

# Marker Search and Results

The TAIR Marker Search window provides three ways of searching for a marker: simple search by name only, feature search using more limits, and search by position. These are offered in three distinct sections of the window. To search for polymorphisms such as SNPS, insertions, deletions and alleles, use the [TAIR Polymorphism/Allele Search](#)

## Search by Name

At the top of the TAIR Marker Search window are the Search by Name options. You can search for markers by marker name or gene/locus name for markers that are associated with genes and loci. For information about marker, gene and locus nomenclature see [Arabidopsis Nomenclature](#)

This simple search is case insensitive and allows you to search for exact matches, names that start with, contain or end with your input string (see "[Using Wildcards](#)").

### Marker Name

*Arabidopsis* markers are usually named by the clones or genes from which the marker was derived.

**Example marker names:** mi192, PAI3

## Restrict by Features

The Restrict by Features options are below the Search by Name options on the TAIR Marker Search window.

These options let you perform more complex searches by type of genetic marker. You can select multiple types within each parameter.

### Genetic Marker

In TAIR, a genetic marker is defined as any polymorphism of a map element between two or more ecotypes or accessions of *Arabidopsis thaliana*. The types of genetic markers in TAIR include

Type	Definition	Reference
All PCR	retrieves all markers that use PCR as the method of detecting polymorphisms (e.g. CAPS, SSLP, AFLP, RAPD, PCR_based)	
CAPS	Cleaved Amplified Polymorphisms	<a href="#">8106085</a>
SSLP	Simple Sequence Length Polymorphism	<a href="#">8188214</a>
AFLP	Amplified Fragment Length Polymorphism	<a href="#">9664423</a>
Hybridization based (hyb_based)	A marker, other than RFLPs where the primary method of detection uses sequence hybridization. For example, SNPs which are detected via hybridization of genomic DNA to oligomers on a chip or by hybridization of an allele specific oligomer to amplified DNA that is bound to a membrane.	
RFLP	Restriction Fragment Length Polymorphism	<a href="#">2901107</a>
RAPD	Randomly Amplified Polymorphic DNA	<a href="#">8332466</a>

You can search one or more marker types using the check boxes. The default option, all will search all marker types.

### Polymorphic Between

The default (unselected) status is "Any", which means that ecotype information is ignored in the query.

Selecting this option lets you limit the selection of markers to those that have known polymorphisms in specific ecotypes. For example, searching for markers polymorphic between Landsberg (Ler) and any ecotype will return all markers for which a polymorphism in Ler is known. A search for polymorphisms between Landsberg erecta (Ler) and Columbia (Col) will return those markers for which polymorphisms are known for both ecotypes. The current selection of ecotypes that can be queried are

Symbol	Full Name
Ws	Wassilewskija

Nd	Niederzenz
No	Nossen
RLD	Rld
Ler	Landsberg erecta
Col	Columbia
C24	C24
Cvi	Cape Verde Islands
En	Enkheim
Be	Bensheim

A search for Col will return results for all accessions (e.g., Col-1 and Col-4 will be treated as Columbia).

### Time Restriction

You can restrict your search to only include markers that have been added or updated in the specified time period.

## Restrict by Map Location

The bottom section of the window lets you restrict your search by location. If you make a mistake and choose the wrong chromosome or map type, use the reset button to reset the parameters. Note that resetting will reset ALL of the search parameters (such as name, type and date restrictions)

The options in this section let you use three parameters to restrict your search: Chromosome, Map Type, and Range.

### Chromosome

Lets you limit your search to a single chromosome. There are five chromosomes in *Arabidopsis*: 1, 2, 3, 4, and 5.

### Map Type

Lets you search entities by their position on a particular map and can be used with or without setting Range parameters. The map choices are: AGI sequence map, Lister and Dean Recombinant Inbred (RI) genetic map and Classical genetic map. You can only choose one map type for each search- the acceptable units for selecting a Range will appear once a map has been selected. To search on multiple map types, use the [TAIR Map Viewer](#). You can also search and view markers down to the nucleotide level on the AGI sequence map using the [SeqViewer](#).

### Range

Lets you specify a range search by the upper and lower bounds (when you select "Between") or a center point (when you select "Around"). The value is interpreted based on the selected range units. You can specify the range by genetic distance (cM), physical distance (kb), and by marker or gene names. When you select "**Between**" from the drop-down menu, your search will be within the range defined by two entities or positions on a particular map. When you select "**Around**" from the drop-down menu, your search will be the area +/-10 cM and/or +/- 100 kb from the specified entity or position. When you choose search **around**, the second value input and units options are disabled.

## Output Options

*This section allows you to specify the number of records to display on each results page for your query, and how you would like your results to be grouped.*

### **number of records/page**

*You can choose to have 25,50,100 or 200 records displayed on the results page for your query.*

### **sort by**

*Allows you to order your results by marker name,type or position. For ordering by position, you do not need to specify a chromosome, but a map type must be defined. The default map for ordering by position is the AGI sequence map (when no map type is specified). If you choose a chromosome and opt to have the output displayed by position, then you must choose from one of the available map types.*

