

How to annotate with brat

Use chrome or Safari browser only

<http://temu.bsc.es/ECO/brat/>

Welcome to the brat annotation tool!

Below is a mini-tutorial for basic usage. For detailed instructions, please see the [brat user manual](#).

Selecting a document

After closing this tutorial, you will see the collection browser, which allows you to access the different text collections and individual documents in those collections on your brat installation. Simply double-click on a collection name to show its contents or on a document name to open it.

You can later return to the collection browser by pressing the TAB key or by clicking on "Collection" in the menu.

Visualization

When a document is selected, the main window area shows a visualization of the text and annotations of that document. Placing the mouse cursor over an annotation shows further information about that annotation.

Menu

Placing the mouse cursor over the blue bar on top of the window opens the tool menu. This provides access to the following features:

- **Collection:** collection browser
- **Data:** export annotation data
- **Search:** search current document or collection
- **Options:** system configuration options
- **Login:** log in for editing


OK

Dismiss

Open

Collection

/

Collection Information

Document

Document

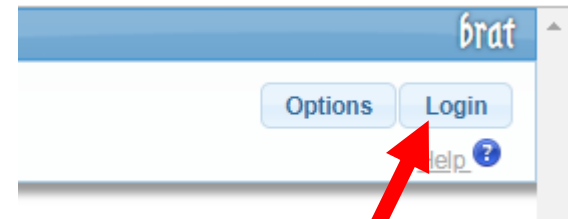
Document	Modified	Entities	Relations	Events	Issues
ECO_annotation1/					

OK Cancel

Don't do anything until logged in. So dismiss this popup

Login

Hover mouse over blue bar (upper right side)



The image shows a standard login dialog box. It has a title bar with the word "Login" and a close button (X). Below the title bar are two input fields. The first field is labeled "Username" and contains the text "Username" with a cursor at the end. The second field is labeled "Password" and contains the text "Password". At the bottom of the dialog are two buttons: "OK" and "Cancel". The dialog is centered on a light gray background. To the left of the dialog, the text "To" is partially visible.

Login ✕

Username
Username

Password
Password

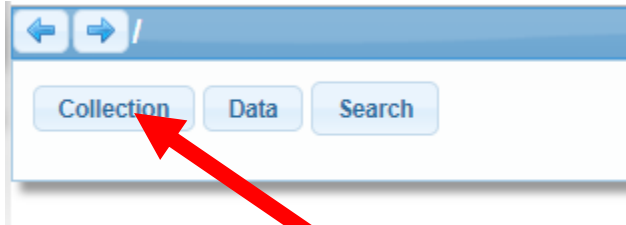
OK Cancel

To

Choose a document to annotate

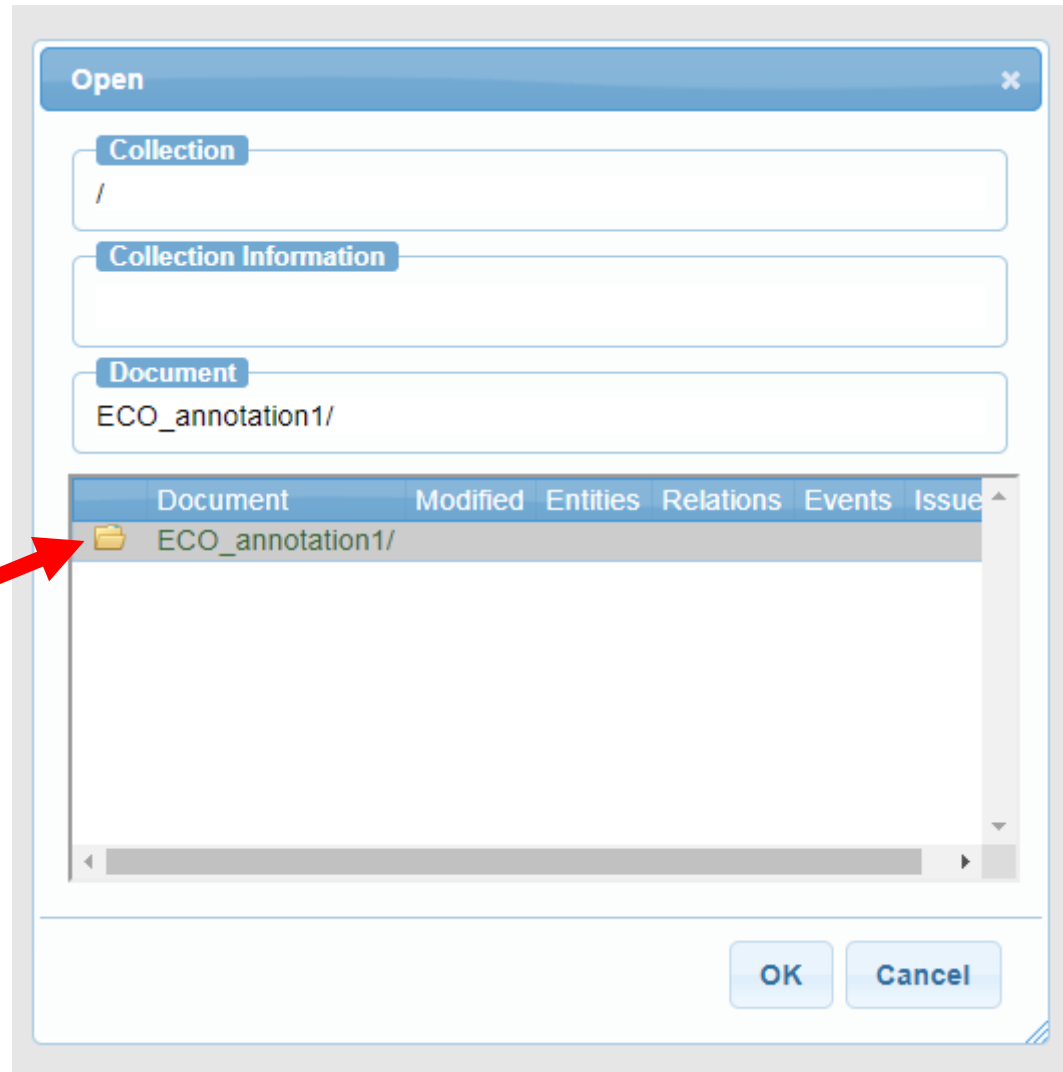
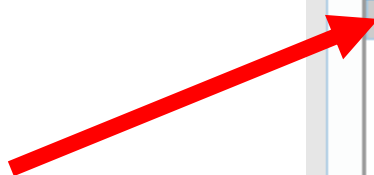


Hover mouse over blue bar (upper left side)

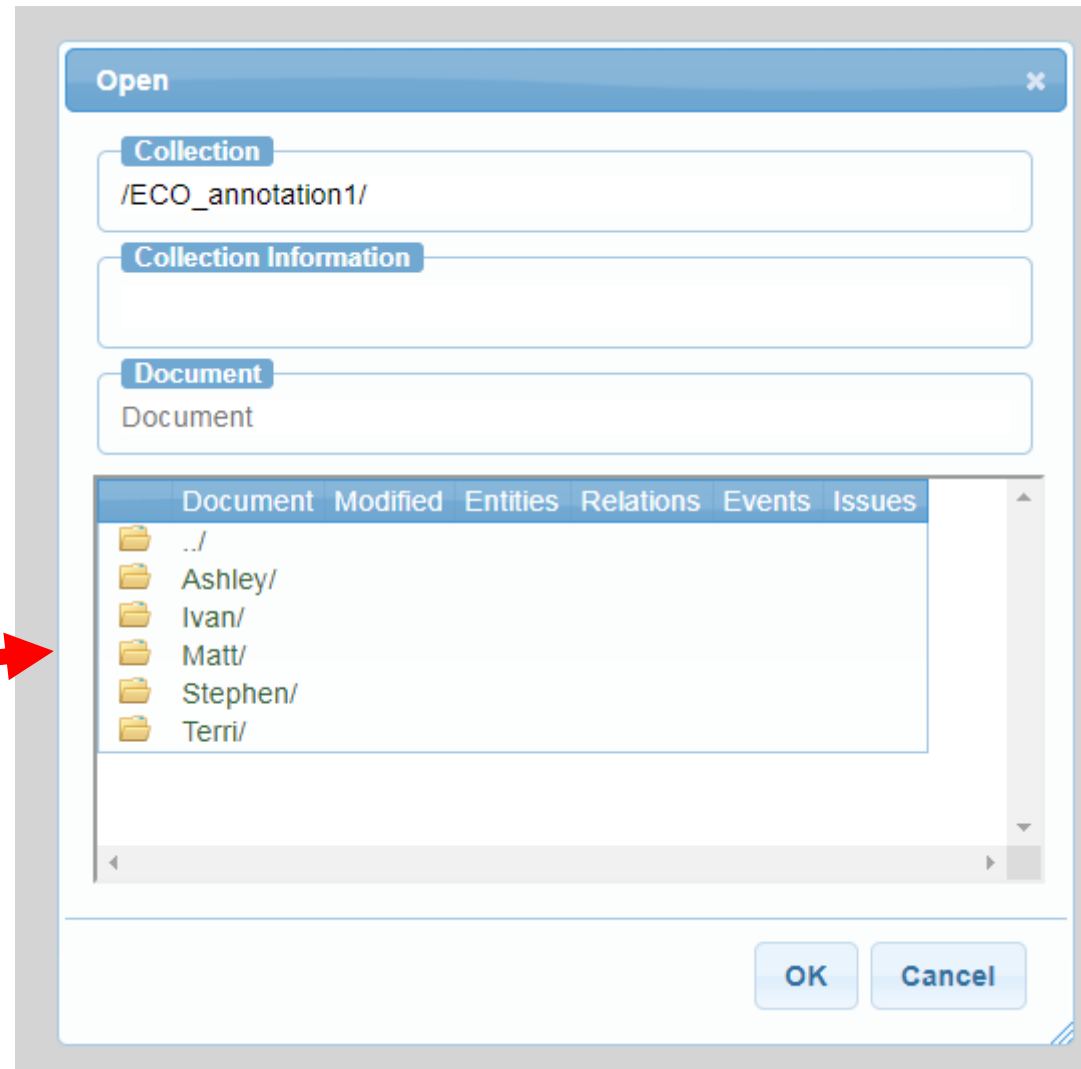


Click on Collection

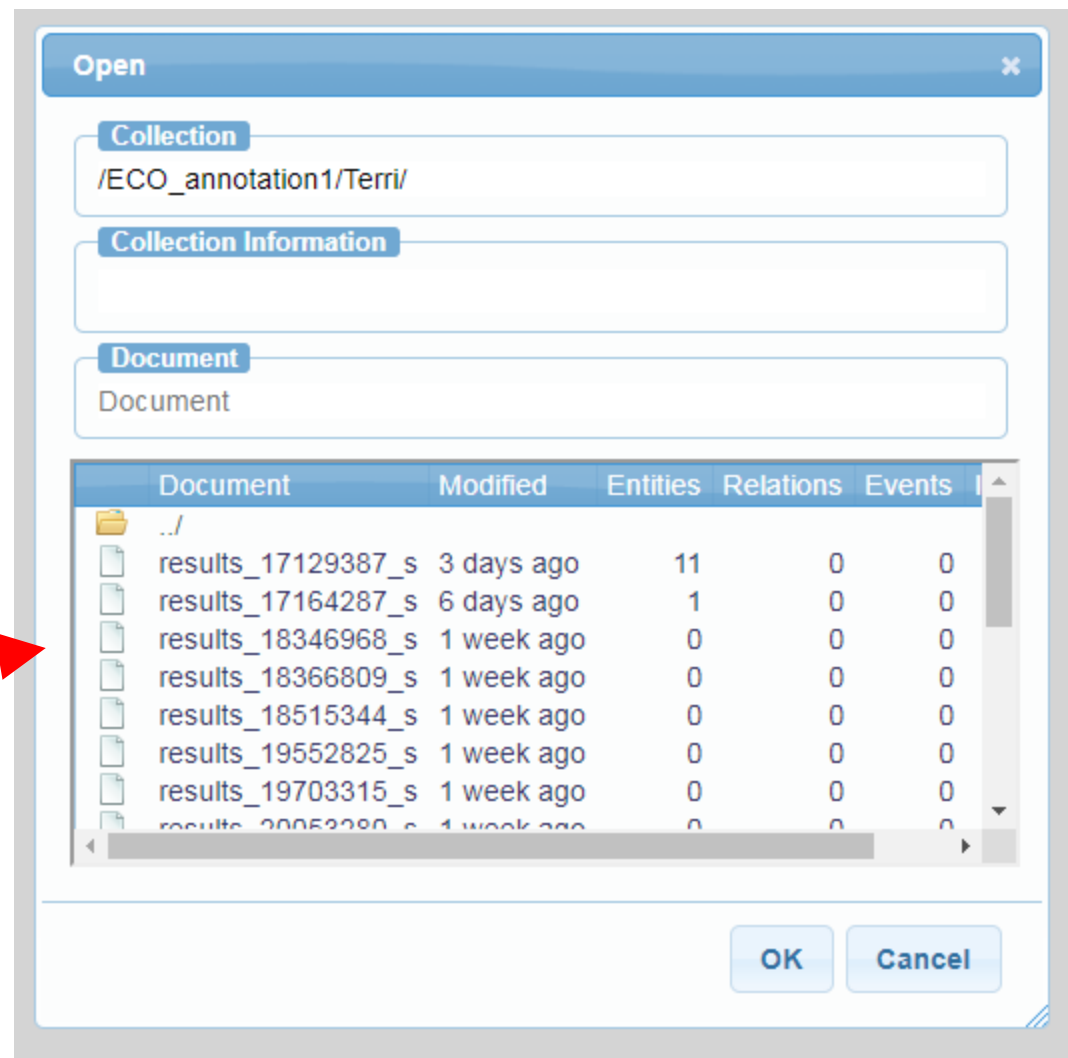
Double click



Double click on
your name

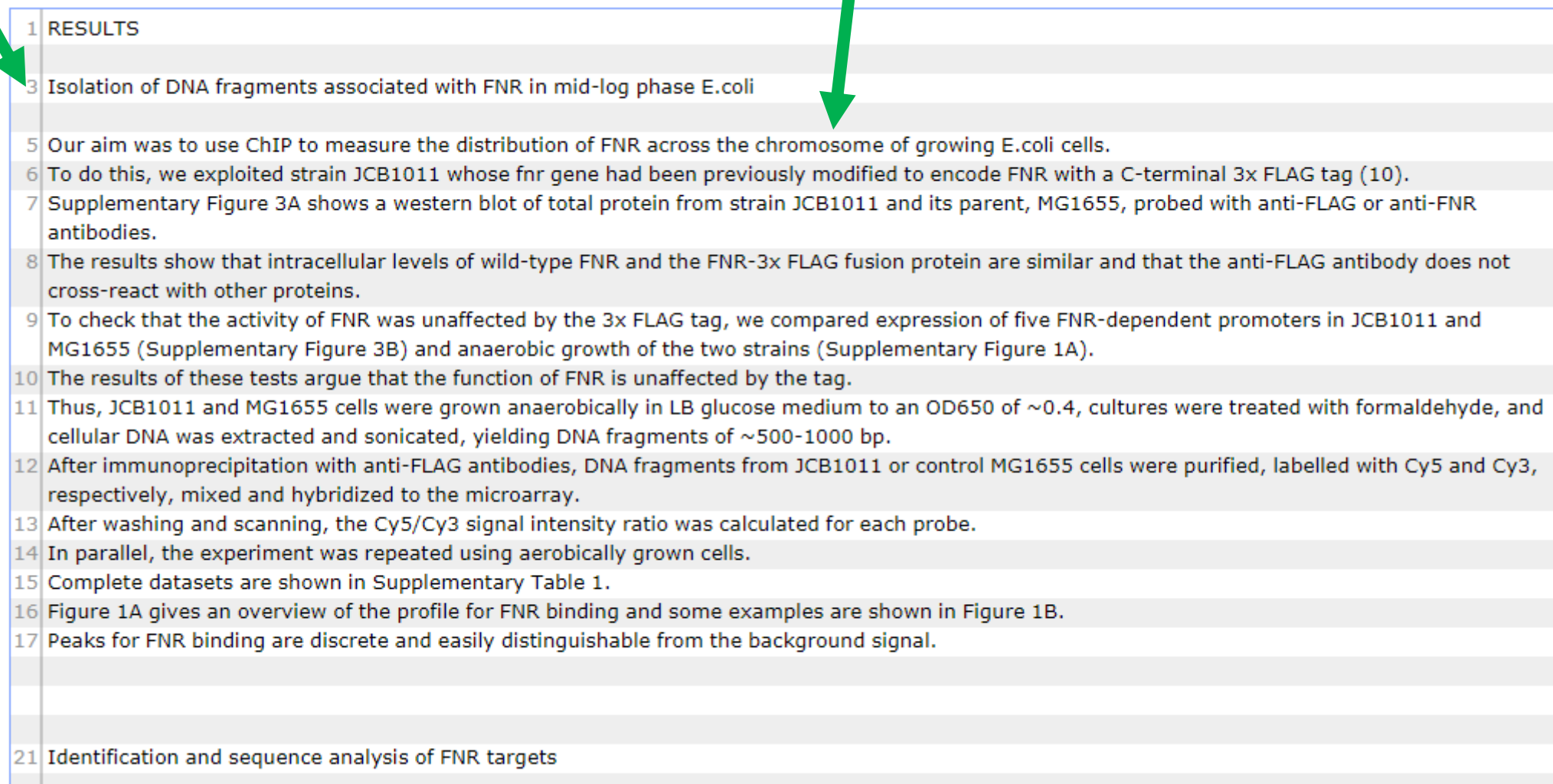


Double click
on a
document



Line numbers, not
sentence numbers

One sentence per colored bar



The screenshot shows a Brat interface with a document text area. The text is divided into sentences, each highlighted with a different colored background bar. Line numbers are displayed on the left side of the text area. Two green arrows point to the line numbers and the colored bars.

1	RESULTS
3	Isolation of DNA fragments associated with FNR in mid-log phase E.coli
5	Our aim was to use ChIP to measure the distribution of FNR across the chromosome of growing E.coli cells.
6	To do this, we exploited strain JCB1011 whose fnr gene had been previously modified to encode FNR with a C-terminal 3x FLAG tag (10).
7	Supplementary Figure 3A shows a western blot of total protein from strain JCB1011 and its parent, MG1655, probed with anti-FLAG or anti-FNR antibodies.
8	The results show that intracellular levels of wild-type FNR and the FNR-3x FLAG fusion protein are similar and that the anti-FLAG antibody does not cross-react with other proteins.
9	To check that the activity of FNR was unaffected by the 3x FLAG tag, we compared expression of five FNR-dependent promoters in JCB1011 and MG1655 (Supplementary Figure 3B) and anaerobic growth of the two strains (Supplementary Figure 1A).
10	The results of these tests argue that the function of FNR is unaffected by the tag.
11	Thus, JCB1011 and MG1655 cells were grown anaerobically in LB glucose medium to an OD650 of ~0.4, cultures were treated with formaldehyde, and cellular DNA was extracted and sonicated, yielding DNA fragments of ~500-1000 bp.
12	After immunoprecipitation with anti-FLAG antibodies, DNA fragments from JCB1011 or control MG1655 cells were purified, labelled with Cy5 and Cy3, respectively, mixed and hybridized to the microarray.
13	After washing and scanning, the Cy5/Cy3 signal intensity ratio was calculated for each probe.
14	In parallel, the experiment was repeated using aerobically grown cells.
15	Complete datasets are shown in Supplementary Table 1.
16	Figure 1A gives an overview of the profile for FNR binding and some examples are shown in Figure 1B.
17	Peaks for FNR binding are discrete and easily distinguishable from the background signal.
21	Identification and sequence analysis of FNR targets

Brat displays the text of the selected document

Create an annotation

r DNA and, in each case
sion vector pRW50 to c
ed in EMSA assays with

r::lacZ fusions was tran

IA and, in each c
vector pRW50 t
EMSA assays w

Highlight some text, but please try not to get trailing spaces

Only highlight text relating to an ECO evidence word or phrase.

When you release the mouse pointer, brat will popup a window. If you don't like what you highlighted, select cancel in that popup.

New
Annotation

New Annotation

Text

EMSA assays

Search

Google, Wikipedia, ECO

Entity type

☒ ECO

☐ Assertion

Entity attributes

ECOConfidence: ?

AssertionStrength: ?

Category: ?

NextSentence: ?

Normalization

brat_eco

ID:

Ref: Click here to search

Notes

OK

Cancel

Keep as ECO

Select selections as appropriate

Category: ?
Category: ?
Category: SeqFeat
Category: MolFn
Category: CellComp
Category: Tax
Category: Phen
Category: BioProc

Always set ECO
Confidence.

If a sentence **pair**,
fill in assertion
strength and
category here, but
use information
from next sentence,
and choose Yes for
Next Sentence.

New Annotation

Text

EMSA assays

Search

Google, Wikipedia, ECO

Entity type

☒ ECO

☐ Assertion

Entity attributes

ECOConfidence: High

AssertionStrength: High

Category: MolFn

NextSentence: Yes

Normalization

brat_eco

ID:

Ref:

Notes

OK

Cancel

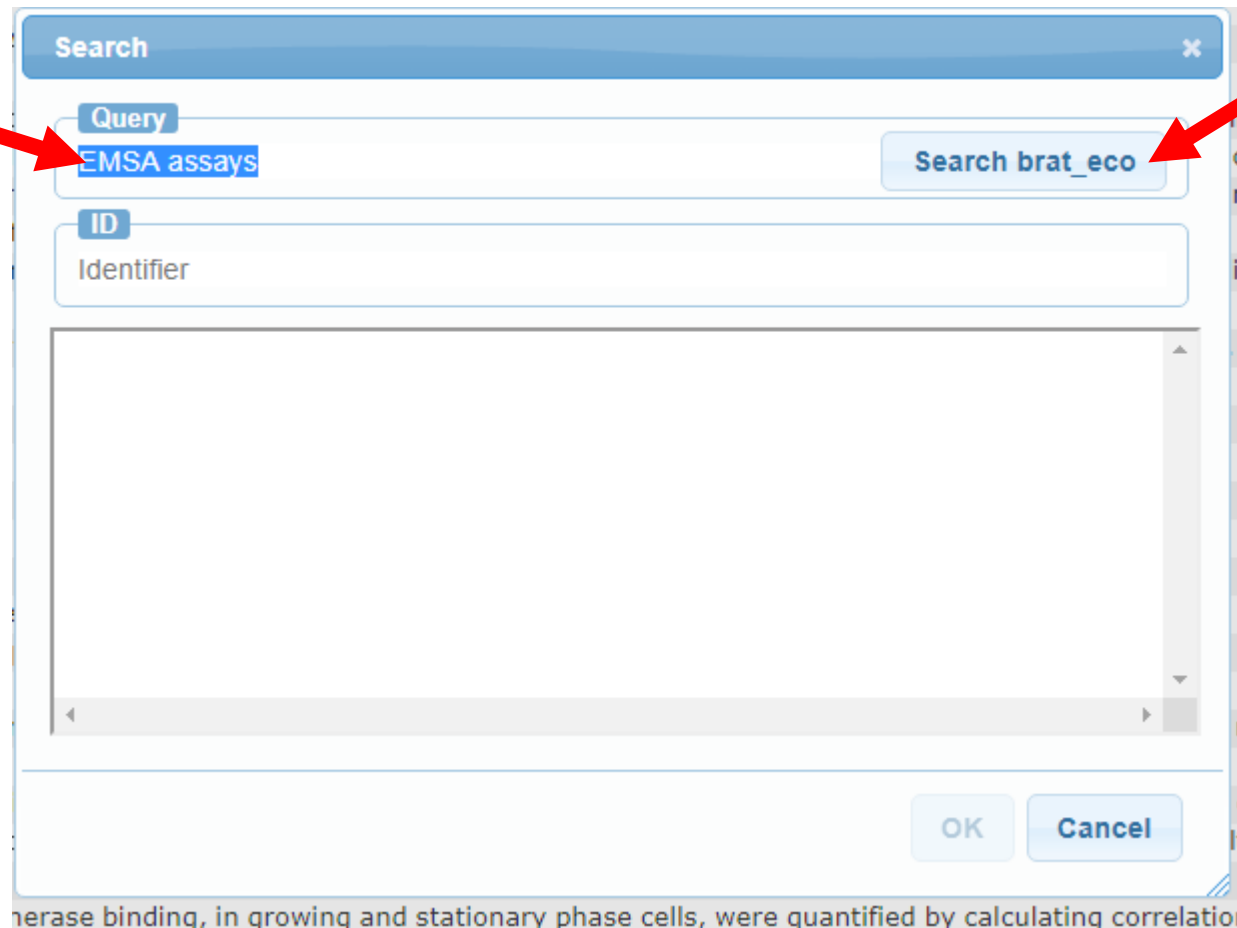
Type in
ECO ID if
known

Or click
here to
search

brat ontology search

Highlighted text. Can edit if you wish

Click here
to search



The image shows a 'Search' dialog box from the Brat interface. It has a title bar with 'Search' and a close button. Inside, there are two main sections. The first section is labeled 'Query' and contains a text input field with the text 'EMSA assays' highlighted in blue. To the right of this field is a button labeled 'Search brat_eco'. The second section is labeled 'ID' and contains a text input field with the placeholder text 'Identifier'. Below these sections is a large, empty rectangular area, likely for displaying search results. At the bottom right of the dialog are 'OK' and 'Cancel' buttons. A red arrow points from the text 'Highlighted text. Can edit if you wish' to the 'EMSA assays' text. Another red arrow points from the text 'Click here to search' to the 'Search brat_eco' button.

Search

Query

EMSA assays

Search brat_eco

ID

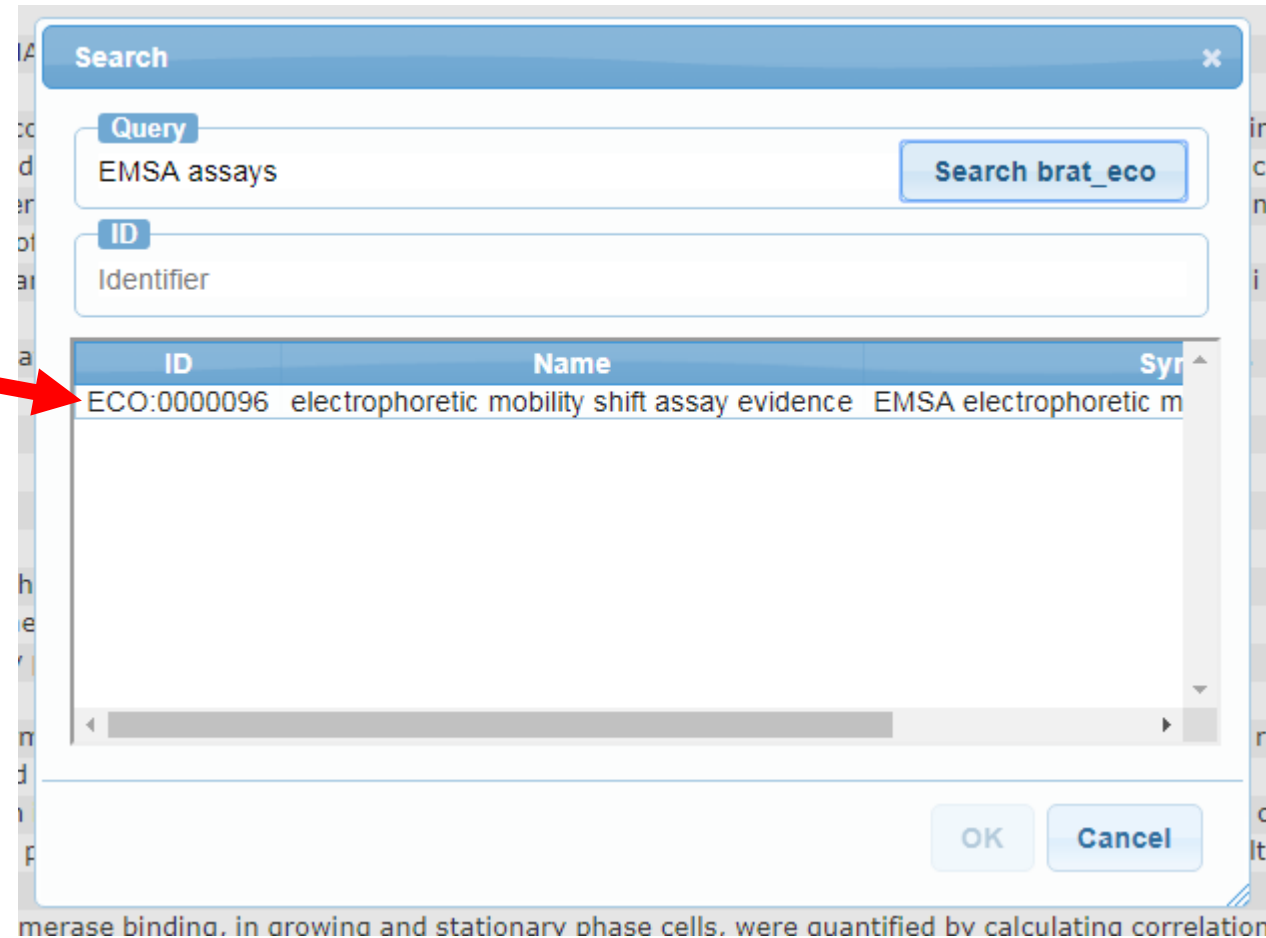
Identifier

OK Cancel

erage binding, in growing and stationary phase cells, were quantified by calculating correlation

brat ontology search

Double click to select



The screenshot shows a 'Search' dialog box with the following components:

- Query:** A text field containing 'EMSA assays' and a 'Search brat_eco' button.
- ID:** A text field labeled 'Identifier'.
- Results Table:** A table with columns 'ID', 'Name', and 'Syn'. It contains one row:

ID	Name	Syn
ECO:0000096	electrophoretic mobility shift assay evidence	EMSA electrophoretic m
- Buttons:** 'OK' and 'Cancel' buttons at the bottom right.

A red arrow points from the text 'Double click to select' to the first row of the results table.

If no match is found, try editing Query and searching again.
(Or can enter ECO ID in the New Annotation popup.)

New Annotation

Text

EMSA assays

Search

Google, Wikipedia, ECO

Entity type

☒ ECO

☐ Assertion

Entity attributes

ECOConfidence: High

AssertionStrength: High

Category: MolFn

NextSentence: Yes

Normalization

brat_eco

ID: ECO:0000096

Ref: electrophoretic mobility shift assay evidence

Notes

OK

Cancel

Optional:
enter GO ID
in Notes

When done,
click OK

Annotation created

r DNA and, in each case, a likely F
sion vector pRW50 to create prom

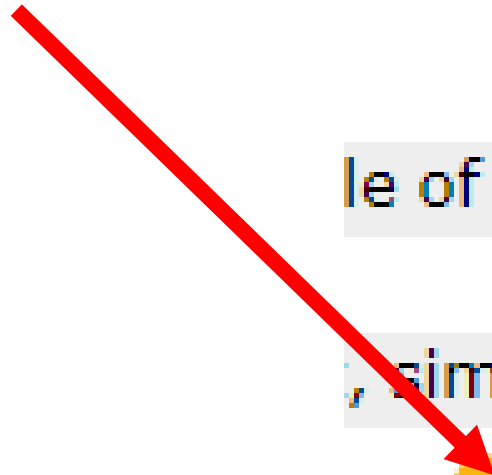
ed in EMSA assays with

ECO → MolFn↑High↑Yes↑High

Brat re-displays the document text with the new annotation highlighted. ECO annotations are light green. Attribute values are shown. Unfortunately, the order of the attribute values is not the same for each annotation.

r::lacZ fusions was transformed ir

To edit or delete an annotation, double click on it



le of FNR binding in stationary ph

, similar analyses were performed

ECO → MolFn↑High→Medium

ied ChIP-chip to stu

polymerase binding are shown in

le of IHF binding in stationary pha

nts for ENP, TUE and DNA polymer

Changing annotations

Edit
Annotation

Edit Annotation

Text

ChIP-chip

Link

Search

Google, Wikipedia, ECO

Entity type

☒ ECO

☐ Assertion

Entity attributes

ECOConfidence: High

AssertionStrength: Medium

Category: MolFn

NextSentence: ?

Normalization

brat_eco

ID: ECO:0000230

Ref: chromatin immunoprecipitation-chip evidence

X

Notes

X

Add Frag.

Delete

Move

OK

Cancel

Or, click
delete to
remove

To edit: Change
attribute values
and/or ECO ID and
click OK

nnotation1/Terri/results_17164287_s


temu.bsc.es says

Are you sure you want to delete this annotation?


OK

Cancel

If choose to remove,
confirm deletion

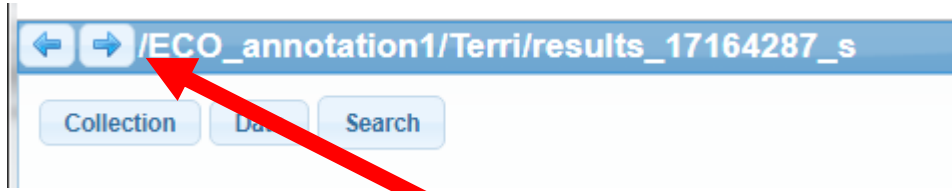


periment, similar analyses were performed. We had used ChIP-chip to study IHF and RNA polymerase binding are shown: the profile of IHF binding in stationary

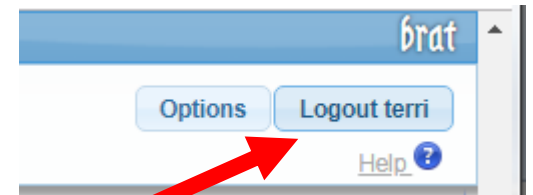


Brat redisplay the
document text, and the
annotation is gone

Another document or logout



When done with document, hover mouse on blue bar (left side). Can use arrows to move to another document.



When done annotating for the session, hover mouse on blue bar (right side) and logout.