

# 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)				AanI .. AxyI	
> B (2, 205)				BaeI .. BveI	
> C (1, 22)				Cac8I .. CviQI	
> D (1, 9)				DdeI .. DseDI	
> E (2, 38)				EaeI .. Esp3I	
<input type="checkbox"/> EaeI	RB00800	R2	YGGCCR	Enterobacter aerogenes	Takara Bio Inc.; N...
<input type="checkbox"/> EaeI	RB00802	R2	CGGCCG	Enterobacter agglomerans	New England Biola...
<input checked="" type="checkbox"/> Eam1104I	RB00805	R2	CTCTTC	Enterobacter amnigenus RFL1104	Thermo Fisher Sci...
<input type="checkbox"/> Eam1105I	RB00806	R2	GACNNNN...	Enterobacter amnigenus RFL1105	Thermo Fisher Sci...
<input type="checkbox"/> EarI	RB00807	R2	CTCTTC	Enterobacter aerogenes	New England Biola...
<input type="checkbox"/> EclI	RB00817	R2	GCGGGA	Escherichia coli	New England Biola...

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

**Selected enzyme info**  
Eam1104I: type 2 restriction enzyme  
3' CTCTTC (N)<sub>1</sub> 5'  
5' GAGAAG (N)<sub>1</sub> (N)<sub>3</sub> 3'

**Result count filter**  
Minimum hits:  Maximum hits:

**Enzyme table filter**  
Suppliers: 15 suppliers     
Recognition sequence length:  to   
Overhang type:   
Keep only: ☐ Palindromic ☐ Uninterrupted ☐ Nondegenerate

**Search region**  
Region:     
☐ Exclude

Total number of enzymes: 656, selected 11

## 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](#)