

# CITRUS GENOME DATABASE



Resources for citrus genomics, genetics, breeding and disease research

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## What is CGD?

CGD is a centralized database containing genomics, genetics, and breeding data and analysis tools for citrus research. Genome sequences are available to view and search and there is also information about genetic maps, molecular markers, and QTL. If you are a breeder who needs to manage private breeding program data, access to the Breeding Information Management System (BIMS) can be requested. Visit us at [www.citrusgenomedb.org](http://www.citrusgenomedb.org) to see everything that is available. Each issue of the newsletter will focus on a different type of data and what features are available.

## New Ortholog/Paralog Search

While ortholog and paralog data are stored in our database as part of the [MCScanX](#) synteny analysis are viewable in the [Synteny Viewer](#) tool, there was not a way to search that data directly. To remedy this, we have designed the new [Ortholog/Paralog Search](#) feature. See the diagram below for details on how to use it.

Remember that clicking on mRNA names opens the details page for that mRNA where you can see all the functional annotation details. Can't find your genome on the list in the new search? Only genomes that are within the Synteny Viewer are currently available. The missing genomes will be added soon. Please [contact us](#) with feedback.

## Ortholog/Paralog Search

Retrieve orthologs/paralogs that are detected using MCScanX (Wang et al. 2012) using default settings between different assemblies/annotations of the same species represents potentially the same gene used in the analysis and genes were used only when mRNAs are not available. The result table

**Genome**

**Chromosome/Scaffold**

**Gene/Transcript Name**   No file chosen

**Compare to**

**Chromosome/Scaffold**

Select the first genome and refine with a chromosome or gene/mRNA name

Refine more by selecting the second genome and chromosome

See the Page 2 for the results!

# Ortholog/Paralog Search Results

Link to download results as file

Genome 1 information

Genome 2 information

1612 records were returned

Download Table

#	Genome1	Chromosome/Scaffold1	Ortholog/Paralog1	Genome2	Chromosome/Scaffold2	Ortholog/Paralog2	Associated Gene
1	Citrus sinensis genome v2.0 (HZAU)	chr1	Cs1g01010.1	Poncirus trifoliata genome v1.3.1 (JGI)	scaffold_7	Ptrif.0007s2566.1.v1.3.1	Ptrif.0007s2566.v1.3.1
2	Citrus sinensis genome v2.0 (HZAU)	chr1	Cs1g01020.1	Poncirus trifoliata genome v1.3.1 (JGI)	scaffold_7	Ptrif.0007s2565.2.v1.3.1	Ptrif.0007s2565.v1.3.1
3	Citrus sinensis genome v2.0 (HZAU)	chr1	Cs1g01040.1	Poncirus trifoliata genome v1.3.1 (JGI)	scaffold_7	Ptrif.0007s2887.1.v1.3.1	Ptrif.0007s2887.v1.3.1
4	Citrus sinensis genome v2.0 (HZAU)	chr1	Cs1g01060.1	Poncirus trifoliata genome v1.3.1 (JGI)	scaffold_7	Ptrif.0007s2562.1.v1.3.1	Ptrif.0007s2562.v1.3.1
5	Citrus sinensis genome v2.0 (HZAU)	chr1	Cs1g01070.1	Poncirus trifoliata genome v1.3.1 (JGI)	scaffold_7	Ptrif.0007s2561.1.v1.3.1	Ptrif.0007s2561.v1.3.1
6	Citrus sinensis genome v2.0 (HZAU)	chr1	Cs1g01090.1	Poncirus trifoliata genome v1.3.1 (JGI)	scaffold_7	Ptrif.0007s2560.2.v1.3.1	Ptrif.0007s2560.v1.3.1
7	Citrus sinensis genome v2.0 (HZAU)	chr1	Cs1g01150.1	Poncirus trifoliata genome v1.3.1 (JGI)	scaffold_7	Ptrif.0007s2881.1.v1.3.1	Ptrif.0007s2881.v1.3.1
8	Citrus sinensis genome v2.0 (HZAU)	chr1	Cs1g01190.1	Poncirus trifoliata genome v1.3.1 (JGI)	scaffold_5	Ptrif.0005s1972.1.v1.3.1	Ptrif.0005s1972.v1.3.1

Hyperlink to mRNA details

Hyperlinks to mRNA and gene details

Hyperlinks to genome information

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