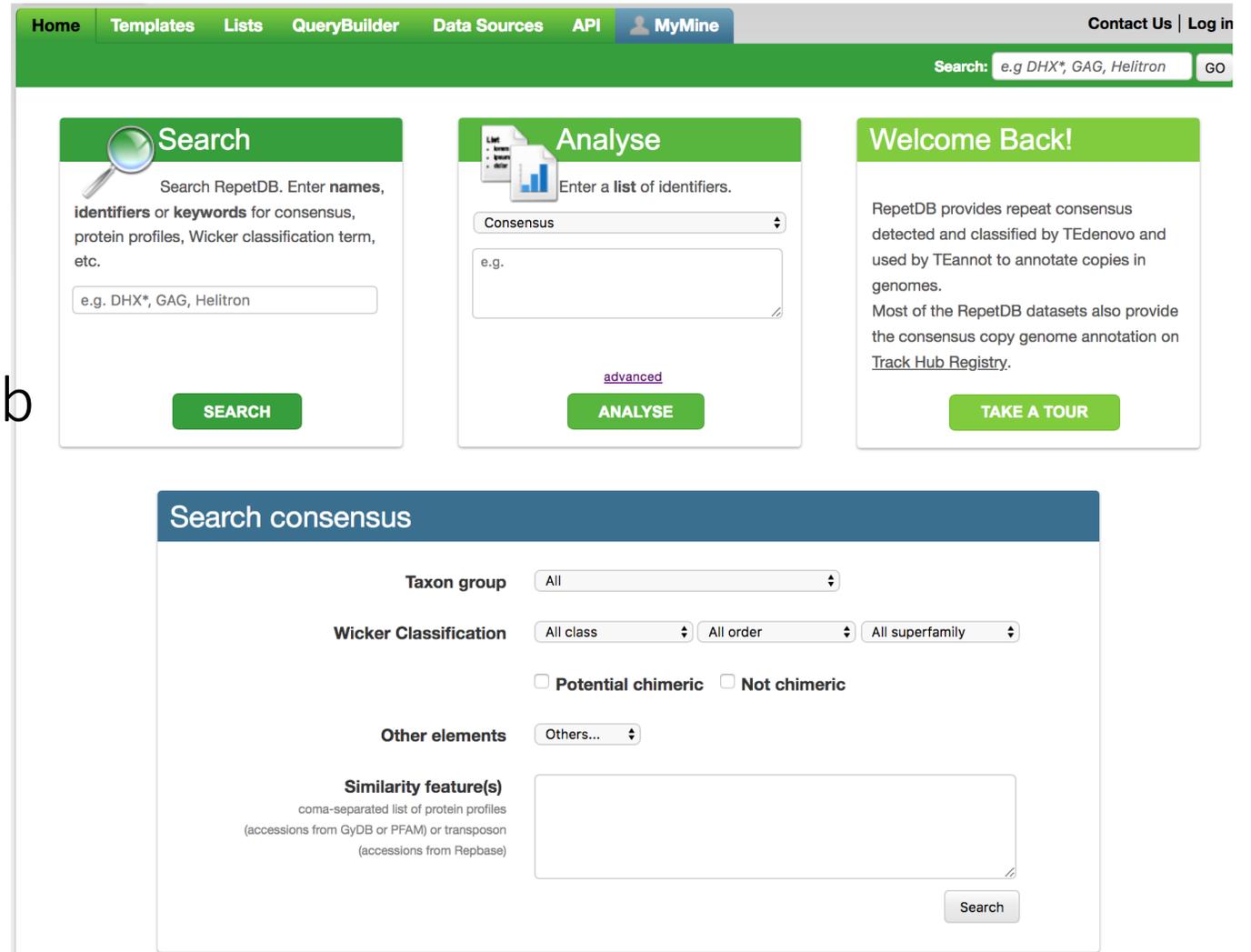


# How to get consensus fasta sequences from a table or a list

<https://urgi.versailles.inra.fr/repetdb>

Amselem J, et al. RepetDB: a unified resource for transposable element references. *Mobile DNA*. 2019;10:6.



The screenshot displays the RepetDB web interface. At the top, there is a navigation menu with links for Home, Templates, Lists, QueryBuilder, Data Sources, API, and MyMine. A search bar on the right contains the text "e.g. DHX\*, GAG, Helitron" and a "GO" button. Below the navigation, there are three main panels: "Search", "Analyse", and "Welcome Back!".

- Search:** Contains a magnifying glass icon and the text "Search RepetDB. Enter names, identifiers or keywords for consensus, protein profiles, Wicker classification term, etc." Below this is a text input field with the example text "e.g. DHX\*, GAG, Helitron" and a green "SEARCH" button.
- Analyse:** Contains a document icon and the text "Enter a list of identifiers." Below this is a dropdown menu labeled "Consensus" and a text input field with "e.g." and a green "ANALYSE" button. A link for "advanced" is also present.
- Welcome Back!:** Contains text about RepetDB's capabilities and a green "TAKE A TOUR" button.

Below these panels is a "Search consensus" section with various filters and a search button:

- Taxon group:** A dropdown menu set to "All".
- Wicker Classification:** Three dropdown menus for "All class", "All order", and "All superfamily".
- Potential chimeric:** Two radio buttons, "Potential chimeric" and "Not chimeric".
- Other elements:** A dropdown menu set to "Others...".
- Similarity feature(s):** A text input field with a small description: "comma-separated list of protein profiles (accessions from GyDB or PFAM) or transposon (accessions from Repbase)".
- A "Search" button is located at the bottom right of this section.

# How to get consensus sequence from a table or a list

Example : from a list you have previously saved

Home Templates **Lists** QueryBuilder Data Sources API MyMine Contact Us | joelle.anselem | Log out

Upload View Search: e.g DHX\*, GAG, Helitron GO

**Lists**  
View your own and public lists, search by keyword and compare the contents of lists. Click on a list to view graphs and summaries in an analysis page, select lists using checkboxes to perform set operations. Click 'Upload' above to import a new list.

Filter: Filter: filter by a tag -- Reset

Actions: Union Intersect Subtract Asymmetric Difference Copy Delete Options: Show descriptions Show Tags

- INT\_crm-galadriel 240 Consensus
- INT\_crm and galadriel 39 Consensus
- protein\_profile=INT\_crm 279 Consensus
- protein\_profile=galadriel 160 Consensus
- Subtract 136 Consensus
- PF09331.10 consensus (search from "classification panel") 236 Consensus
- Consensus List (Wed Jul 31 2019 10:00:10 GMT+0200 (heure d'été d'Europe centrale)) DUF1985 consensus 100 Consensus
- ap+gag+termLTR 1581 Consensus
- Consensus with LTR 8316 Consensus
- GAG+AP 2914 Consensus**
- Consensus with Asp AP 5957 Consensus
- Consensus with GAG domain 5041 Consensus

Home Templates Lists QueryBuilder Data Sources API MyMine

Upload View

**List Analysis for GAG+AP (2914 Consensus)**

Manage Columns Manage Filters

Manage Relationships Save as List Generate Python code Export

Showing 1 to 25 of 2,914 rows Rows per page: 25 page 1

Consensus identifier	Consensus Length	Consensus TE classification code	Consensus Miscellaneous classification	Consensus Potential Chimeric	Consensus Cumulative genome coverage	Consensus Fragments	Consensus Full-length fragments	Consensus Copies	Consensus Full-length copies
DHX-chim_CoII-B-G203-Map4_reversed	18549	Class I : LTR : ?		true	118203	41	4	39	4
DHX-incomp-chim_denovoPeach-B-R4306-Map4_reversed	10851	Class II : Helitron : ?		true	92547	316	1	285	1
DHX-incomp-chim_MCL19_Tpar_TEdenovo-B-R1169-Map11	6293	Class II : Helitron : ?		true	73852	174	1	139	1
DTX-chim_Tmel28-B-G11914-Map3_reversed	8458	Class II : TIR : ?		true	47244	101	0	83	0
DTX-incomp-chim_3b_ltr1_300M-B-G22427-Map7_reversed	9318	Class II : TIR : ?		true	306167	179	4	165	5
DTX-incomp-chim_3b_ltr1_300M-B-G23116-Map3_reversed	7819	Class II : TIR : ?		true	284832	194	3	180	5
DTX-incomp-chim_3b_ltr1_300M-B-G23311-Map3_reversed	8372	Class II : TIR : ?		true	60231	38	1	36	1

# Manage columns

1

2

Manage Columns

Showing 1 to 25 of 2,914 rows

Consensus identifier	Consensus Length	Consensus TE classification code	Consensus Miscellaneous classification	Consensus Potential Chimeric	Consensus Cumulative genome coverage	Consensus Fragments	Consensus Full-length fragments	Consensus Copies	Consensus Full-length copies
DHX-chim_CollID-B-G203-Map4_reversed	18549	Class I : LTR : ?		true	118203	41	4	39	4
DHX-incomp-chim_denovoPeach-B-R4306-Map4_reversed	10851	Class II : Helitron : ?		true	92547	316	1	285	1
DHX-incomp-chim_MCL19_Tpar_TEdenovo-B-R1169-Map11	6293	Class II : Helitron : ?		true	73852	174	1	139	1
DTX-chim_Tmel28-B-G11914-Map3_reversed	8458	Class II : TIR : ?		true	47244	101	0	83	0
DTX-incomp-chim_3b_itr1_300M-B-G22427-Map7_reversed	9318	Class II : TIR : ?		true	306167	179	4	165	5
DTX-incomp-chim_3b_itr1_300M-B-G23116-Map3_reversed	7819	Class II : TIR : ?		true	284832	194	3	180	5
DTX-incomp-chim_3b_itr1_300M-B-G23311-Map3_reversed	8372	Class II : TIR : ?		true	60231	38	1	36	1

Manage Columns

Selected Columns Sort Order

10 Columns Selected

Re-arrange or remove columns by dragging, or by using the buttons

- Consensus = Consensus identifier
- Consensus = Length
- Consensus = TE classification code
- Consensus = Miscellaneous classification
- Consensus = Potential Chimeric
- Consensus = Cumulative genome coverage
- Consensus = Fragments
- Consensus = Full-length fragments
- Consensus = Copies
- Consensus = Full-length copies

Cancel Apply Changes

3 : delete all columns not needed

Manage Columns

Selected Columns Sort Order

2 Columns Selected, 8 Removed

Re-arrange or remove columns by dragging, or by using the buttons

- Consensus = Consensus identifier
- Consensus = Length

+ Add a Column

Cancel Apply Changes

Manage Columns

Selected Columns Sort Order

Choose a path from Consensus

+ Add 1 new column

- Full-length fragments
- Symbol
- Fragments
- Score
- TE classification code
- Secondary Identifier
- Full-length copies
- Score Type
- Copies
- Consensus Identifier
- Miscellaneous classification
- Potential Chimeric
- Consensus.description
- Name
- Length
- Cumulative genome coverage
- Family
- Sequence
- Residues
- MDS Checksum
- Length
- Chromosome Location
- Chromosome
- Parent Feature
- Sequence Ontology Term
- Organism
- Data Set
- Ontology Annotations
- Classification
- Cross References
- Publications
- Locations
- Copy statistics
- Located Features
- Synonyms
- Child Features
- Data Sets

Cancel Apply Changes

4 : Add « sequence->Residues » column



Fasta sequences of consensus could also be obtained from a particular data source, following the same steps in slides 2 - 3 - 4

Home Templates Lists QueryBuilder **Data Sources** API My Account Contact Us | Log in

Search: e.g DHX\*, GAG, Helitron GO

### Search

Search RepetDB. Enter names, identifiers or keywords for consensus, protein profiles, Wicker classification term, etc.

e.g. DHX\*, GAG, Helitron

**SEARCH**

### Analyse

Enter a list of identifiers.

Consensus

e.g.

[advanced](#)

**ANALYSE**

### Welcome Back!

RepetDB provides repeat consensus detected and classified by TEdenovo and used by TEannot to annotate copies in genomes.

Most of the RepetDB datasets also provide the consensus copy genome annotation on [Track Hub Registry](#).

**TAKE A TOUR**

**Data source: Botrytis\_cinerea\_T4**

Organism: Botrytis cinerea T4      Genome assembly: Name: BotFuc\_Mar2011, Accession: GCA\_000227075.1

Software used: TEdenovo v1.2, TEannot v2.1, PastecClassifier v1.0

Comments: The TEdenovo (v1.2) pipeline was launched on Botrytis cinerea strain T4 whole genome assembly (118 scaffolds) to provide a TE library of 31 consensus. This library was filtered for SSR, then 2 consensus from Repbase (BOTY and FLIPPER) were added. These 24 TE consensus including BOTY and FLIPPER were used to annotate the genome using TEannot pipeline (v2.1). We provide here a new refined classification (v2017) with PastecClassifier (v1.0) to obtain the TE consensus library of B. cinerea T4 inserted in RepetDB. Genome annotation files and TE consensus ID mapping between previous and new classification are [available for download](#). Other genome annotations are also available on an [online Gbrowse](#).

Contact: [Joelle Amselem \(mail to urgi-contact\)](#)

2 Publications

Year	First author	Title
2011	Amselem Joelle	Genomic Analysis of the Necrotrophic Fungal Pathogens Sclerotinia sclerotiorum and Botrytis cinerea
2015	Amselem Joelle	Whole genome comparative analysis of transposable elements provides new insight into mechanisms of their inactivation in fungal genomes

### Search consensus

Taxon group: All

Wicker Classification: All class | All order | All superfamily

Potential chimeric    Not chimeric

Other elements: Others...

Similarity feature(s): coma-separated list of protein profiles (accessions from GyDB or PFAM) or transposon (accessions from Repbase)

**Search**

- ✓ Select one of the dataset
- ✓ Manage columns
  - Consensus >> Consensus Identifier
  - Sequence >> Residues
- ✓ Export the consensus in fasta format