



Search copies of a consensus located in a genome region

<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 bar with links for Home, Templates, Lists, QueryBuilder, Data Sources, API, MyMine, Contact Us, and Log in. A search bar on the right contains the text "e.g DHX*, GAG, Helitron" and a "GO" button. Below the navigation bar, the page is divided into three main sections: "Search", "Analyse", and "Welcome Back!".

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

Below these sections is a detailed "Search consensus" form with the following fields and options:

- 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 icon on the right. Below the field is a note: "comma-separated list of protein profiles (accessions from GyDB or PFAM) or transposon (accessions from Repbase)".
- Search:** A grey "Search" button at the bottom right of the form.

Search all the TE copies located in a genome region

Request : Search all the TE copies located in a genome region

- Get All the copies corresponding to:

Genome genus = "Malus"

Region= Chr4: 13000000..15000000

- Display the copies coordinates, the consensus classification and identifier

QueryBuilder

Advanced users can use a flexible query interface to construct their own data mining queries. The QueryBuilder lets you view the data model, apply constraints and select output. You can also export queries to share them with others.

[Browse data model](#) [Import query from XML](#) [Login to view saved queries](#)

Select a Data Type to Begin a Query

Click on a class name for a description or double click on a class name to create a new query starting at that class

Consensus

- Bio-Entity
- Blast hit
- BlastN hit
- BlastX hit
- Chromosome
- Consensus
- Consensus copy**

Query History

Queries that you have run during this session - [Log in to save your queries permanently](#)

[nothing to display]

[Import query from XML](#)

[Show results](#)

Model browser

Browse through the classes and attributes. Click on [SUMMARY](#) links to add summary of fields to the results table or on [SHOW](#) links to add individual fields to the results. Use [CONSTRAIN](#) links to constrain a value in the query.

- [Consensus copy](#) [SUMMARY](#) [CONSTRAIN](#)
- [Genome Jbrowse Url](#) [SHOW](#) [CONSTRAIN](#)
- [Identity Double](#) [SHOW](#) [CONSTRAIN](#)
- [Length Integer](#) [SHOW](#) [CONSTRAIN](#)
- [DB Identifier](#) [SHOW](#) [CONSTRAIN](#)
- [Target Chromosome](#) [SHOW](#) [CONSTRAIN](#)
- [Target End Integer](#) [SHOW](#) [CONSTRAIN](#)
- [Target Segment](#) [SHOW](#) [CONSTRAIN](#)
- [Target Start Integer](#) [SHOW](#) [CONSTRAIN](#)
- [Used For Classification Boolean](#) [SHOW](#) [CONSTRAIN](#)
- [Child Features Sequence Feature](#) [SUMMARY](#) [CONSTRAIN](#)
- [Consensus Consensus](#) [SUMMARY](#) [CONSTRAIN](#)
- [Data Sets Data Set](#) [SUMMARY](#) [CONSTRAIN](#)
- [Locations Location](#) [SUMMARY](#) [CONSTRAIN](#)
- [Organism Organism](#) [SUMMARY](#) [CONSTRAIN](#)
- [Parent Feature Sequence Feature](#) [SUMMARY](#) [CONSTRAIN](#)
- [Target Sequence Feature](#) [SUMMARY](#) [CONSTRAIN](#)

Show empty fields

Fields selected for output

Columns to Display

Use the [SHOW](#) or [SUMMARY](#) links to add fields to the results table.

No fields selected for output

[Show results](#)

Query Overview

no fields constrained

Constraint logic:

no constraints

Questions? Comments? Click here!



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Model browser

Browse through the classes and attributes. Click on **Summary** links to add summary of fields to the results table or on **Show** links to add individual fields to the results. Use **Constrain** links to constrain a value in the query.

- Consensus copy **Summary** **Constrain**
- Genome Jbrowse Url **Show** **Constrain**
- Identity Double **Show** **Constrain**
- Length Integer **Show** **Constrain**
- DB identifier **Show** **Constrain**
- Target Chromosome **Show** **Constrain**
- Target End Integer **Show** **Constrain**
- Target Segment **Show** **Constrain**
- Target Start Integer **Show** **Constrain**
- Used For Classification Boolean **Show** **Constrain**
- Child Features Sequence Feature **Summary** **Constrain**
- Consensus Consensus **Summary** **Constrain**
- Data Sets Data Set **Summary** **Constrain**
- Locations Location **Summary** **Constrain**
- Organism Organism **Summary** **Constrain**
 - Genus **Show** **Constrain**
 - Name **Show** **Constrain**
 - Species **Show** **Constrain**
 - Taxon Id Integer **Show** **Constrain**
- Taxonomy Node Taxonomy Node **Summary** **Constrain**
- Parent Feature Sequence Feature **Summary** **Constrain**
- Target Sequence Feature **Summary** **Constrain**

Query Overview

Constraint logic:

Constraint for Consensus copy > Organism > Genus

Constrain

Choose a filter

Filter query results on this field having a specific value

Consensus copy > Organism > Genus

= Malus Add to query

Filter query results on this field having any value or not

Has no value Has a value Add to query

Add a constraint
Organism genus = "Malus"

Add columns to show
genus
species

Model browser

add summary of fields to the results table or on **Show** links to add individual fields to the results. Use **Constrain** links to constrain a value in the query.

- Consensus copy **Summary** **Constrain**
- Genome Jbrowse Url **Show** **Constrain**
- Identity Double **Show** **Constrain**
- Length Integer **Show** **Constrain**
- DB identifier **Show** **Constrain**
- Target Chromosome **Show** **Constrain**
- Target End Integer **Show** **Constrain**
- Target Segment **Show** **Constrain**
- Target Start Integer **Show** **Constrain**
- Used For Classification Boolean **Show** **Constrain**
- Child Features Sequence Feature **Summary** **Constrain**
- Consensus Consensus **Summary** **Constrain**
- Data Sets Data Set **Summary** **Constrain**
- Locations Location **Summary** **Constrain**
- Organism Organism **Summary** **Constrain**
 - Genus **Show** **Constrain**
 - Name **Show** **Constrain**
 - Species **Show** **Constrain**
 - Taxon Id Integer **Show** **Constrain**
- Taxonomy Node Taxonomy Node **Summary** **Constrain**
- Parent Feature Sequence Feature **Summary** **Constrain**
- Target Sequence Feature **Summary** **Constrain**

Show empty fields

Fields selected for output

Columns to Display

Use the **Show** or **Summary** links to add fields to the results table. Click and drag the blue output boxes to choose the output column order. Click **?** to choose a column to sort results by, click again to select ascending **?** or descending **?**. Use the **Remove All** link to remove all fields from the results table.

REMOVE ALL

Consensus copy > Organism > Genus (no description) **?**

Consensus copy > Organism > Species (no description) **?**

Query Overview

Consensus copy

Organism Organism **?**

Genus **?**

= Malus **?** (A)

Species **?**

Constraint logic:

one constraint

Show results

Model browser

Browse through the classes and attributes. Click on **SUMMARY** links to add summary of fields to the results table or on **SHOW** links to add individual fields to the results. Use **CONSTRAIN** links to constrain a value in the query.

Query Overview

Constraint logic:

Constrain for Consensus copy > Target Chromosome

Constrain

Choose a filter

Filter query results on this field having a specific value

Consensus copy > Target Chromosome

= Chr04 Add to query

Filter query results on this field having any value or not

Has no value Has a value Add to query

Add a constraint
Target Chromosome = "Chr4"

Model browser

individual fields to the results. Use **CONSTRAIN** links to constrain a value in the query.

Consensus copy **SUMMARY** **CONSTRAIN**

Genome Jbrowse Url **SHOW** **CONSTRAIN**

Identity Double **SHOW** **CONSTRAIN**

Length Integer **SHOW** **CONSTRAIN**

DB Identifier **SHOW** **CONSTRAIN**

Target Chromosome **SHOW** **CONSTRAIN**

Target End Integer **SHOW** **CONSTRAIN**

Target Segment **SHOW** **CONSTRAIN**

Target Start Integer **SHOW** **CONSTRAIN**

Used For Classification Boolean **SHOW** **CONSTRAIN**

Child Features Sequence Feature **SUMMARY** **CONSTRAIN**

Consensus Consensus **SUMMARY** **CONSTRAIN**

Data Sets Data Set **SUMMARY** **CONSTRAIN**

Locations Location **SUMMARY** **CONSTRAIN**

Organism Organism **SUMMARY** **CONSTRAIN**

Parent Feature Sequence Feature **SUMMARY** **CONSTRAIN**

Target Sequence Feature **SUMMARY** **CONSTRAIN**

Show empty fields

Query Overview

Consensus-copy

Target Chromosome **X**

= Chr04 **X** **B**

Organism Organism **X** **B**

Genus **X**

= Malus **X** **A**

Species **X**

Constraint logic: A and B

A and B

Add column to show
Chromosome column

Fields selected for output

Columns to Display

Use the **SHOW** or **SUMMARY** links to add fields to the results table. Click and drag the blue output boxes to choose the output column order. Click **?** to choose a column to sort results by, click again to select ascending **↑** or descending **↓**. Use the **REMOVE ALL** link to remove all fields from the results table.

REMOVE ALL

Consensus copy > Organism > Genus **X**
(no description) **?**

Consensus copy > Organism > Species **X**
(no description) **?**

Consensus copy > Target Chromosome **X**
(no description) **?**

Show results



Show results

Model browser

- Consensus copy [SUMMARY](#) [CONSTRAIN](#)
- Genome Jbrowse Url [SHOW](#) [CONSTRAIN](#)
- Identity Double [SHOW](#) [CONSTRAIN](#)
- Length Integer [SHOW](#) [CONSTRAIN](#)
- DB identifier [SHOW](#) [CONSTRAIN](#)
- Target Chromosome [SHOW](#) [CONSTRAIN](#)
- Target End Integer [SHOW](#) [CONSTRAIN](#)
- Target Segment [SHOW](#) [CONSTRAIN](#)
- Target Start Integer [SHOW](#) [CONSTRAIN](#)
- Used For Classification Boolean [SHOW](#) [CONSTRAIN](#)
- Child Features Sequence Feature [SUMMARY](#) [CONSTRAIN](#)
- Consensus Consensus [SUMMARY](#) [CONSTRAIN](#)
 - TE classification code [SHOW](#) [CONSTRAIN](#)
 - Copies Integer [SHOW](#) [CONSTRAIN](#)
 - Cumulative genome coverage Integer [SHOW](#) [CONSTRAIN](#)
 - Fragments Integer [SHOW](#) [CONSTRAIN](#)
 - Full-length copies Integer [SHOW](#) [CONSTRAIN](#)
 - Full-length fragments Integer [SHOW](#) [CONSTRAIN](#)
 - Length Integer [SHOW](#) [CONSTRAIN](#)
 - Miscellaneous classification [SHOW](#) [CONSTRAIN](#)
 - Potential Chimeric Boolean [SHOW](#) [CONSTRAIN](#)
 - Consensus identifier [SHOW](#) [CONSTRAIN](#)
- Classification Wicker Classif Term [SUMMARY](#) [CONSTRAIN](#)

Show empty fields

Query Overview

Consensus copy

- Target Chromosome
 - = Chr04 (B)
- Target End
 - < 15000000 (D)
- Target Start
 - > 13000000 (C)
- Consensus Consensus
 - TE classification code
 - Copies
 - Consensus identifier
- Organism Organism
 - Genus
 - = Malus (A)
 - Species

Constraint logic: A and B and C and D

A and B and C and D

Fields selected for output

Columns to Display

Use the [SHOW](#) or [SUMMARY](#) links to add fields to the results table. Click and drag the blue output boxes to choose the output column order. Click [?](#) to choose a column to sort results by, click again to select ascending [?](#) or descending [?](#). Use the [REMOVE ALL](#) link to remove all fields from the results table.

[REMOVE ALL](#)

Consensus copy > Organism > Genus <input checked="" type="checkbox"/> (no description) ?	Consensus copy > Organism > Species <input checked="" type="checkbox"/> (no description) ?	Consensus copy > Target Chromosome <input checked="" type="checkbox"/> (no description) ?	Consensus copy > Target Start <input checked="" type="checkbox"/> (no description) ?
Consensus copy > Target End <input checked="" type="checkbox"/> (no description) ?	Consensus copy > Consensus > TE classification code <input checked="" type="checkbox"/> (no description) ?	Consensus copy > Consensus > Consensus identifier <input checked="" type="checkbox"/> (no description) ?	
Consensus copy > Consensus > Copies <input checked="" type="checkbox"/> (no description) ?			

Add constraints on Chromosome target location

Target start > 13000000

Target end < 15000000

Add column to show

Target start

Target end

TE classification code

Consensus identifier

Total number of genome copies



Show results

Model browser

- Consensus copy [SUMMARY](#) [CONSTRAIN](#)
- Genome Jbrowse Url [SHOW](#) [CONSTRAIN](#)
- Identity Double [SHOW](#) [CONSTRAIN](#)
- Length Integer [SHOW](#) [CONSTRAIN](#)
- DB identifier [SHOW](#) [CONSTRAIN](#)
- Target Chromosome [SHOW](#) [CONSTRAIN](#)
- Target End Integer [SHOW](#) [CONSTRAIN](#)
- Target Segment [SHOW](#) [CONSTRAIN](#)
- Target Start Integer [SHOW](#) [CONSTRAIN](#)
- Used For Classification Boolean [SHOW](#) [CONSTRAIN](#)
- Child Features Sequence Feature [SUMMARY](#) [CONSTRAIN](#)
- Consensus Consensus [SUMMARY](#) [CONSTRAIN](#)
 - TE classification code [SHOW](#) [CONSTRAIN](#)
 - Copies Integer [SHOW](#) [CONSTRAIN](#)
 - Cumulative genome coverage Integer [SHOW](#) [CONSTRAIN](#)
 - Fragments Integer [SHOW](#) [CONSTRAIN](#)
 - Full-length copies Integer [SHOW](#) [CONSTRAIN](#)
 - Full-length fragments Integer [SHOW](#) [CONSTRAIN](#)
 - Length Integer [SHOW](#) [CONSTRAIN](#)
 - Miscellaneous classification [SHOW](#) [CONSTRAIN](#)
 - Potential Chimeric Boolean [SHOW](#) [CONSTRAIN](#)
 - Consensus identifier [SHOW](#) [CONSTRAIN](#)
- Classification Wicker Classif Term [SUMMARY](#) [CONSTRAIN](#)

Show empty fields

Query Overview

- Consensus copy
 - Target Chromosome [X](#)
 - = Chr04 [X](#) [B](#)
 - Target End [X](#)
 - < 15000000 [X](#) [D](#)
 - Target Start [X](#)
 - > 13000000 [X](#) [C](#)
- Consensus Consensus [X](#) [B](#)
 - TE classification code [X](#)
 - Copies [X](#)
 - Consensus identifier [X](#)
- Organism Organism [X](#) [B](#)
 - Genus [X](#)
 - = Malus [X](#) [A](#)
 - Species [X](#)

Constraint logic: A and B and C and D

A and B and C and D

Fields selected for output

Columns to Display

Use the [SHOW](#) or [SUMMARY](#) links to add fields to the results table. Click and drag the blue output boxes to choose the output column order. Click [↑↓](#) to choose a column to sort results by, click again to select ascending [↑](#) or descending [↓](#). Use the [REMOVE ALL](#) link to remove all fields from the results table.

[REMOVE ALL](#)

Consensus copy > Organism > Genus X (no description) ↑↓	Consensus copy > Organism > Species X (no description) ↑↓	Consensus copy > Target Chromosome X (no description) ↑↓	Consensus copy > Target Start X (no description) ↑↓
Consensus copy > Target End X (no description) ↑↓	Consensus copy > Consensus > TE classification code X (no description) ↑↓	Consensus copy > Consensus > Consensus identifier X (no description) ↑↓	
Consensus copy > Consensus > Copies X (no description) ↑↓			



Trail: [Query](#) > Results

Showing 1 to 25 of 543 rows

Rows per page:

 page 1

Organism Genus	Organism Species	Consensus copy Target Chromosome	Consensus copy Target Start	Consensus copy Target End	Consensus TE classification code	Consensus Consensus identifier	Consensus Copies
Malus	domestica	Chr04	13000126	13000212	Class I : LTR : Gypsy	RLG_denovoMDO_kr-B-R7325-Map7_reversed	162
Malus	domestica	Chr04	13000282	13000325	Class II : TIR : hAT	DTX-hAT_denovoMDO_kr-B-G6122-Map17	104
Malus	domestica	Chr04	13000350	13000441	Class II : TIR : hAT	DTX-hAT_denovoMDO_kr-B-G6025-Map15	171
Malus	domestica	Chr04	13000442	13000711	Class II : TIR : hAT	DTX-hAT_denovoMDO_kr-B-G6122-Map17	104
Malus	domestica	Chr04	13000712	13003346	Class I : LTR : Gypsy	RLG_denovoMDO_kr-B-G8388-Map5	724
Malus	domestica	Chr04	13003350	13004845	Class I : LTR : Gypsy	RLG_denovoMDO_kr-B-R12988-Map5_reversed	54
Malus	domestica	Chr04	13003511	13003577	Class I : LTR : Gypsy	RLG_denovoMDO_kr-B-R507-Map8_reversed	12
Malus	domestica	Chr04	13004846	13004882	Class I : LTR : Gypsy	RLG_denovoMDO_kr-B-R15553-Map9	168
Malus	domestica	Chr04	13005322	13005445	Class I : LTR : Copia	HODOR-RLC-tork-like_denovoMDO_kr-B-G8255-Map20	414
Malus	domestica	Chr04	13006438	13006727	Class II : ? : ?	DXX_denovoMDO_kr-B-G10439-Map5	1304
Malus	domestica	Chr04	13006909	13007012	Class I : LTR : ?	RLX_denovoMDO_kr-B-G1136-Map20	198
Malus	domestica	Chr04	13008031	13008182	Class II : TIR : PIF-Harbinger	DTX-PIF-Harbinger_denovoMDO_kr-B-R1096-Map6	661
Malus	domestica	Chr04	13008306	13008729	Class I : LTR : Gypsy	RLG_denovoMDO_kr-B-R15959-Map7	477
Malus	domestica	Chr04	13009142	13009290	Class II : TIR : hAT	DTX-hAT_denovoMDO_kr-B-R5292-Map9	174
Malus	domestica	Chr04	13009437	13009600	Class II : TIR : Mutator	DTX-MuDR_denovoMDO_kr-B-R8793-Map6	427
Malus	domestica	Chr04	13010776	13012193	Class I : LTR : Gypsy	RLG_denovoMDO_kr-B-R2550-Map9_reversed	2462
Malus	domestica	Chr04	13011447	13011479	Class I : LTR : ?	RLX-solo-LTR_denovoMDO_kr-B-R799-Map14	705
Malus	domestica	Chr04	13011818	13011854	Class I : LTR : ?	RLX-solo-LTR_denovoMDO_kr-B-R799-Map14	705



Download results for query

Download TSV file

File name

results

.tsv

All Columns

All Rows

A flat file format suitable for spreadsheet programmes

No Compression

Destination

Formatted Column Headers

Preview

- Download file
- Send to Galaxy
- Upload to Genomespace

Close

Download file

Export

Trail: Query > Results

Manage Columns

Manage




showing 1 to 25 of 543 rows




Organism Genus	Organism Species	Consensus Target					Consensus Copies
Malus	domestica	Chr04					162
Malus	domestica	Chr04					104
Malus	domestica	Chr04					171
Malus	domestica	Chr04	13000442	13000711	Class II : TIR : hAT	DTX-hAT_denovoMDO_kr-B-G6122-Map17	104
Malus	domestica	Chr04	13000712	13003346	Class I : LTR : Gypsy	RLG_denovoMDO_kr-B-G8388-Map5	724
Malus	domestica	Chr04	13003350	13004845	Class I : LTR : Gypsy	RLG_denovoMDO_kr-B-R12988-Map5_reversed	54
Malus	domestica	Chr04	13003511	13003577	Class I : LTR : Gypsy	RLG_denovoMDO_kr-B-R507-Map8_reversed	12
Malus	domestica	Chr04	13004846	13004882	Class I : LTR : Gypsy	RLG_denovoMDO_kr-B-R15553-Map9	168
Malus	domestica	Chr04	13005322	13005445	Class I : LTR : Copia	HODOR-RLC-tork-like_denovoMDO_kr-B-G8255-Map20	414
Malus	domestica	Chr04	13006438	13006727	Class II : ? : ?	DXX_denovoMDO_kr-B-G10439-Map5	1304
Malus	domestica	Chr04	13006909	13007012	Class I : LTR : ?	RLX_denovoMDO_kr-B-G1136-Map20	198
Malus	domestica	Chr04	13008031	13008182	Class II : TIR : PIF-Harbinger	DTX-PIF-Harbinger_denovoMDO_kr-B-R1096-Map6	661
Malus	domestica	Chr04	13008306	13008729	Class I : LTR : Gypsy	RLG_denovoMDO_kr-B-R15959-Map7	477
Malus	domestica	Chr04	13009142	13009290	Class II : TIR : hAT	DTX-hAT_denovoMDO_kr-B-R5292-Map9	174
Malus	domestica	Chr04	13009437	13009600	Class II : TIR : Mutator	DTX-MuDR_denovoMDO_kr-B-R8793-Map6	427
Malus	domestica	Chr04	13010776	13012193	Class I : LTR : Gypsy	RLG_denovoMDO_kr-B-R2550-Map9_reversed	2462
Malus	domestica	Chr04	13011447	13011479	Class I : LTR : ?	RLX-solo-LTR_denovoMDO_kr-B-R799-Map14	705
Malus	domestica	Chr04	13011818	13011854	Class I : LTR : ?	RLX-solo-LTR_denovoMDO_kr-B-R799-Map14	705
Malus	domestica	Chr04	13012249	13012468	Class I : SINE : ?	RSX-chim_denovoMDO_kr-B-R18724-Map13	5403









Consensus copy > Target End	Organism > Genus	Consensus copy > Consensus	TE classification code	Consensus copy > Consensus	Consensus copy > Consensus	Consensus copy > Consensus identifier	Consensus copy > Target Start	Consensus copy > Consensus > Copies
Malus domestica	Chr04	13000126	13000212	Class I : LTR : Gypsy	RLG_denovoMDO_kr-B-R7325-Map7_reversed	162		
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Malus domestica	Chr04	13011447	13011479	Class I : LTR : ?	RLX-solo-LTR_denovoMDO_kr-B-R799-Map14	705		
Malus domestica	Chr04	13011818	13011854	Class I : LTR : ?	RLX-solo-LTR_denovoMDO_kr-B-R799-Map14	705		
Malus domestica	Chr04	13012249	13012468	Class I : SINE : ?	RSX-chim_denovoMDO_kr-B-R18724-Map13	5403		
Malus domestica	Chr04	13015880	13015964	""	PHG_denovoMDO_kr-B-R15757-Map5	624		
Malus domestica	Chr04	13015976	13016083	Class II : TIR : Mutator	DTX-MuDR_denovoMDO_kr-B-R6665-Map5	546		
Malus domestica	Chr04	13016213	13018386	Class I : LTR : Gypsy	RLG_denovoMDO_kr-B-R2115-Map14_reversed	418		
Malus domestica	Chr04	13018387	13018976	Class I : LTR : Gypsy	RLG_denovoMDO_kr-B-G1880-Map5	288		
Malus domestica	Chr04	13019040	13019070	Class I : LTR : Gypsy	RLG_denovoMDO_kr-B-R2156-Map20	346		
Malus domestica	Chr04	13019071	13022351	Class I : LTR : Gypsy	RLG_denovoMDO_kr-B-G8309-Map6_reversed	382		
Malus domestica	Chr04	13022352	13024607	Class I : LTR : Gypsy	RLG_denovoMDO_kr-B-R2156-Map20	346		
Malus domestica	Chr04	13024637	13025005	Class I : LTR : Gypsy	RLG_denovoMDO_kr-B-G5089-Map5	149		
Malus domestica	Chr04	13025006	13026050	Class I : LTR : ?	RLX_denovoMDO_kr-B-R24618-Map8	42		
Malus domestica	Chr04	13026066	13027459	Class I : LTR : Gypsy	RLG_denovoMDO_kr-B-R2115-Map14_reversed	418		
Malus domestica	Chr04	13027631	13027752	Class II : TIR : Mutator	DTX-MuDR_denovoMDO_kr-B-R6665-Map5	546		
Malus domestica	Chr04	13027767	13027898	Class I : LTR : ?	RLX_denovoMDO_kr-B-R14839-Map5	931		
Malus domestica	Chr04	13028077	13028190	Class II : TIR : Mutator	DTX-MuDR_denovoMDO_kr-B-R6665-Map5	546		
Malus domestica	Chr04	13028487	13028621	Class II : TIR : Mutator	DTX-MuDR_denovoMDO_kr-B-R6665-Map5	546		
Malus domestica	Chr04	13028958	13029823	Class II : TIR : hAT	DTX-hAT_denovoMDO_kr-B-G2078-Map20	257		
Malus domestica	Chr04	13030040	13031717	Class I : LTR : Gypsy	RLG_denovoMDO_kr-B-G7816-Map7	660		
Malus domestica	Chr04	13030289	13030467	Class I : LTR : Gypsy	RLG_denovoMDO_kr-B-P166.84-Map20_reversed	108		
Malus domestica	Chr04	13030811	13031109	Class I : LTR : Gypsy	RLG_denovoMDO_kr-B-G4335-Map6_reversed	118		
Malus domestica	Chr04	13033327	13033391	Class I : LTR : Copia	RLC_denovoMDO_kr-B-G8285-Map10_reversed	43		




REMOVE ALL




Consensus copy > Organism > Genus 
(no description) 





Consensus copy > Organism > Species 
(no description) 





Consensus copy > Target Chromosome 
(no description) 


Consensus copy > Target Start 
(no description) 


Consensus copy > Target End 
(no description) 


Consensus copy > Consensus > TE classification code 
(no description) 


Consensus copy > Consensus > Consensus identifier 
(no description) 



Consensus copy > Consensus > Copies 
(no description) 


Show results

 web service URL

[Perl](#) | [Python](#) | [Ruby](#) | [Java \[help\]](#)

[Export XML](#)

 Start building a template query

Save the query

is_13000000-15000000

Save query

Malus_Chr4_consensus_copies_13000000-15000000

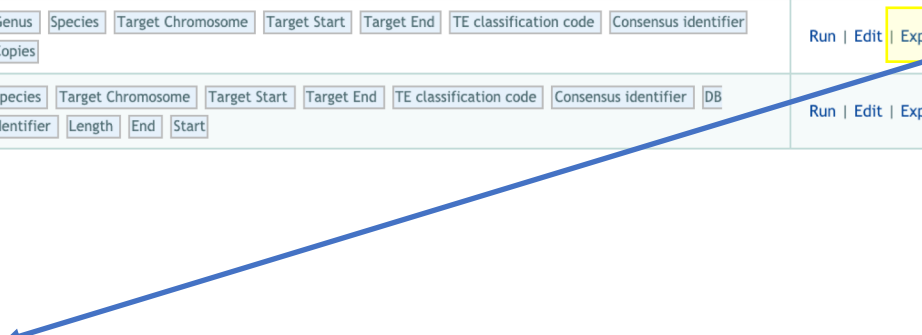
Query builder

view saved queries

Queries that you have saved

QUERY NAME	CREATED	APPROX ROWS	START	RESULTS FORMAT	ACTIONS
Malus_Chr4_consensus_copies_13000000-15000000	2018-12-26 12:50	n/a	Consensus copy	Genus Species Target Chromosome Target Start Target End TE classification code Consensus identifier Copies	Run Edit Export
query_11	2018-04-27 13:24	n/a	Consensus copy	Species Target Chromosome Target Start Target End TE classification code Consensus identifier DB identifier Length End Start	Run Edit Export

Delete Export



```
<query name="Malus_Chr4_consensus_copies_13000000-15000000" model="genomic" view="ConsensusCopy.organism.genus ConsensusCopy.organism.species ConsensusCopy.targetChromosome ConsensusCopy.targetStart ConsensusCopy.targetEnd ConsensusCopy.consensus.classificationCode ConsensusCopy.consensus.primaryIdentifier ConsensusCopy.consensus.copies" longDescription="" sortOrder="ConsensusCopy.organism.genus asc" constraintLogic="A and B and C and D">
  <constraint path="ConsensusCopy.organism.genus" code="A" op="=" value="Malus"/>
  <constraint path="ConsensusCopy.targetChromosome" code="B" op="=" value="Chr04"/>
  <constraint path="ConsensusCopy.targetStart" code="C" op=">" value="13000000"/>
  <constraint path="ConsensusCopy.targetEnd" code="D" op="<" value="15000000"/>
</query>
```



Home

Generated Python Code for Query



Log in

GO

Trail: [Query](#) > Results

Manage Columns

Manage

Showing 1 to 25 of 543 rows

Organism Genus	Organism Species	Cons Target					Consensus Copies
Malus	domestica	Chr04					162
Malus	domestica	Chr04					104
Malus	domestica	Chr04					171
Malus	domestica	Chr04					104
Malus	domestica	Chr04					724
Malus	domestica	Chr04	13003350	13004845	Class I : LTR : Gypsy	RLG_denovoMDO_kr-B-R12988-Map5_reversed	54
Malus	domestica	Chr04	13003511	13003577	Class I : LTR : Gypsy	RLG_denovoMDO_kr-B-R507-Map8_reversed	12
Malus	domestica	Chr04	13004846	13004882	Class I : LTR : Gypsy	RLG_denovoMDO_kr-B-R15553-Map9	168
Malus	domestica	Chr04	13005322	13005445	Class I : LTR : Copia	HODOR-RLC-tork-like_denovoMDO_kr-B-G8255-Map20	414
Malus	domestica	Chr04	13006438	13006727	Class II : ? : ?	DXX_denovoMDO_kr-B-G10439-Map5	1304
Malus	domestica	Chr04	13006909	13007012	Class I : LTR : ?	RLX_denovoMDO_kr-B-G1136-Map20	198
Malus	domestica	Chr04	13008031	13008182	Class II : TIR : PIF-Harbinger	DTX-PIF-Harbinger_denovoMDO_kr-B-R1096-Map6	661
Malus	domestica	Chr04	13008306	13008729	Class I : LTR : Gypsy	RLG_denovoMDO_kr-B-R15959-Map7	477
Malus	domestica	Chr04	13009142	13009290	Class II : TIR : hAT	DTX-hAT_denovoMDO_kr-B-R5292-Map9	174
Malus	domestica	Chr04	13009437	13009600	Class II : TIR : Mutator	DTX-MuDR_denovoMDO_kr-B-R8793-Map6	427
Malus	domestica	Chr04	13010776	13012193	Class I : LTR : Gypsy	RLG_denovoMDO_kr-B-R2550-Map9_reversed	2462
Malus	domestica	Chr04	13011447	13011479	Class I : LTR : ?	RLX-solo-LTR_denovoMDO_kr-B-R799-Map14	705
Malus	domestica	Chr04	13011818	13011854	Class I : LTR : ?	RLX-solo-LTR_denovoMDO_kr-B-R799-Map14	705

Python ▾

Show comments

Highlight Syntax

```

from intermine.webservice import Service
service = Service("http://urgi.versailles.inra.fr//repetdb/service")
query = service.new_query("ConsensusCopy")
query.add_view(
    "organism.genus", "organism.species", "targetChromosome", "targetStart",
    "targetEnd", "consensus.classificationCode", "consensus.primaryIdentifier",
    "consensus.copies"
)
query.add_constraint("organism.genus", "=", "Malus", code = "A")
query.add_constraint("targetChromosome", "=", "Chr04", code = "B")
query.add_constraint("targetStart", ">", "13000000", code = "C")
query.add_constraint("targetEnd", "<", "15000000", code = "D")

for row in query.rows():
    print row["organism.genus"], row["organism.species"], row["targetChromosome"], \
          row["targetStart"], row["targetEnd"], row["consensus.classificationCode"], \
          row["consensus.primaryIdentifier"], row["consensus.copies"]

```

Close

Save

Export



```
query.py > No Selection
1 #!/usr/bin/env python
2
3 # This is an automatically generated script to run your query
4 # to use it you will require the intermine python client.
5 # To install the client, run the following command from a terminal:
6 #
7 #     sudo easy_install intermine
8 #
9 # For further documentation you can visit:
10 #     http://intermine.readthedocs.org/en/latest/web-services/
11
12 # The following two lines will be needed in every python script:
13 from intermine.webservice import Service
14 service = Service("http://urgi.versailles.inra.fr//repetdb/service")
15
16 # Get a new query on the class (table) you will be querying:
17 query = service.new_query("ConsensusCopy")
18
19 # The view specifies the output columns
20 query.add_view(
21     "organism.genus", "organism.species", "targetChromosome", "targetStart",
22     "targetEnd", "consensus.classificationCode", "consensus.primaryIdentifier",
23     "consensus.copies"
24 )
25
26 # Uncomment and edit the line below (the default) to select a custom sort order:
27 # query.add_sort_order("ConsensusCopy.organism.genus", "ASC")
28
29 # You can edit the constraint values below
30 query.add_constraint("organism.genus", "=", "Malus", code = "A")
31 query.add_constraint("targetChromosome", "=", "Chr04", code = "B")
32 query.add_constraint("targetStart", ">", "13000000", code = "C")
33 query.add_constraint("targetEnd", "<", "15000000", code = "D")
34
35 # Uncomment and edit the code below to specify your own custom logic:
36 # query.set_logic("A and B and C and D")
37
38 for row in query.rows():
39     print row["organism.genus"], row["organism.species"], row["targetChromosome"], \
40           row["targetStart"], row["targetEnd"], row["consensus.classificationCode"], \
41           row["consensus.primaryIdentifier"], row["consensus.copies"]
42
43
```

Request : reuse the previous query and change the query name and coordinates

- Get All the copies corresponding to:

Genome genus = “Malus”

Region= Chr4: 10000000..13000000

- Display the copies coordinates, the consensus classification and identifier



QueryBuilder

Advanced users can use a flexible query interface to construct their own data mining queries. The QueryBuilder lets you view the data model, apply constraints and select output. You can also export queries to share them with others.

[Browse data model](#)

[Import query from XML](#)

[View saved queries](#)

Select a Data Type to Begin a Query

Click on a class name for a description or double click on a class name to create a new query starting at that class

Consensus

-
- Bio-Entity
- Blast hit
- BlastN hit
- tBlastX hit
- BlastX hit
- Chromosome
- Consensus
- Consensus copy

Select

Query History

Queries that you have run during this session

<input type="checkbox"/>	QUERY NAME	CREATED	APPROX ROWS	START	RESULTS FORMAT	ACTIONS
<input type="checkbox"/>	query_1	2018-12-26 12:28	n/a	Consensus copy	<input type="text" value="Genus"/> <input type="text" value="Species"/> <input type="text" value="Target Chromosome"/> <input type="text" value="Target Start"/> <input type="text" value="Target End"/> <input type="text" value="TE classification code"/> <input type="text" value="Consensus identifier"/> <input type="text" value="Copies"/>	Run Edit Save Export

Enter a query in XML format or upload a query from a file and press 'Submit' to load the query into your account.

Type/Paste in the query XML:

```
<query name="Malus_Chr4_consensus_copies_10000000-13000000"
model="genomic" view="ConsensusCopy.organism.genus
ConsensusCopy.organism.species ConsensusCopy.targetChromosome
ConsensusCopy.targetStart ConsensusCopy.targetEnd
ConsensusCopy.consensus.classificationCode
ConsensusCopy.consensus.primaryIdentifier ConsensusCopy.consensus.copies"
longDescription="" sortOrder="ConsensusCopy.organism.genus asc"
constraintLogic="A and B and C and D">
  <constraint path="ConsensusCopy.organism.genus" code="A" op="="
value="Malus"/>
  <constraint path="ConsensusCopy.targetChromosome" code="B" op="="
value="Chr04"/>
  <constraint path="ConsensusCopy.targetStart" code="C" op=">";"
value="10000000"/>
  <constraint path="ConsensusCopy.targetEnd" code="D" op="&lt;"
value="13000000"/>
</query>
```

OR upload the template from
a .txt file...:

Aucun fichier choisi

NOTE:

- Queries with names identical to existing queries will get an automatic extension to make it unique, e.g. dmel-proteins-1, dmel-proteins-2
- Names may not contain special characters. Special characters in names will be replaced with their word-equivalent, e.g. "a&b" will be imported as "a_AMPERSAND_b"

Copy-Paste the
previous request
in XML format

And submit



Model browser



Browse through the classes and attributes. Click on [SUMMARY](#) links to add summary of fields to the results table or on [SHOW](#) links to add individual fields to the results. Use [CONSTRAIN](#) links to constrain a value in the query.

- Consensus copy [SUMMARY](#) [CONSTRAIN](#)
- Genome Jbrowse Url [SHOW](#) [CONSTRAIN](#)
- Identity Double [SHOW](#) [CONSTRAIN](#)
- Length Integer [SHOW](#) [CONSTRAIN](#)
- DB identifier [SHOW](#) [CONSTRAIN](#)
- Target Chromosome [SHOW](#) [CONSTRAIN](#)
- Target End Integer [SHOW](#) [CONSTRAIN](#)
- Target Segment [SHOW](#) [CONSTRAIN](#)
- Target Start Integer [SHOW](#) [CONSTRAIN](#)
- Used For Classification Boolean [SHOW](#) [CONSTRAIN](#)
- Child Features Sequence Feature [SUMMARY](#) [CONSTRAIN](#)
- Consensus Consensus [SUMMARY](#) [CONSTRAIN](#)
- Data Sets Data Set [SUMMARY](#) [CONSTRAIN](#)
- Locations Location [SUMMARY](#) [CONSTRAIN](#)
- Organism Organism [SUMMARY](#) [CONSTRAIN](#)
- Parent Feature Sequence Feature [SUMMARY](#) [CONSTRAIN](#)
- Target Sequence Feature [SUMMARY](#) [CONSTRAIN](#)

Show empty fields

Query Overview

Consensus copy

Target Chromosome

= Chr04 (B)

Target End

< 13000000 (D)

Target Start

> 10000000 (C)

Consensus Consensus

TE classification code

Copies

Consensus identifier

Organism Organism

Genus

= Malus (A)

Species

Constraint logic: A and B and C and D

A and B and C and D

Fields selected for output

Columns to Display

Use the [SHOW](#) or [SUMMARY](#) links to add fields to the results table. Click and drag the blue output boxes to choose the output column order. Click [?](#) to choose a column to sort results by, click again to select ascending [?](#) or descending [?](#). Use the [REMOVE ALL](#) link to remove all fields from the results table.

[REMOVE ALL](#)

Consensus copy > Organism > Genus <input type="checkbox"/> (no description) <input type="checkbox"/>	Consensus copy > Organism > Species <input type="checkbox"/> (no description) <input type="checkbox"/>	Consensus copy > Target Chromosome <input type="checkbox"/> (no description) <input type="checkbox"/>	Consensus copy > Target Start <input type="checkbox"/> (no description) <input type="checkbox"/>
Consensus copy > Target End <input type="checkbox"/> (no description) <input type="checkbox"/>	Consensus copy > Consensus > TE classification code <input type="checkbox"/> (no description) <input type="checkbox"/>	Consensus copy > Consensus > Consensus identifier <input type="checkbox"/> (no description) <input type="checkbox"/>	
Consensus copy > Consensus > Copies <input type="checkbox"/> (no description) <input type="checkbox"/>			

Request : reuse the previous query

- Get All the copies corresponding to:

Genome genus = “Malus”

Region= Chr4: 10000000..13000000

- Display the genome copies coordinates, the consensus classification and identifier

and new columns to display

- copy identifier
- consensus fragment coordinates (One copy may be constituted by 2 or more fragments joined)

Query builder

➤ view saved queries

3000000" Hide

QUERY NAME	CREATED	APPROX ROWS	START	RESULTS FORMAT	ACTIONS
query_11	2018-04-27 13:24	n/a	Consensus copy	Species Target Chromosome Target Start Target End TE classification code Consensus identifier DB identifier Length End Start	Run Edit Export
Malus_Chr4_consensus_copies_13000000-15000000	2018-12-26 12:50	10	Consensus copy	Genus Species Target Chromosome Target Start Target End TE classification code Consensus identifier Copies	Run Edit Export
Malus_Chr4_consensus_copies_10000000-13000000	2018-12-26 13:24	11	Consensus copy	Genus Species Target Chromosome Target Start Target End TE classification code Consensus identifier Copies	Run Edit Export

Delete Export

[Import query from XML](#)



Browse through the classes and attributes. Click on [SUMMARY](#) links to add summary of fields to the results table or on [SHOW](#) links to add individual fields to the results. Use [CONSTRAIN](#) links to constrain a value in the query.

Consensus copy [SUMMARY](#) [CONSTRAIN](#)

- Genome Jbrowse Url [SHOW](#) [CONSTRAIN](#)
- Identity Double [SHOW](#) [CONSTRAIN](#)
- Length Integer [SHOW](#) [CONSTRAIN](#)
- DB identifier [SHOW](#) [CONSTRAIN](#)
- Target Chromosome [SHOW](#) [CONSTRAIN](#)
- Target End Integer [SHOW](#) [CONSTRAIN](#)
- Target Segment [SHOW](#) [CONSTRAIN](#)
- Target Start Integer [SHOW](#) [CONSTRAIN](#)
- Used For Classification Boolean [SHOW](#) [CONSTRAIN](#)
- Child Features Sequence Feature [SUMMARY](#) [CONSTRAIN](#)
 - Length Integer [SHOW](#) [CONSTRAIN](#)
 - Name [SHOW](#) [CONSTRAIN](#)
 - DB identifier [SHOW](#) [CONSTRAIN](#)
- Cross References Cross Reference [SUMMARY](#) [CONSTRAIN](#)
- Data Sets Data Set [SUMMARY](#) [CONSTRAIN](#)
- Located Features Location [SUMMARY](#) [CONSTRAIN](#)
- Locations Location [SUMMARY](#) [CONSTRAIN](#)
- Ontology Annotations Ontology Annotation [SUMMARY](#) [CONSTRAIN](#)
- Organism Organism [SUMMARY](#) [CONSTRAIN](#)
- Parent Feature Sequence Feature [SUMMARY](#) [CONSTRAIN](#)
- Sequence Sequence [SUMMARY](#) [CONSTRAIN](#)
- Consensus Consensus [SUMMARY](#) [CONSTRAIN](#)
- Data Sets Data Set [SUMMARY](#) [CONSTRAIN](#)
- Locations Location [SUMMARY](#) [CONSTRAIN](#)
- Feature Bio-Entity
 - End Integer [SHOW](#) [CONSTRAIN](#)
 - Start Integer [SHOW](#) [CONSTRAIN](#)

Consensus copy

- Target Chromosome [X](#)
 - = Chr04 [X](#) [\(B\)](#)
- Target End [X](#)
- < 13000000 [X](#) [\(D\)](#)
- Target Start [X](#)
 - > 10000000 [X](#) [\(C\)](#)
- Child Features Sequence Feature collection [X](#) [\(E\)](#)
 - Length [X](#)
 - DB identifier [X](#)
- Consensus Consensus [X](#) [\(F\)](#)
 - TE classification code [X](#)
 - Copies [X](#)
 - Consensus identifier [X](#)
- Locations Location collection [X](#) [\(G\)](#)
 - End [X](#)
 - Start [X](#)
- Organism Organism [X](#) [\(H\)](#)
 - Genus [X](#)
 - = Malus [X](#) [\(A\)](#)
 - Species [X](#)

Constraint logic: A and B and C and D

A and B and C and D

Columns to Display

Use the [SHOW](#) or [SUMMARY](#) links to add fields to the results table. Click and drag the blue output boxes to choose the output column order. Click [\[1\]](#) to choose a column to sort results by, click again to select ascending [\[1\]](#) or descending [\[1\]](#). Use the [REMOVE ALL](#) link to remove all fields from the results table.

[REMOVE ALL](#)

Consensus copy > Organism > Genus X (no description) [1]	Consensus copy > Organism > Species X (no description) [1]	Consensus copy > Target Chromosome X (no description) [1]	Consensus copy > Target Start X (no description) [1]
Consensus copy > Target End X (no description) [1]	Consensus copy > Consensus > TE classification code X (no description) [1]	Consensus copy > Consensus > Consensus identifier X (no description) [1]	
Consensus copy > Consensus > Copies X (no description) [1]	Consensus copy > Child Features > DB identifier X (no description) [1]	Consensus copy > Child Features > Length X (no description) [1]	
Consensus copy > Locations > Start X (no description) [1]	Consensus copy > Locations > End X (no description) [1]		



Trail: Query > Results

Manage Columns d'écran

Manage Filters

Manage Relationships

Save as List

Generate Python code

Export

Showing 1 to 25 of 6,090 rows

Rows per page:

25 [Navigation icons]

Organism Genus	Organism Species	Consensus copy Target Chromosome	Consensus copy Target Start	Consensus copy Target End	Consensus TE classification code	Consensus identifier	Consensus Copies	Child Features DB Identifier	Child Features Length	Locations Start	Locations End
Malus	domestica	Chr04	10002796	10002837	Class I : LTR : Gypsy	RLG_denovoMDO_kr-B-G8337-Map5	110	mp52473-1_RLG_denovoMDO_kr-B-G8337-Map5_Ch04	43	6776	6819
Malus	domestica	Chr04	10002796	10002837	Class I : LTR : Gypsy	RLG_denovoMDO_kr-B-G8337-Map5	110	mp52473-1_RLG_denovoMDO_kr-B-G8337-Map5_Ch04	43	10002796	10002837
Malus	domestica	Chr04	10002850	10007409	Class I : LTR : Gypsy	RLG-tat-like_denovoMDO_kr-B-G539-Map11	391	mp52464-1_RLG-tat-like_denovoMDO_kr-B-G539-Map11_Ch04	726	3818	8344
Malus	domestica	Chr04	10002850	10007409	Class I : LTR : Gypsy	RLG-tat-like_denovoMDO_kr-B-G539-Map11	391	mp52464-1_RLG-tat-like_denovoMDO_kr-B-G539-Map11_Ch04	726	10002850	10007409
Malus	domestica	Chr04	10002850	10007409	Class I : LTR : Gypsy	RLG-tat-like_denovoMDO_kr-B-G539-Map11	391	mp52464-2_RLG-tat-like_denovoMDO_kr-B-G539-Map11_Ch04	3673	3818	8344
Malus	domestica	Chr04	10002850	10007409	Class I : LTR : Gypsy	RLG-tat-like_denovoMDO_kr-B-G539-Map11	391	mp52464-2_RLG-tat-like_denovoMDO_kr-B-G539-Map11_Ch04	3673	10002850	10007409
Malus	domestica	Chr04	10007417	10007972	Class I : LTR : Gypsy	RLG_denovoMDO_kr-B-G8376-Map12_reversed	1569	mp52525-1_RLG_denovoMDO_kr-B-G8376-Map12_reversed_Ch04	283	7622	8284
Malus	domestica	Chr04	10007417	10007972	Class I : LTR : Gypsy	RLG_denovoMDO_kr-B-G8376-Map12_reversed	1569	mp52525-1_RLG_denovoMDO_kr-B-G8376-Map12_reversed_Ch04	283	10007417	10007972
Malus	domestica	Chr04	10007417	10007972	Class I : LTR : Gypsy	RLG_denovoMDO_kr-B-G8376-Map12_reversed	1569	mp52525-2_RLG_denovoMDO_kr-B-G8376-Map12_reversed_Ch04	305	7622	8284
Malus	domestica	Chr04	10007417	10007972	Class I : LTR : Gypsy	RLG_denovoMDO_kr-B-G8376-Map12_reversed	1569	mp52525-2_RLG_denovoMDO_kr-B-G8376-Map12_reversed_Ch04	305	10007417	10007972
Malus	domestica	Chr04	10007978	10008447	Class I : LTR : Copia	RLC_denovoMDO_kr-B-P299.362-Map20_reversed	108	mp52531-1_RLC_denovoMDO_kr-B-P299.362-Map20_reversed_Ch04	498	7	505

