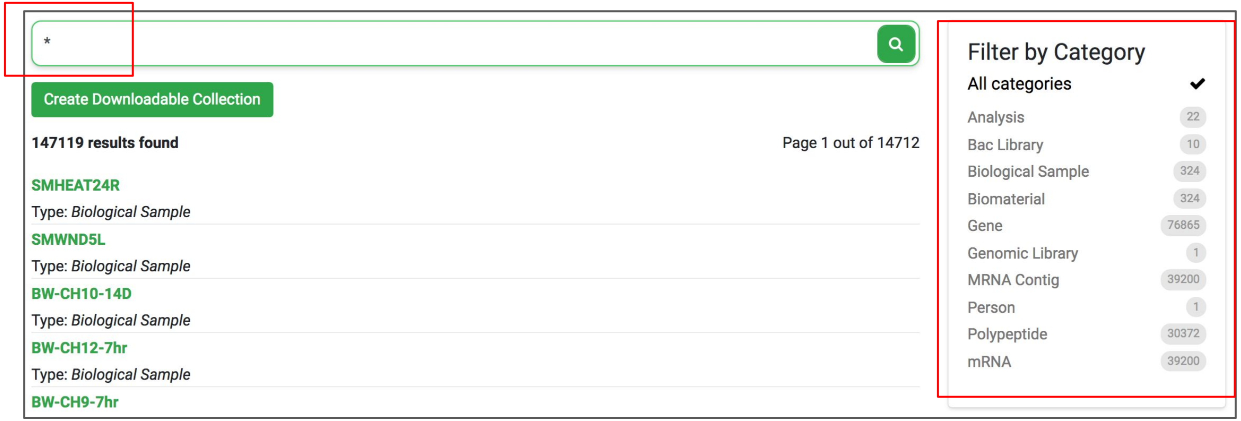
Site Wide Search
elastic

# Tripal Elasticsearch: quick and easy access to data



## Site wide search (Advanced search)

- **Wildcard search** with `*`. Examples:
    - `genom* sequence` -> `genome`, `genomic`, `genomics` ...
    - `Lir*dron tulipifera` -> `Liriodendron tulipifera`
- **Fuzzy search**: When you don't know how to exactly spell your keywords, you use `fuzzy` search. `fuzzy` search allows you to search for similar words. You use the `~` at the end of your keyword for `fuzzy` search (`keyword~`). Examples:
    - `sequeeence~` -> `sequence`
    - `Alnus rhmifolia~` -> `Alnus rhombifolia`
- `AND`, `OR`, `NOT` **operator and combination search**. Examples:
    - `"heat stress" AND ("Castanea mollissima" OR "green ash") NOT "heat shock"`



*

**147119 results found**

Page 1 out of 14712

**SMHEAT24R**
Type: *Biological Sample*

**SMWND5L**
Type: *Biological Sample*

**BW-CH10-14D**
Type: *Biological Sample*

**BW-CH12-7hr**
Type: *Biological Sample*

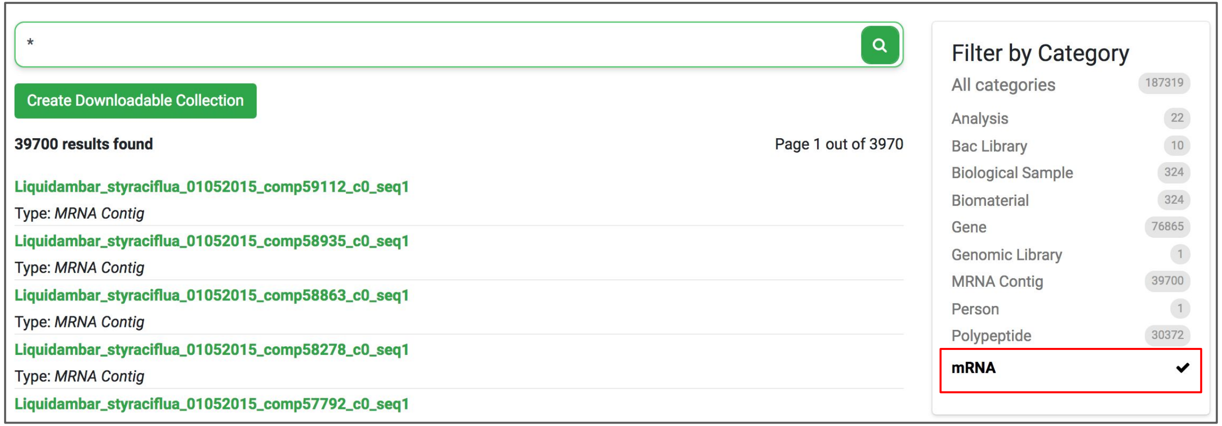
**BW-CH9-7hr**

Filter by Category

| | |
|---|---|
| All categories | ✓ |
| Analysis | 22 |
| Bac Library | 10 |
| Biological Sample | 324 |
| Biomaterial | 324 |
| Gene | 76865 |
| Genomic Library | 1 |
| MRNA Contig | 39200 |
| Person | 1 |
| Polypeptide | 30372 |
| mRNA | 39200 |

First time using HWG, don't know what's available.

Use a simple wildcard to display all.



*

**39700 results found**

Page 1 out of 3970

**Liquidambar_styraciflua_01052015_comp59112_c0_seq1**
Type: *MRNA Contig*

**Liquidambar_styraciflua_01052015_comp58935_c0_seq1**
Type: *MRNA Contig*

**Liquidambar_styraciflua_01052015_comp58863_c0_seq1**
Type: *MRNA Contig*

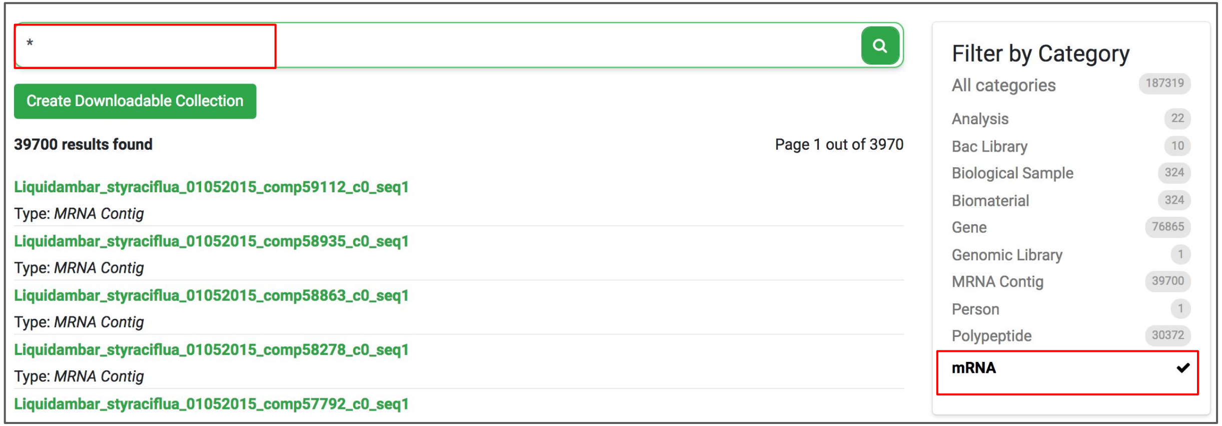
**Liquidambar_styraciflua_01052015_comp58278_c0_seq1**
Type: *MRNA Contig*

**Liquidambar_styraciflua_01052015_comp57792_c0_seq1**

Filter by Category

| | |
|---|---|
| All categories | 187319 |
| Analysis | 22 |
| Bac Library | 10 |
| Biological Sample | 324 |
| Biomaterial | 324 |
| Gene | 76865 |
| Genomic Library | 1 |
| MRNA Contig | 39700 |
| Person | 1 |
| Polypeptide | 30372 |
| **mRNA** | ✓ |

Filter by category



*

Create Downloadable Collection

**39700 results found**

Page 1 out of 3970

**Liquidambar_styraciflua_01052015_comp59112_c0_seq1**

Type: *MRNA Contig*

**Liquidambar_styraciflua_01052015_comp58935_c0_seq1**

Type: *MRNA Contig*

**Liquidambar_styraciflua_01052015_comp58863_c0_seq1**

Type: *MRNA Contig*

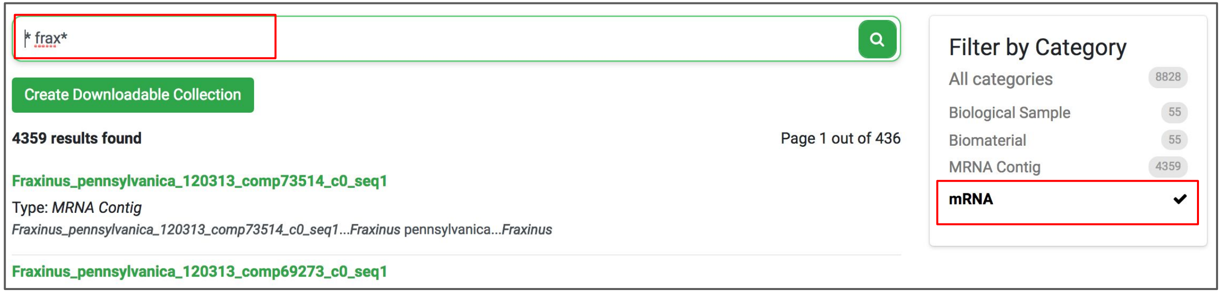
**Liquidambar_styraciflua_01052015_comp58278_c0_seq1**

Type: *MRNA Contig*

**Liquidambar_styraciflua_01052015_comp57792_c0_seq1**

Filter by Category

| | |
|---|---|
| All categories | 187319 |
| Analysis | 22 |
| Bac Library | 10 |
| Biological Sample | 324 |
| Biomaterial | 324 |
| Gene | 76865 |
| Genomic Library | 1 |
| MRNA Contig | 39700 |
| Person | 1 |
| Polypeptide | 30372 |
| **mRNA** | ✓ |



* frax*

Create Downloadable Collection

**4359 results found**

Page 1 out of 436

**Fraxinus_pennsylvanica_120313_comp73514_c0_seq1**

Type: *MRNA Contig*

*Fraxinus_pennsylvanica_120313_comp73514_c0_seq1*...*Fraxinus* pennsylvanica...*Fraxinus*

**Fraxinus_pennsylvanica_120313_comp69273_c0_seq1**

Filter by Category

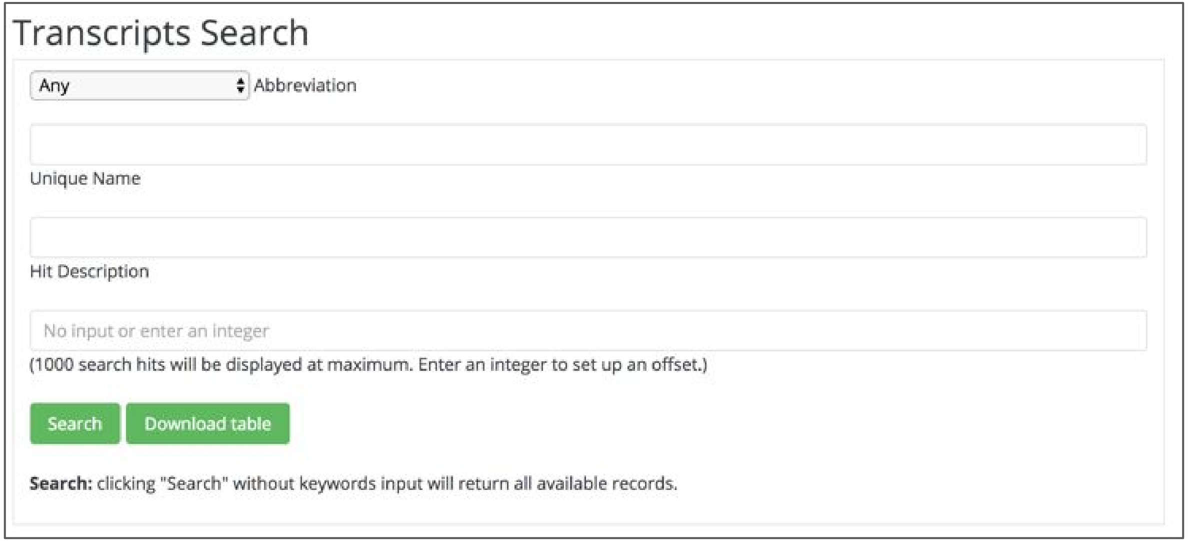
| | |
|---|---|
| All categories | 8828 |
| Biological Sample | 55 |
| Biomaterial | 55 |
| MRNA Contig | 4359 |
| **mRNA** | ✓ |

Only interested in green ash! But don't know how to spell its scientific name.

Wildcard again! Easy!

# Gene search

Old gene search interface



## Transcripts Search

Any
Abbreviation

Unique Name

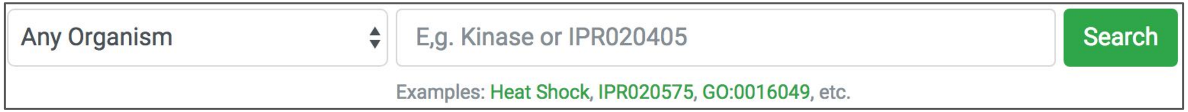
Hit Description

No input or enter an integer

(1000 search hits will be displayed at maximum. Enter an integer to set up an offset.)

Search
Download table

**Search:** clicking "Search" without keywords input will return all available records.

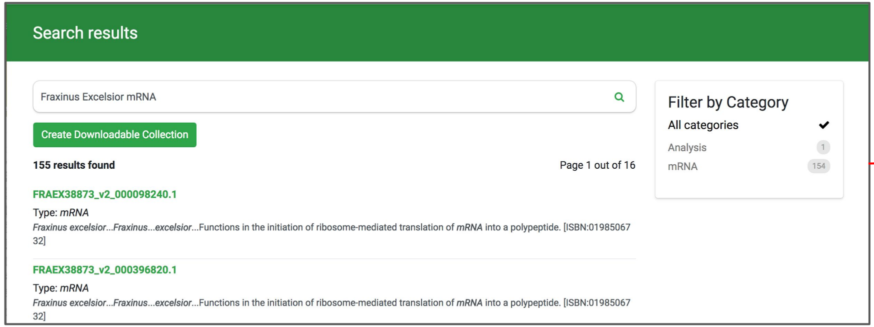


Any Organism
E,g. Kinase or IPR020405
Search

Examples: Heat Shock, IPR020575, GO:0016049, etc.

New: simplified search interface, improved “download” functionality

# Download data with data collections



**Search results**

Fraxinus Excelsior mRNA

Create Downloadable Collection

**155 results found**

Page 1 out of 16

**FRAEX38873_v2_000098240.1**

Type: *mRNA*

*Fraxinus excelsior*...*Fraxinus*...*excelsior*...Functions in the initiation of ribosome-mediated translation of *mRNA* into a polypeptide. [ISBN:0198506732]

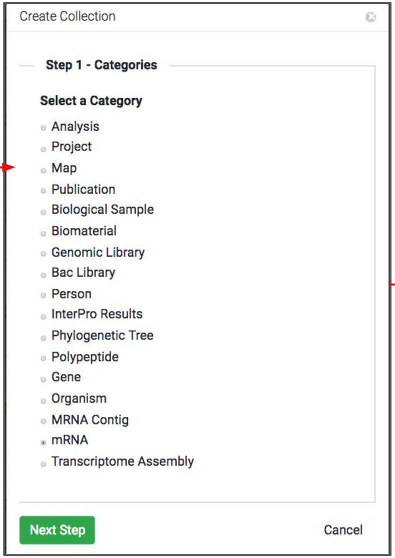
**FRAEX38873_v2_000396820.1**

Type: *mRNA*

*Fraxinus excelsior*...*Fraxinus*...*excelsior*...Functions in the initiation of ribosome-mediated translation of *mRNA* into a polypeptide. [ISBN:0198506732]

Filter by Category

| | |
|---|---|
| All categories | ✓ |
| Analysis | 1 |
| mRNA | 154 |



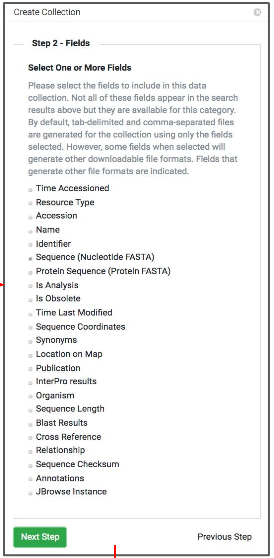
Create Collection

**Step 1 - Categories**

**Select a Category**

- ○ Analysis
- ○ Project
- ○ Map
- ○ Publication
- ○ Biological Sample
- ○ Biomaterial
- ○ Genomic Library
- ○ Bac Library
- ○ Person
- ○ InterPro Results
- ○ Phylogenetic Tree
- ○ Polypeptide
- ○ Gene
- ○ Organism
- ○ MRNA Contig
- ● mRNA
- ○ Transcriptome Assembly

Next Step     Cancel



Create Collection

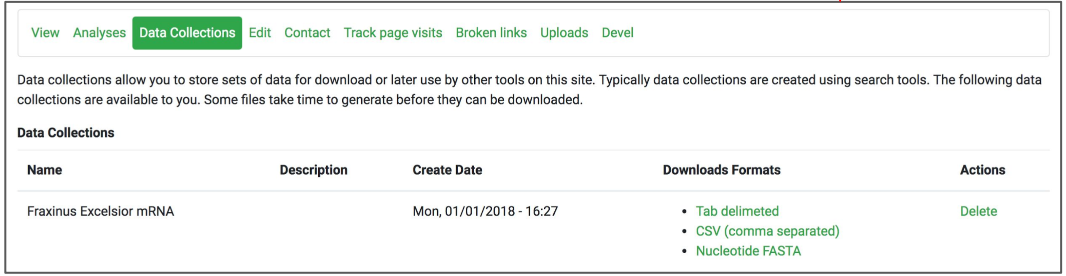
**Step 2 - Fields**

**Select One or More Fields**

Please select the fields to include in this data collection. Not all of these fields appear in the search results above but they are available for this category. By default, tab-delimited and comma-separated files are generated for the collection using only the fields selected. However, some fields when selected will generate other downloadable file formats. Fields that generate other file formats are indicated.

- ☐ Time Accessioned
- ☐ Resource Type
- ☐ Accession
- ☐ Name
- ☐ Identifier
- ☑ Sequence (Nucleotide FASTA)
- ☐ Protein Sequence (Protein FASTA)
- ☐ Is Analysis
- ☐ Is Obsolete
- ☐ Time Last Modified
- ☐ Sequence Coordinates
- ☐ Synonyms
- ☐ Location on Map
- ☐ Publication
- ☐ InterPro results
- ☐ Organism
- ☐ Sequence Length
- ☐ Blast Results
- ☐ Cross Reference
- ☐ Relationship
- ☐ Sequence Checksum
- ☐ Annotations
- ☐ JBrowse Instance

Next Step     Previous Step



View | Analyses | Data Collections | Edit | Contact | Track page visits | Broken links | Uploads | Devel

Data collections allow you to store sets of data for download or later use by other tools on this site. Typically data collections are created using search tools. The following data collections are available to you. Some files take time to generate before they can be downloaded.

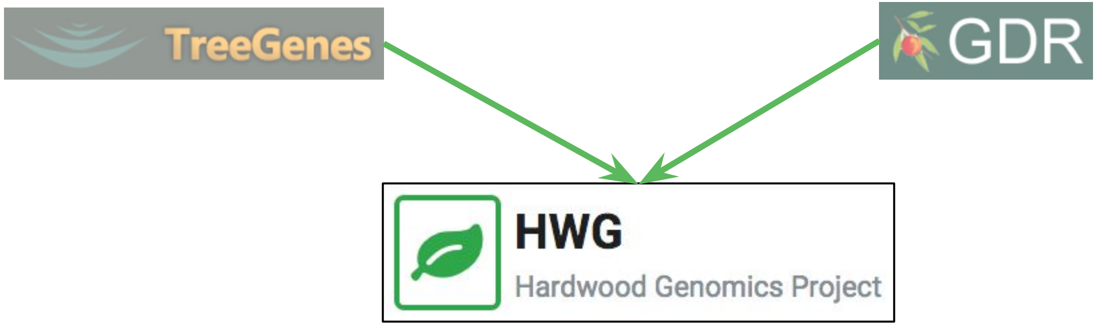
**Data Collections**

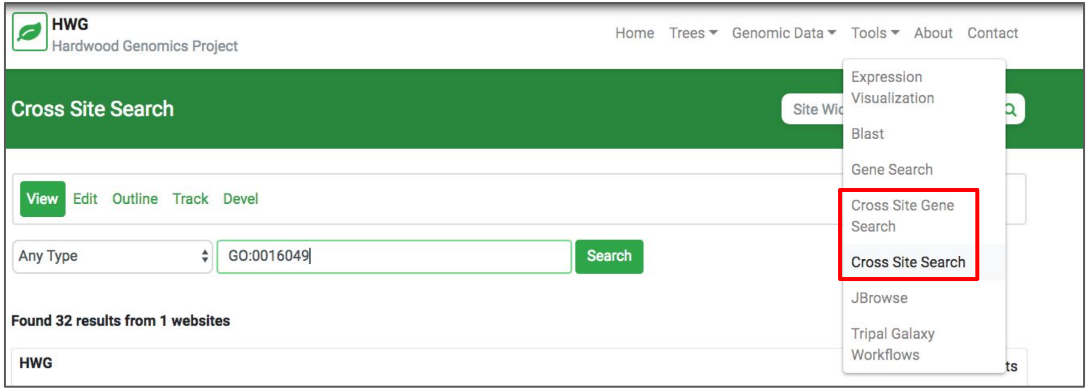
| Name | Description | Create Date | Downloads Formats | Actions |
|---|---|---|---|---|
| Fraxinus Excelsior mRNA | | Mon, 01/01/2018 - 16:27 | • Tab delimeted<br>• CSV (comma separated)<br>• Nucleotide FASTA | Delete |

**HWG**
Hardwood Genomics Project

https://beta.hardwoodgenomics.org/

# Cross site search

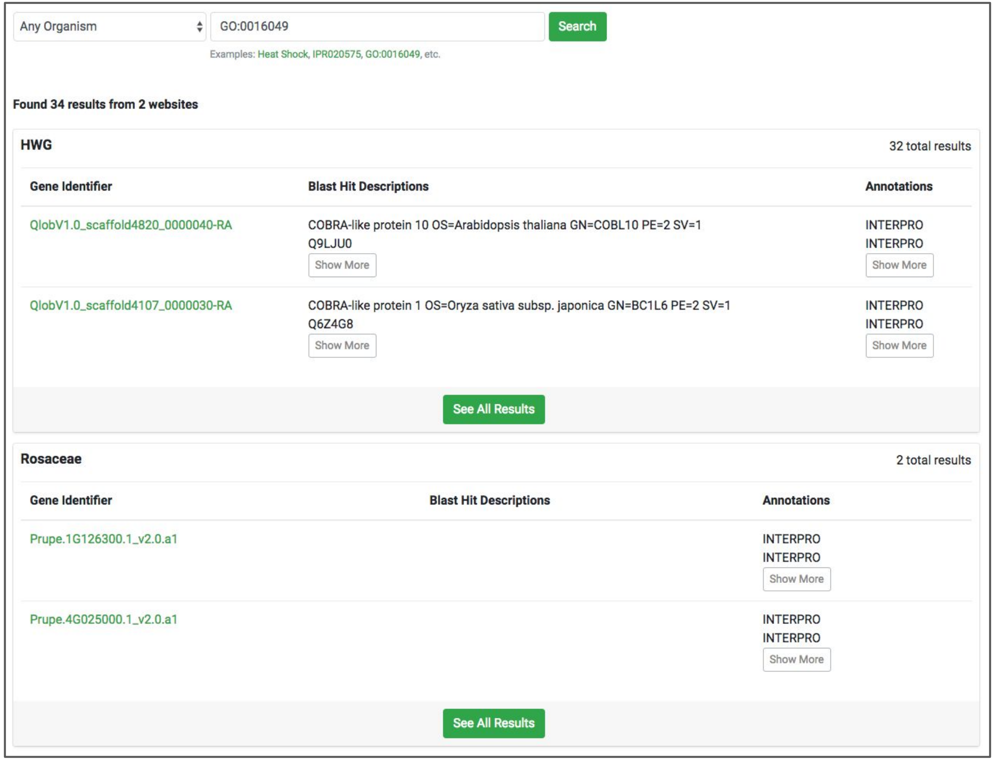

TreeGenes
GDR
HWG
Hardwood Genomics Project


HWG
Hardwood Genomics Project
Home
Trees
Genomic Data
Tools
About
Contact
Cross Site Search
Site Wic
Expression Visualization
Blast
Gene Search
Cross Site Gene Search
Cross Site Search
JBrowse
Tripal Galaxy Workflows
View
Edit
Outline
Track
Devel
Search
HWG
ts

Any Type: GO:0016049

**Found 32 results from 1 websites**

# Cross site search



Examples: Heat Shock, IPR020575, GO:0016049, etc.

**Found 34 results from 2 websites**

**HWG**

32 total results

| Gene Identifier | Blast Hit Descriptions | Annotations |
|---|---|---|
| QlobV1.0_scaffold4820_0000040-RA | COBRA-like protein 10 OS=Arabidopsis thaliana GN=COBL10 PE=2 SV=1<br>Q9LJU0<br>Show More | INTERPRO<br>INTERPRO<br>Show More |
| QlobV1.0_scaffold4107_0000030-RA | COBRA-like protein 1 OS=Oryza sativa subsp. japonica GN=BC1L6 PE=2 SV=1<br>Q6Z4G8<br>Show More | INTERPRO<br>INTERPRO<br>Show More |

**Rosaceae**

2 total results

| Gene Identifier | Blast Hit Descriptions | Annotations |
|---|---|---|
| Prupe.1G126300.1_v2.0.a1 | | INTERPRO<br>INTERPRO<br>Show More |
| Prupe.4G025000.1_v2.0.a1 | | INTERPRO<br>INTERPRO<br>Show More |

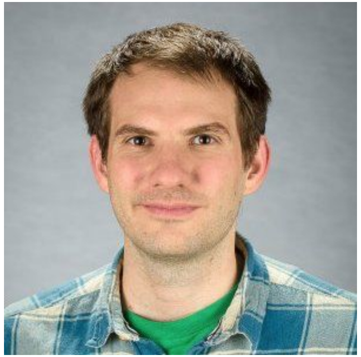
Want to know more about Tripal Elasticsearch?

# Tripal Elasticsearch: Bringing Simple and Powerful Sitewide Search to Tripal Websites

Abdullah Almsaeed

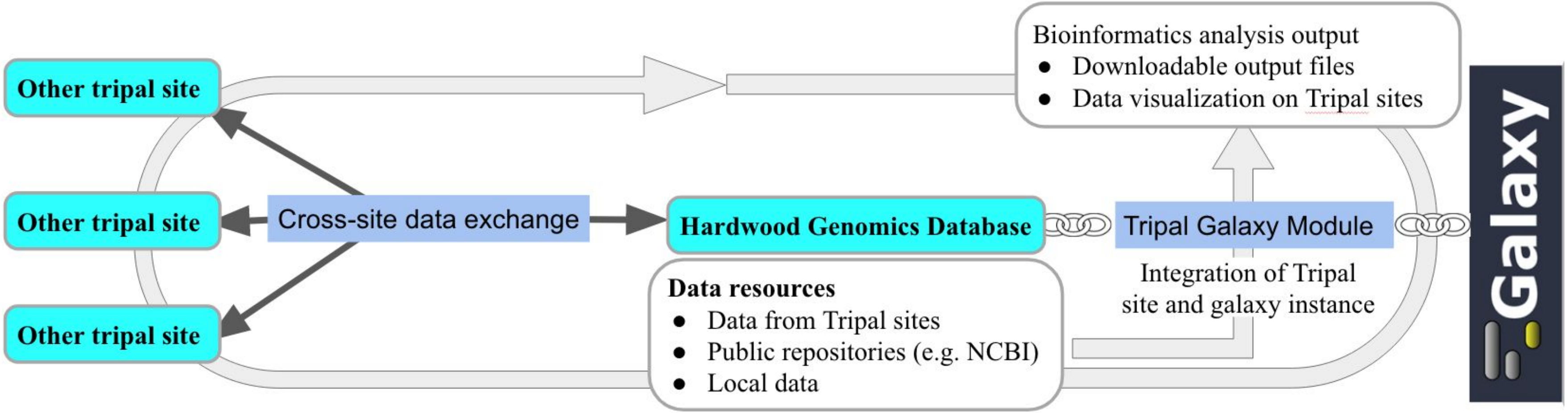
## Abdullah Almsaeed

Sunday, January 14, 2018 05:12 PM - 05:30 PM
California room



Bradford Condon

# Tripal gateway: bridge from Tripal to Galaxy



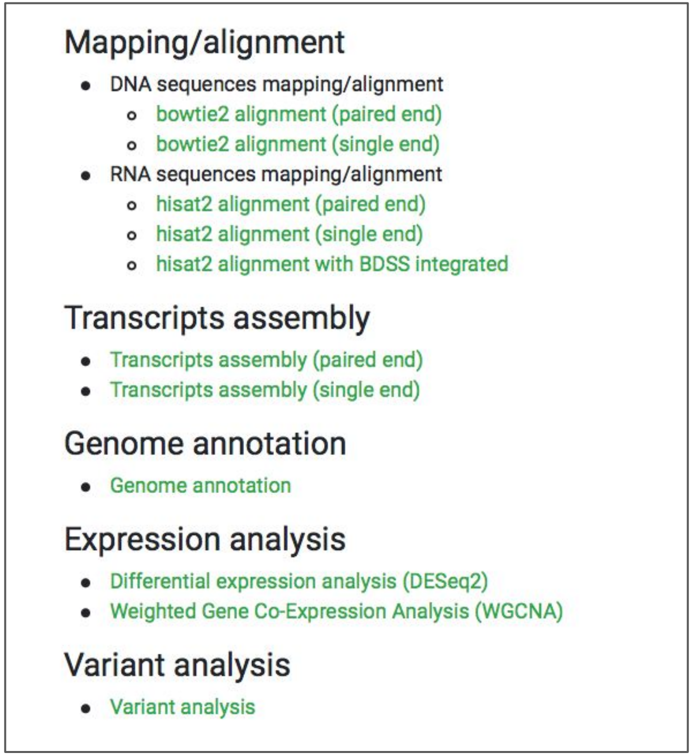
Other tripal site
Other tripal site
Other tripal site
Cross-site data exchange
Hardwood Genomics Database
Tripal Galaxy Module
Galaxy

Bioinformatics analysis output
- Downloadable output files
- Data visualization on Tripal sites

**Data resources**
- Data from Tripal sites
- Public repositories (e.g. NCBI)
- Local data

Integration of Tripal site and galaxy instance

# Tripal gateway: bridge from Tripal to Galaxy



## Mapping/alignment

- DNA sequences mapping/alignment
  - bowtie2 alignment (paired end)
  - bowtie2 alignment (single end)
- RNA sequences mapping/alignment
  - hisat2 alignment (paired end)
  - hisat2 alignment (single end)
  - hisat2 alignment with BDSS integrated

## Transcripts assembly

- Transcripts assembly (paired end)
- Transcripts assembly (single end)

## Genome annotation

- Genome annotation

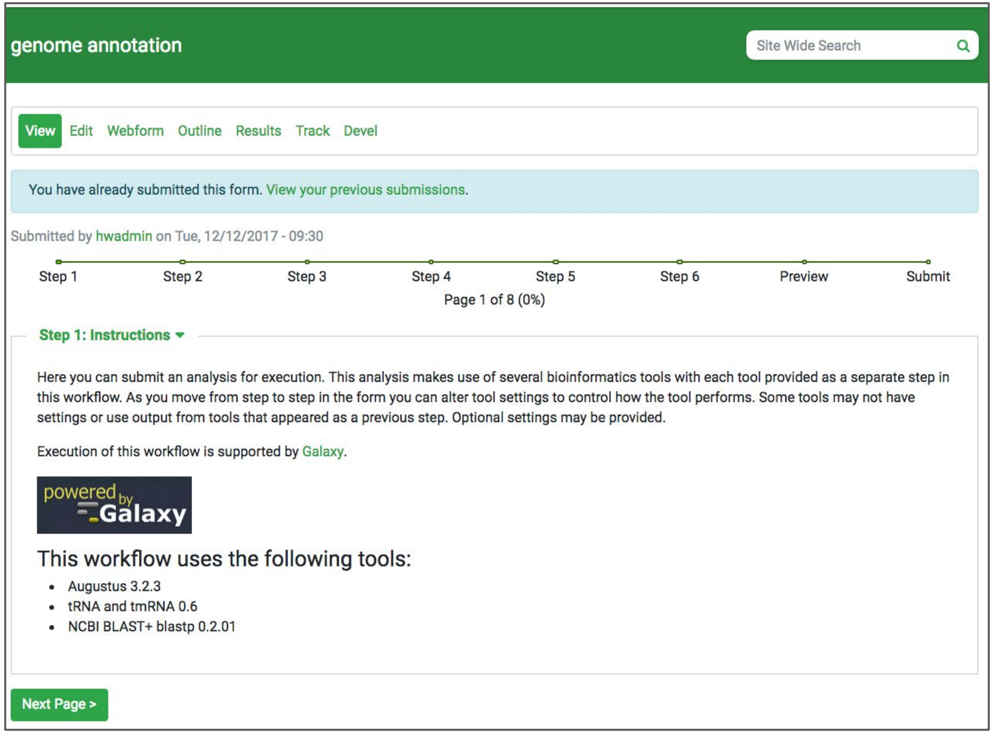
## Expression analysis

- Differential expression analysis (DESeq2)
- Weighted Gene Co-Expression Analysis (WGCNA)

## Variant analysis

- Variant analysis

# Running a Galaxy workflow


genome annotation
Site Wide Search
View
Edit
Webform
Outline
Results
Track
Devel

You have already submitted this form. View your previous submissions.

Submitted by hwadmin on Tue, 12/12/2017 - 09:30

Step 1
Step 2
Step 3
Step 4
Step 5
Step 6
Preview
Submit

Page 1 of 8 (0%)

**Step 1: Instructions**

Here you can submit an analysis for execution. This analysis makes use of several bioinformatics tools with each tool provided as a separate step in this workflow. As you move from step to step in the form you can alter tool settings to control how the tool performs. Some tools may not have settings or use output from tools that appeared as a previous step. Optional settings may be provided.

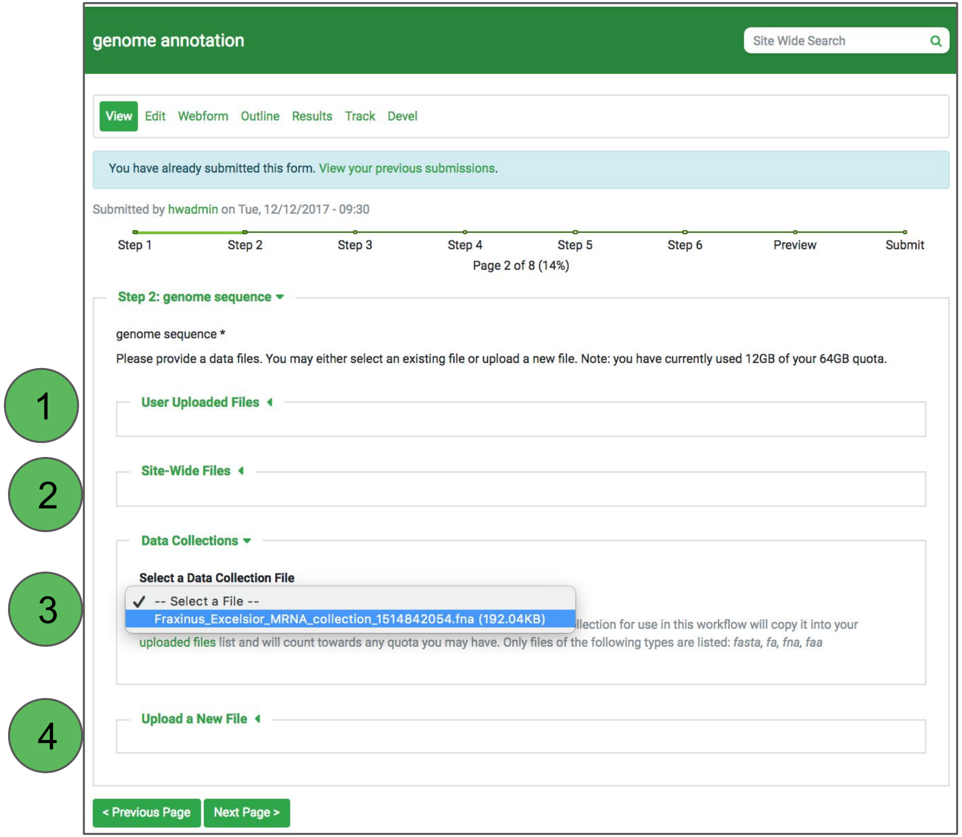
Execution of this workflow is supported by Galaxy.

powered by Galaxy

This workflow uses the following tools:

- Augustus 3.2.3
- tRNA and tmRNA 0.6
- NCBI BLAST+ blastp 0.2.01

# Running a Galaxy workflow


genome annotation
Site Wide Search
View
Edit
Webform
Outline
Results
Track
Devel
Step 1
Step 2
Step 3
Step 4
Step 5
Step 6
Preview
Submit
1
2
3
4
User Uploaded Files
Site-Wide Files
Data Collections
Upload a New File
< Previous Page
Next Page >

You have already submitted this form. View your previous submissions.

Submitted by hwadmin on Tue, 12/12/2017 - 09:30

Page 2 of 8 (14%)

**Step 2: genome sequence**

genome sequence *

Please provide a data files. You may either select an existing file or upload a new file. Note: you have currently used 12GB of your 64GB quota.

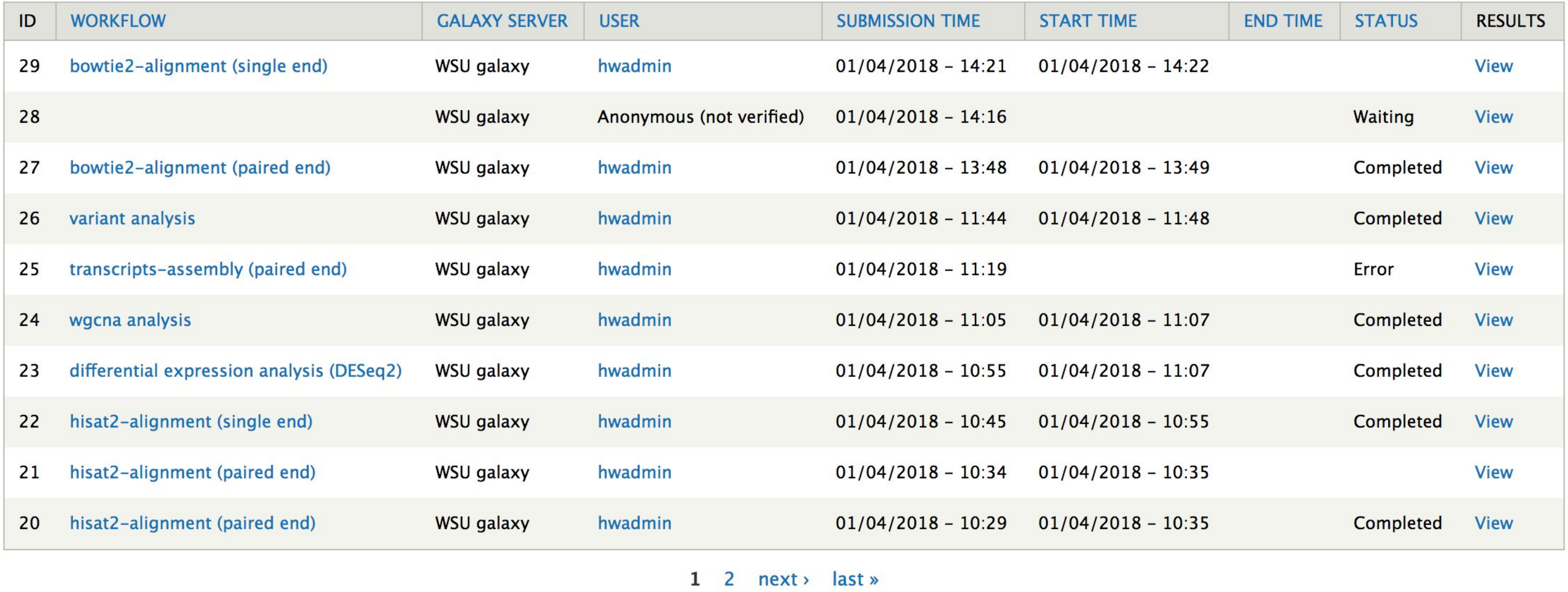
**Select a Data Collection File**

✓ -- Select a File --

Fraxinus_Excelsior_MRNA_collection_1514842054.fna (192.04KB)

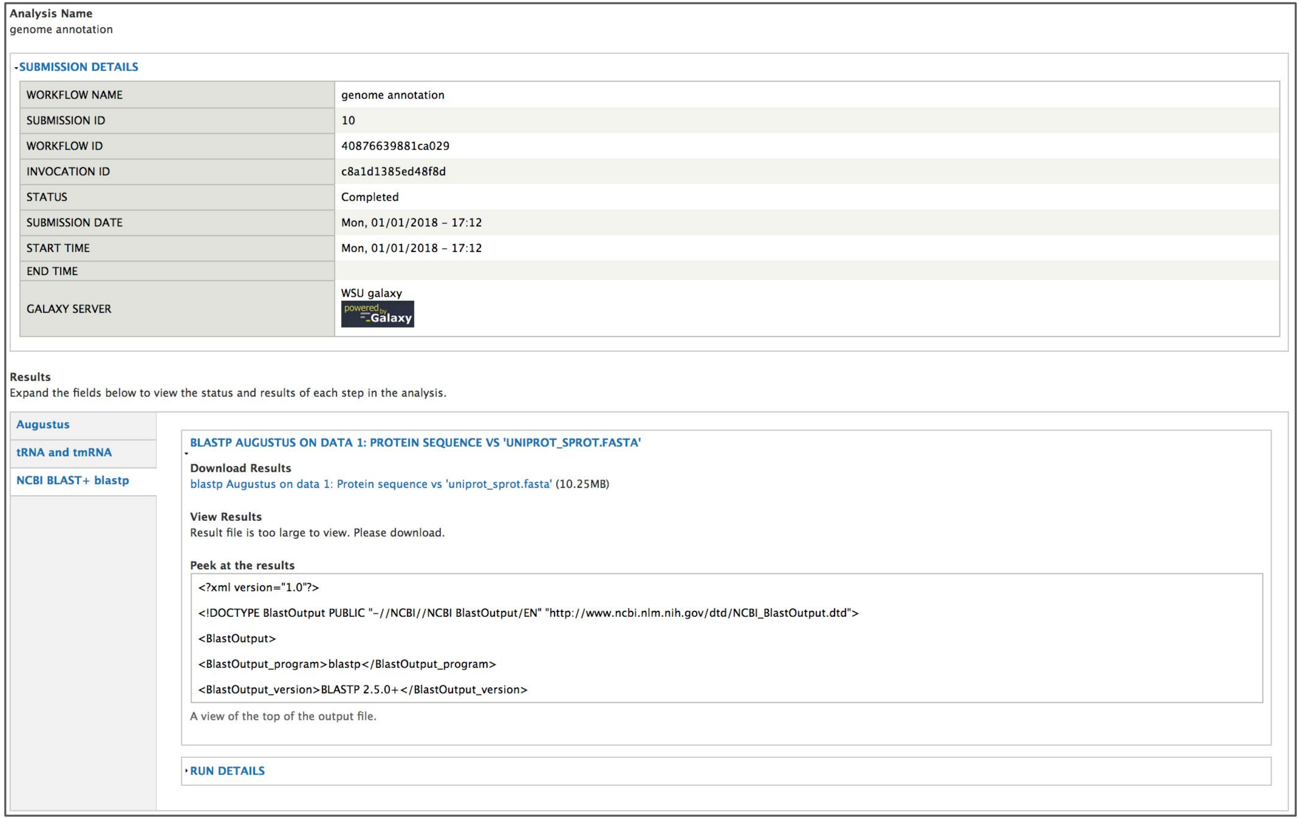
…llection for use in this workflow will copy it into your uploaded files list and will count towards any quota you may have. Only files of the following types are listed: *fasta, fa, fna, faa*

# Workflow status



| ID | WORKFLOW | GALAXY SERVER | USER | SUBMISSION TIME | START TIME | END TIME | STATUS | RESULTS |
|---|---|---|---|---|---|---|---|---|
| 29 | bowtie2-alignment (single end) | WSU galaxy | hwadmin | 01/04/2018 - 14:21 | 01/04/2018 - 14:22 | | | View |
| 28 | | WSU galaxy | Anonymous (not verified) | 01/04/2018 - 14:16 | | | Waiting | View |
| 27 | bowtie2-alignment (paired end) | WSU galaxy | hwadmin | 01/04/2018 - 13:48 | 01/04/2018 - 13:49 | | Completed | View |
| 26 | variant analysis | WSU galaxy | hwadmin | 01/04/2018 - 11:44 | 01/04/2018 - 11:48 | | Completed | View |
| 25 | transcripts-assembly (paired end) | WSU galaxy | hwadmin | 01/04/2018 - 11:19 | | | Error | View |
| 24 | wgcna analysis | WSU galaxy | hwadmin | 01/04/2018 - 11:05 | 01/04/2018 - 11:07 | | Completed | View |
| 23 | differential expression analysis (DESeq2) | WSU galaxy | hwadmin | 01/04/2018 - 10:55 | 01/04/2018 - 11:07 | | Completed | View |
| 22 | hisat2-alignment (single end) | WSU galaxy | hwadmin | 01/04/2018 - 10:45 | 01/04/2018 - 10:55 | | Completed | View |
| 21 | hisat2-alignment (paired end) | WSU galaxy | hwadmin | 01/04/2018 - 10:34 | 01/04/2018 - 10:35 | | | View |
| 20 | hisat2-alignment (paired end) | WSU galaxy | hwadmin | 01/04/2018 - 10:29 | 01/04/2018 - 10:35 | | Completed | View |

# Results



**Analysis Name**
genome annotation

- **SUBMISSION DETAILS**

| | |
|---|---|
| WORKFLOW NAME | genome annotation |
| SUBMISSION ID | 10 |
| WORKFLOW ID | 40876639881ca029 |
| INVOCATION ID | c8a1d1385ed48f8d |
| STATUS | Completed |
| SUBMISSION DATE | Mon, 01/01/2018 – 17:12 |
| START TIME | Mon, 01/01/2018 – 17:12 |
| END TIME | |
| GALAXY SERVER | WSU galaxy<br>powered by Galaxy |

**Results**
Expand the fields below to view the status and results of each step in the analysis.

**BLASTP AUGUSTUS ON DATA 1: PROTEIN SEQUENCE VS 'UNIPROT_SPROT.FASTA'**

**Download Results**
blastp Augustus on data 1: Protein sequence vs 'uniprot_sprot.fasta' (10.25MB)

**View Results**
Result file is too large to view. Please download.

**Peek at the results**

```
<?xml version="1.0"?>

<!DOCTYPE BlastOutput PUBLIC "-//NCBI//NCBI BlastOutput/EN" "http://www.ncbi.nlm.nih.gov/dtd/NCBI_BlastOutput.dtd">

<BlastOutput>

<BlastOutput_program>blastp</BlastOutput_program>

<BlastOutput_version>BLASTP 2.5.0+</BlastOutput_version>
```

A view of the top of the output file.

Want to know more about Tripal Galaxy?

# Building a Bridge from the Tripal Community Database to Galaxy

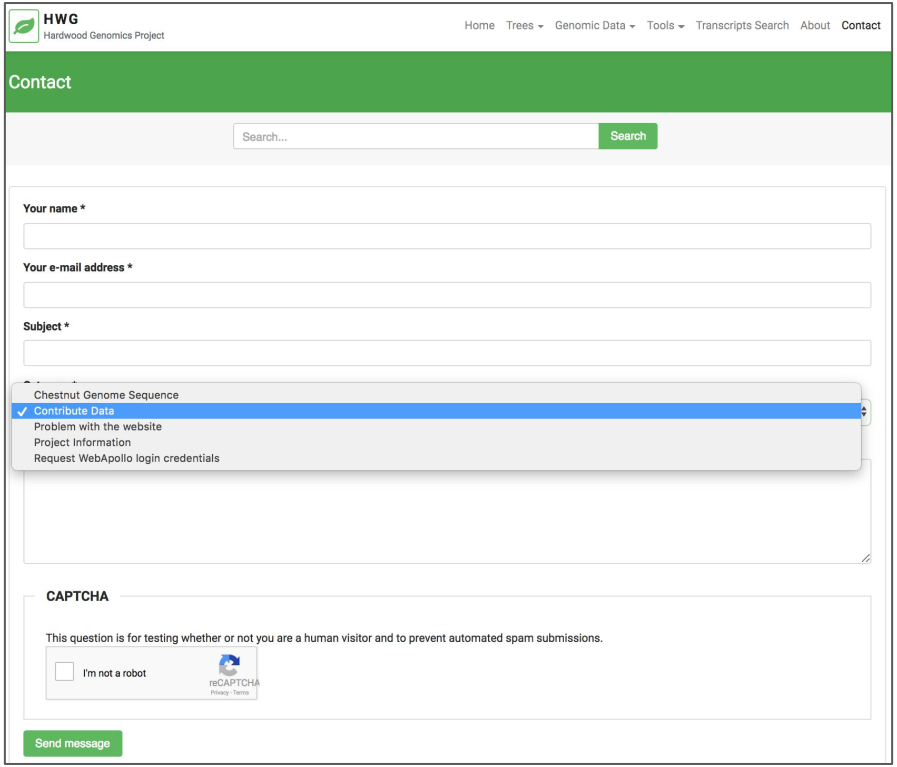
## Margaret Staton

Tuesday, January 16, 2018 05:50 PM - 06:10 PM
California room

# Summary

- New data
  - Genetic markers and maps
  - phenotype data
- Improved user experience
  - Gene search
  - Site wide search
  - Data collection to download search results
  - Cross-site search
  - Gene expression visualization
- Tripal Gateway
  - Collect data from HWG
  - Run Galaxy workflows from HWG

# Interested in adding your data to HWG? Contact us!


HWG
Hardwood Genomics Project
Home
Trees
Genomic Data
Tools
Transcripts Search
About
Contact
Search...
Search
I'm not a robot
reCAPTCHA
Privacy - Terms
Send message

## Contact

Your name *

Your e-mail address *

Subject *

- Chestnut Genome Sequence
- ✓ Contribute Data
- Problem with the website
- Project Information
- Request WebApollo login credentials

**CAPTCHA**

This question is for testing whether or not you are a human visitor and to prevent automated spam submissions.

☐ I'm not a robot

**HWG**
Hardwood Genomics Project

https://beta.hardwoodgenomics.org/

# Acknowledgements

Meg Staton, PI
- Abdullah Almsaeed
- Bradford Condon
- Ming Chen

Stephen Ficklin, PI
- Connor Wytko
- Brian Soto

Dorrie Main, PI
- Chunhuai Cheng
- Heidi hough

Lacey-Anne Sanderson

Jill Wegrzyn, PI
- Nic Herndon
- Sean Buehler

Tripal Community

**Penn State University**
**John Carlson**, PI
Teodora Best, Research Associate
Nicole Zembower, Technician
Di Wu, PhD Student
**Nick Wheeler, Manager**

**University of Notre Dame**
**Jeanne Romero-Severson**, Co-PI
Dan Borkowski, PhD Student
Arpita Konar, PhD Student
Andrea Noakes, PhD Student
Lauren Fiedler, Technician
Olivia Choudhary

**Michigan Tech University**
**Oliver Gailing**, Co-PI
Sandra Owusu, PhD Student
Sudhir Khodwekar, PhD Student

**University Tennessee**
**Scott Schlarbaum**, Co-PI
Ami Sharp, Research Associate
Jason Hogan, Research Associate
James Simons, Research Associate

**Margaret Staton**, Bioinformatics,
Jack Davitt, Research Associate
Nathan Henry, Research Associate
Thomas Lane, Research Associate

**University of Missouri**
**Mark Coggeshall**, Co-PI
Christopher Heim, MS student

**Clemson University**
**Haiying Liang**, Co-PI
**Chris Saski**, Director of CUGI
Tatyana Zhebentyayev, Research Associate

**Ketia Shumaker**, Co-PI