

Restriction Analysis

From this chapter you can learn how to search for restriction sites on a DNA sequence.

The restriction sites found are stored as automatic annotations. This means that if the automatic annotations highlighting is enabled then the restriction sites are searched and highlighted for each nucleotide sequence opened. Refer [Automatic Annotations Highlighting](#) to learn more.

Open a DNA sequence in and click the following button on the *Sequence View* toolbar:



The *Find restriction sites* dialog appears:

Find Restriction Sites

Name filter

Name

Accession

Type

Sequence

Organism / Details

Suppliers

> A (0, 74)

> B (2, 205)

> C (1, 22)

> D (1, 9)

> E (2, 38)

☐ EaeI

RB00800

R2

YGGCCR

Enterobacter aerogenes

Takara Bio Inc.; N...

☐ EaeI

RB00802

R2

CGGCCG

Enterobacter agglomerans

New England Biola...

☒ Eam1104I

RB00805

R2

CTCTTC

Enterobacter amnigenus RFL1104

Thermo Fisher Sci...

☐ Eam1105I

RB00806

R2

GACNNNN...

Enterobacter amnigenus RFL1105

Thermo Fisher Sci...

☐ EarI

RB00807

R2

CTCTTC

Enterobacter aerogenes

New England Biola...

☐ EclI

RB00817

R2

GCGGGA

Escherichia coli

New England Biola...

Open enzymes

Export enzymes

Select All

Select None

Select by length

Invert selection

Load selection

Save selection

REBASE Info

Checked enzymes

BamHI, BglII, ClaI, DraI, EcoRI, EcoRV, HindIII, PstI, SalI, SmaI, XmaI

Selected enzyme info

Eam1104I: type 2 restriction enzyme

3' C T C T T C (N) 1 5'

5' G A G A A G (N) 1 (N) 3 3'

Result count filter

Minimum hits: 1 Maximum hits: 2

Enzyme table filter

Suppliers 15 suppliers All None Invert

Recognition sequence length 1 to 9+

Overhang type Any

Keep only ☐ Palindromic ☐ Uninterrupted ☐ Nondegenerate

Search region

Region Whole sequence 1 199950

☐ Exclude 1 199950

Total number of enzymes: 656, selected 11

Help Cancel OK

The tree of restriction enzymes

Restriction enzymes are collected in a tree view. Enzymes are grouped by their names first letter here. Click on the > icon of a group (or just double click on the entire line) to show the whole group. Check the checkbox to include enzyme to the search list and uncheck to exclude. Use **Name filter** to find certain enzyme by its name.

Checked enzymes

Here you may see the all checked enzymes. This enzymes will be searched after clicking **OK**.

Selected enzyme info

Some information about the enzyme selected. It includes name, link to the [REBASE](#) database, the enzyme type detailed information, number of enzymes in the current sequence and sites and cuts location.

Control buttons (right side)

- **Open enzymes** - open file with enzymes in [the bairoch format](#). It is required if you want to update enzymes database or open a database with some limited amount of enzymes. See [Using Custom File with Enzymes](#) for details.
- **Export enzymes** - export selected enzymes to the separate file (using [the bairoch format](#)).
- **Select all** - check all enzymes in the tree.
- **Select none** - uncheck all enzymes in the tree.
- **Select by length** - check enzymes only if its recognition site has length more than you set in the dialog window appeared.
- **Invert selection** - switch checked and unchecked enzymes.
- **Load selection** - load selected enzymes from the file. This file should contain comma-separated enzyme name list, for example: [BamHI,BglII,ClaI,DraI,EcoRI,EcoRV,HindIII,PstI,Sall,SmaI,XmaI](#)
- **Save selection** - save checked enzymes to the separate file using the format, described above.
- **REBASE info** - open the [REBASE](#) database page of the selected enzyme.

The filter of the results number

Show enzyme only if there are not less than "Minimum hints" and not more than "Maximum hints" values.

Enzyme table filter

Show/hide enzymes depending on certain parameters:

- **Suppliers** - check/uncheck suppliers, whose enzymes will be shown. By default, enzymes with undefined commercial suppliers are not shown.
- **Recognition sequence length** - show only enzymes, whose recognition sequence length is in bounds. **NOTE:** **N** bases are not included in recognition site. That means, that if enzyme has the following sequence:

C C N N N N N N N G G

its recognition site length will be **four**, not eleven.

- **Overhang type** - show only enzymes with certain overhang type. The following options are presented:

- [Any](#) - show all enzymes.
- [No overhang](#) - site has no cuts at all. *Example:*

3' **CTCGAG** 5'
5' **GAGCTC** 3'

- [5'](#) - the cut of the forward strand is to the **left** of the cut of the reverse-complementary strand. *Example:*

3' **C CT** N A G G 5'
5' **G G A** N T C C 3'

- [3'](#) - the cut of the forward strand is to the **right** of the cut of the reverse-complementary strand. *Example:*

3' **C G A** T C G 5'
5' **G C T** A G C 3'

- [Blunt](#) - cuts are located in the middle of the site.
- [Sticky](#) - cuts are located anywhere but the middle of the site. It is [5'](#) and [3'](#) both.
- [Nondegenerate sticky](#) - the same as [Sticky](#), but the overhang between cuts has only A, C, G or T (no extended) symbols.
- [Blunt or sticky](#) - [Blunt](#) + [Sticky](#).
- [Blunt or nondegenerate sticky](#) - [Blunt](#) + [Nondegenerate sticky](#).

- **Keep only** - show most interesting enzymes only:
 - [Palindromic](#) - forward and reverse-complementary strands are equal.
 - [Uninterrupted](#) - no internal **N** bases.
 - [Nondegenerate](#) - no extended DNA alphabet symbols (only **A, C, G, T** and **N**).

Search region

The region to search enzymes in. You may also **Exclude** some region and not to search in it.

The information about enzymes was obtained from the [REBASE](#) database. For each enzyme in the list a brief description is available (the accession ID in the database, the recognition sequence, etc.). If you're online you can get more detailed information about an enzyme selected by clicking the [REBASE Info](#) button.

- [Selecting Restriction Enzymes](#)
- [Using Custom File with Enzymes](#)
- [Filtering by Number of Hits](#)
- [Excluding Region](#)
- [Circular Molecule](#)
- [Results](#)