

# RMA Path Syntax

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Use the RMA path syntax to describe a path connecting associated models in the schema. It is used in the `include=` and `criteria=` URL parameters. Please note that the path syntax does not support spaces between operators and values, but values enclosed in single quotes can include them (i.e. `name$eq'value with spaces'`).

### Comma-Separated Lists for Multiple Associations

The RMA Path specifies a set of associations from a resource. The simplest form is a comma-separated list of association names. Association names are lower case and may be singular or plural depending on the type of association.

```
probes,organism,chromosome
```

### Nested Parentheses for Association Paths

Indicate multiple levels of association with nested parentheses. Follow multiple associations from a model by using commas.

```
probes(orientation,predicted_sequence)
```

### Square Brackets for Filters

Filter the resources that are included in the query results using square brackets following an association. Operators include equal (`$eq`), not equal (`$ne`), like (`$li`), greater than (`$gt`), less than (`$lt`), greater or equal (`$ge`) less or equal (`$le`) in (`$in`) and case-insensitive like (`$il`).

```
genes[acronym$eq'ABAT']
```

The left hand side of the filter is an attribute name. It may be qualified with a lower case plural table name to resolve ambiguity using the form `table.attribute`. At times the model name in a filter may not match the association name due to inheritance.

```
predicted_sequence[sequences.sequence_length$eq948]
```

The right hand side may be a number, a string or a qualified attribute or association name. Strings should be enclosed in single quotes, but the quotes may be omitted when there is no ambiguity. The asterisk (\*) is treated as a wildcard for the like and ilike string comparison operators.

```
genes[chromosome.name$eq'X']  
ontologies[name$il'*human*']
```

A filter without an operator or a right hand side is treated as an existence test. It removes records with null values for an attribute. In many cases an `_id` attribute can be used to test whether any associated resources exist.

```
probes[orientation_id]
```

Apply multiple filters to a set of resources using extra filter clauses in square brackets. The effect is a boolean 'and'.

```
chromosome[organism_id$eq1][name$ne'X'][name$ne'Y']
```

Use filters without any association at the start of the criteria field of a query URL to filter resources from the model in the URL.

```
http://api.brain-map.org/api/v2/data/Organism/query.xml?criteria=[name$il'*human*']  
http://api.brain-map.org/api/v2/data/Gene/query.xml?criteria=[acronym$il'abat']&include=organism
```

## Double Colon for Axis

The double colon (::) operator can be used to change the axis of an RMA query. The five defined axes are `attribute::`, `model::`, `service::`, `pipe::` and `rma::`. The double colon axis operator is combined with an id to create a single step along the axis. Examples include `service::differential`, `pipe::list`, `model::Gene`, and `rma::options`. Each axis behaves slightly differently. They can be used in combination to form a service pipeline.

The `model` axis begins an API data query. The right hand side of a `model` step is a model name. Use the `model` axis is used in combination with steps along the `attribute` axis and filters to form a complete model stage.

```
model::Gene,probes(orientation,predicted_sequence)
```

Use the `rma` axis to modify the RMA query. The right hand side of an `rma` step is the name of the option. An `rma::criteria` step will cause following `attribute` steps to specify what associations are used in retrieving the data. An `rma::include` step will cause following `attribute` steps to specify what associations are displayed in the message response body. Use an `rma::options` step to specify sorting, paging and ordering options.

```
model::Gene,rma::criteria,organism[name$il'Homo Sapiens'],rma::include,probes,chromosome,rma::options  
[num_rows$eq10]
```

The above request will find human genes (the `criteria`), display the genes along with the probes and chromosome (the `includes`) ten genes at a time (the `options`). Options specified on the URL as described above are treated as steps on the `rma` axis.

The `service` and `pipe` axes are discussed in depth in the following section. They are used in combination with the other axes to create multiple stage service pipelines.

The `attribute::` axis is the assumed axis used for the RMA path syntax, but it is almost never used explicitly.