

NEXPLORER USER GUIDE

1. General Information

1.1. PURPOSE OF NEXPLORER

Nexplorer is a database containing authorised GMO events and links to their respective annotated DNA sequences. It is made available as a web-application offering a user-friendly interface that allows non-IT experts to manage the database and the sequences. This application gives the GMOLab a secure way to store the data by the use of functionalities such as change tracking and confidentiality management.

1.2. SYSTEM REQUIREMENTS

Nexplorer can be used with Chrome or Firefox (with both cookies and JavaScript enabled) inside a Windows or Linux operating system. The web application is not compatible with Internet Explorer due to its lack of support for standardised CSS format, leading to display issues.

1.3. ACCESSIBILITY

The dedicated web interface can be reached at the following address: <https://nexplorer.sciensano.be>. Only public data are available to anonymous users; confidential data are restricted to authenticated users. The database administrators are responsible of the account creation. They will provide the credentials to the new users upon request.

1.4. HOME PAGE

Two sections are available from the home page: the 'Search' and the 'Login' sections. The 'Align' link is a placeholder for future developments and is not active yet.

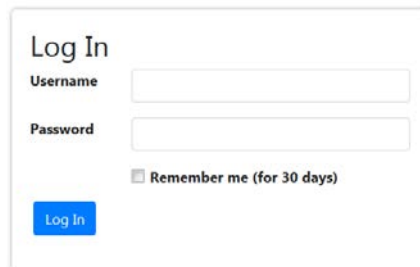


Welcome to Nexplorer !
Version 1.0



2. User Account

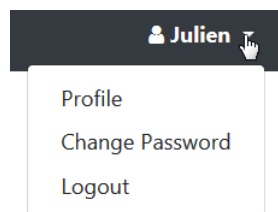
2.1. LOGIN FORM



A login form titled "Log In". It contains two input fields: "Username" and "Password". Below the password field is a checkbox labeled "Remember me (for 30 days)". At the bottom left is a blue button labeled "Log In".

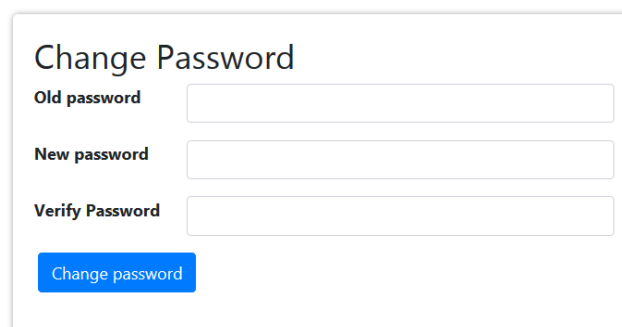
2.2. ONCE LOGGED

Once logged in, you will be able to see confidential data. You also will have access to three additional options, which can be found under your username.



A user profile dropdown menu. The header bar is dark grey and contains a user icon, the name "Julien", and a cursor icon. The dropdown menu is white and contains three options: "Profile", "Change Password", and "Logout".

The password change requires your previous password and a duplicate of the new one as double confirmation method.



A form titled "Change Password". It contains three input fields: "Old password", "New password", and "Verify Password". At the bottom is a blue button labeled "Change password".

Profile

First name

Last name

E-mail

bioit@sciensano.be

Username

Apply changes

You can also change your first name, last name and username through the profile menu. Your e-mail can only be changed by a database administrator.

3. Search for Events

3.1. THE SEARCH FORM

Search event

Search all events fulfilling the provided criteria. The lookup apply exact match (full and case sensitive) to all filters but 'Names', use their respective suggestions dropdown in case of doubt.

Names

OECD UIs

Organisms

Traits

Elements

☒ AND ☐ OR ☐ NOT

☒ AND ☐ OR ☐ NOT

☒ Include complex transformations

☒ Include confidential entries

Search

Reset

3.1.1. Names

Search terms match against event's name in a partial case-insensitive way. If several comma-separated terms are provided, an event will be returned if a least one term matches a subpart of its name.

3.1.2. OECD UIs

A full match (case sensitive) to a OECD UI will lead to the corresponding events to be returned. In case of multiple values, at least one of them must match. In case of doubt, feel free to use the provided suggestion dropdown list.

3.1.3. Organisms

A full match to organism's common name will lead to the corresponding linked events to be returned. Works identically to OECD UI search.

3.1.4. Traits

The search terms must match exactly the trait name. Furthermore, thanks to the hierarchical structure of traits, the trait search is (top-down) recursive. Simply said if you search for 'Pest resistance', all events linked to 'Coleoptera resistance' will also show up in the results.

Multiple value operators

- **Or** has an equivalent behaviour to others fields without logical operators: an event will be returned if it has at least one of the given traits (or descendants).
- **And** matches an event only if it is linked to each input trait (or respective descendants).
- **Not** matches all events not linked to any of the specified traits (and descendants).

3.1.5. Elements

A full match is applied for elements search terms against element's aliases. Aliases are the multiple alternative names of an element, defined by administrators. All available aliases are listed next to the search box.

Multiple value operators

- **Or** means that each returned event is linked to at least one of the selected elements.
- **And** returns events that are linked indirectly to all matching elements (aliases).
- **Not** matches all events not linked to any selected elements.

3.1.6. Reset button

The latest value of each search field of the form is saved by Nexplorer and automatically re-filled at the next search. This allows you to repeat the previous search when you go back to the search page as long as you do not change your session: delete your cookies, login/logout or close/change your browser. You can manually clean the form by clicking the reset button.

3.2. THE SEARCH RESULTS

Search results

Query filters

Data confidentiality: All
Stacked events: Included
Organisms: rice

Matching events All

											3 records found
Id	Host organism	OECD unique ID	Confidential	Descriptions	Type	Name	Alternatives names	Tradename	Company	Remarks	
☐ 34	rice	BCS-OS003-7	No	LLRice601 contain...	single	LLRICE601	GAT-OS3	Liberty Link	Bayer CropScience	NULL	Q View
☐ 35	rice	ACS-OS001-4	No	The rice line LLR...	single	LLRICE06	GAT-OS2	Liberty Link	Bayer CropScience	probably the same...	Q View
☐ 36	rice	ACS-OS002-5	No	The rice line LLR...	single	LLRICE62	GAT-OS1	Liberty Link	Bayer CropScience	probably the same...	Q View

Export: [CSV](#) [TSV \(Spreadsheets\)](#) [Tabular overview](#) [Elements overview](#)

Under 'Query filters' all search restrictions used to generate the results are listed. At the bottom, 'Matching Events' section displays the returned events in the form of an (CSV) exportable grid. After a selection of the events of interest, two overview visualisations are available: 'Tabular overview' and 'Elements overview'. Additionally, any displayed event is reachable through the corresponding 'View' button provided at the right side of the grid. Finally, the 'All' button allow you to (de)select all events in one go.

3.3. TABULAR OVERVIEW

Tabular Overview

	flank	RB	35S	nos	LB	35S	pat	bar
I_52_ACS-OS001-4	2		1			2	1	
I_51_BCS-OS003-7	2	1		2	1	2		1
All inserts	4	1	1	2	1	4	1	1

Lists all the elements that are present in the inserts of the selected events. Therefore, the application makes use of the sequences' annotations. The numbers represent the occurrence of each element in the sequences linked to each insert. Please note that this value can be different from the number of times the element is found in the insert, e.g. if a fraction of the insert is covered by multiple overlapping sequences or if a fraction of the insert is not covered by any sequences at all. By clicking on these numbers, you can download the corresponding insert-element sequences as a single multi-FASTA file. More detailed information about inserts or elements is available through the respective line/column header links.

3.4. ELEMENTS OVERVIEW

Elements Overview

I_51_BCS-OS003-7

flank

35S

bar

nos

flank

I_52_ACS-OS001-4

flank

35S

pat

35S

flank

Aligns all the archetypes of the inserts present in the selected events. Archetypes are visualisations made by the database administrators to illustrate the elements order in the insert, based on its related annotated sequences. As previously, all insert-specific details can be obtained through the inserts links.

4. Detailed Views

4.1. ELEMENT

Element 35S

Long name	CaMV 35S terminator	Standard name	T_35S_CaMV
Donor organism	Cauliflower mosaic virus	Abbreviation	35S
Subgroup	terminator	Description 	

Terminator sequence from the 35S RNA from the cauliflower mosaic virus genome (Similar to GenBank Accession Number AF140604, positions 7412-7680). Its function is to provide a polyadenylation sequence (Franck et al., 1980, Sanfaçon et al., 1991)

All the details on the selected element are accessible from the tabular overview column header (see section 3.3). The standard name is composed by joining the first letter(s) of the functional group of the element, its abbreviation and the element's donor organism abbreviation. Description can be hidden/shown by clicking on the blue arrow.

4.2. SEQUENCE

Sequence S_5_I_5_DP-073496-4 Not confidential

Elements



Full sequence FASTA

[Download file](#)

Traceable True

Description and sources ⓘ

sequence 11 obtained from patent US 8993238, which could be identified as a sequence of the transgenic insertion as it is (a) the longest sequence provided within the patent and (b) is composed of/completely covered by sequences 2, 12, 13, 14, 15, 16, 17, 18, and/or 19 that are stated to be the examples of the junction DNA in the patent and sequences 8, 9 and 3; includes insert and flanks

The upper part of the page gives an overview of the various elements present in the sequence, including their direction and order. You can download the sequence of any element by clicking on its representation or of the full sequence with the dedicated button.

The lower part of the page displays additional sequence-related information such as its traceability or sources. A sequence is traceable if it has a known linked patent.

4.3. INSERT

Insert I_6_DP-098140-6 Not confidential

Archetype



Sequences

No sequence

Transformation method

Agrobacterium tumefaciens

Real insert

True

Copy number

1

Vectors

ID	Name	Is confidential	Remarks
6	pHP24279	False	NULL

Remarks ⓘ

Related events

No event

Gives all the available information about the selected insert. If defined by the database administrators, the archetype is displayed under the insert name. It reflects the positions of the various elements inside the insert, summarising the information available from the underlying annotated sequences. Sequences section groups links to all insert sequences (see section 1.1).

If the field “Real insert” is true, the insert is identified unambiguously by at least one flanking sequence. Otherwise, the entry concerns a hypothetical insert, or a group of hypothetical inserts derived from the same vector(s).

Finally, more information about the insert itself is shown, including other events in which the insert is found, and a table of details about the vector(s) from which the insert has been derived.

4.4. EVENT

Event 123.2.38 Not confidential

OECD UI	FLO-40644-6	Alternatives names	40644
Organism	carnation	Company	Florigene Pty
Tradename	Moonlite, Florigene Moonlite	Stacked type	simple

Description ⓘ

Remarks

former oecd_ui: FLO-40644-4

Traits

- Colour modification
- Sulfonyleurea tolerance

The page summarises event details. OECD UI is the ID of the GMO event in the OECD [BioTrack](#) database. Stacked type indicates whether the event belongs to the ‘simple’, ‘stacked’ or ‘re-transform’ types. At the bottom of the page, a dedicated section provides an overview of the related inserts (see section 4.3), shown inside contiguous tabs to allow a quick navigation between them.