

# Polymorphism/Allele Search and Results

## Using the Polymorphism/Allele Search

The TAIR Polymorphism/Allele Search window provides three ways of narrowing your search in three distinct sections of the window: specifying name, specifying features, and specifying map location. If you make a mistake, 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).

## Search by Name

At the top of the TAIR Polymorphism/Allele Search window are the Search by Name options.

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. You may specify the full name or symbol of the polymorphism/allele, the full name or symbol of the wild type gene, the locus name (i.e. AT2g54790), or the last name of the person or organization who submitted the polymorphism/allele. You may select two different types of criteria (i.e. name **and** submitter last name) that will be searched together. (see "[Using Wildcards](#)").

## Restrict by Features

The Restrict by Features options are below the Search by Name options on the TAIR Polymorphism/Allele Search window.

These options let you perform more complex searches. You may select multiple options within each parameter by clicking on one selection and then clicking on additional ones while holding down either the CTRL key (PCs) or the Apple key (Mac).

### Polymorphism Features

Checking the "has associated genetic markers" box allows you to select only those polymorphisms/alleles with detection methods associated to them. You may also limit your search to only those polymorphisms that are also alleles by ticking the appropriate button.

### Polymorphism Type

In TAIR, a polymorphism/allele is defined as any genetic variation between two ecotypes or within one ecotype that can be assessed experimentally by sequencing, PCR amplification, restriction digest analysis or phenotypic inspection. You can search one or more polymorphism/allele types . To select more than one type of polymorphism, hold down the CTRL key (PC) or Apple (Mac) while clicking on the selection with the mouse. The default option, any, finds all polymorphisms regardless of type.

### Insertion Type

Limit your selection by the insertion type . To select more than one type of insertion hold down the CTRL key (PC) or Apple (Mac) while clicking on the selection with the mouse. The default option any, does not restrict the search by insertion type.

### Polymorphism Site

Limit your selection by the location in the gene/genome where the polymorphism occurs. The sites are:

Polymorphism Site	Comment
Any	
exon	
intron	
splice junction	May be either 5' or 3' splice site.

### Inheritance

Limit your selection by the mode of inheritance. You can select only one mode of inheritance. The modes are:

Inheritance mode	Comment	Reference
Any	Returns all polymorphisms/alleles regardless of inheritance.	
dominant	Allele that produces the same character whether present in the homozygous or heterozygous state.	Oxford Dictionary of Biochemistry and Molecular Biology
incompletely dominant	(also semi-dominant) Allele combination that produces a separate phenotype in the heterozygous state from the dominant homozygote and the recessive homozygote phenotypes	
recessive	Allele that lacks effect when accompanied in the same diploid by a dominant form of the same gene.	Oxford Dictionary of Biochemistry and Molecular Biology

### Polymorphic Between

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

Limit your selection to those that have known polymorphisms in specific ecotypes. For example, searching between Landsberg erecta (Ler) and any ecotype will return all polymorphism/alleles for which a polymorphism in Ler is known. A search for polymorphisms between Landsberg erecta (Ler) and Columbia (Col) will return those polymorphism/alleles for which polymorphisms are known for both ecotypes. The current selection of ecotypes that can be queried are:

Symbol	Full Name
Be	Bensheim
C24	C24
Co	Coimbra
Col	Columbia
Cvi	Cape Verde Islands
En	Enkheim
Ler	Landsberg erecta
Nd	Niederzenz
No	Nossen
Po	Poppelsdorf
RLD	Rld
Ws	Wassilewskija

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

### Time Restriction

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

### Mutagen

Limit your selection by the type of mutagen used to induce the polymorphism. The mutagens are:

Mutagen Name	Comment
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Any	returns all polymorphisms/alleles regardless of the mutagen used
transposon insertion	
T-DNA insertion	
Agrobacterium transformation	Covers both seed and whole plant transformation.
diepoxybutane (DEB)	
ethylmethane sulfonate (EMS)	
ethyl-nitrosourea (ENU)	
gamma-rays	
fast neutrons	
nitrosomethyl urea (NMU)	also methylNitrosourea (MNU)
tissue culture	
X-rays	
unknown	

## Restrict by Map Location

This section 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) map and Classical 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 polymorphism/alleles 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 distance (cM), physical distance (kb), and by polymorphism/allele 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 each results page for your query.

**sort by**

Allows you to order your results by polymorphism/allele 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.