

Global information sharing: EUginius

GMO analysis and new genomic techniques

March 16th, Theo Prins (Wageningen food Safety Research)

The screenshot shows the top navigation bar with tabs for 'Protection', 'Analysis', and 'Assessment'. Below this is the 'Database System' header. The main content area is titled 'The European GMO database' and includes the following text:

EUginius (European GMO Initiative for a Unified Database System) is an initiative of BVL - the Federal Office (Berlin, DE) and VFSR - Wageningen Food Safety Research (formerly FSQ/L) of Wageningen UR (Wageningen, competent authorities and private users who seek accurate information on genetically modified organisms).

EUginius provides detailed information of major and relevant issues regarding the presence, detection and identification.

- with a focus on the situation in the European Union
- as well as world-wide coverage

Since the European Union classifies organisms developed using 'new genomic techniques' (NGTs) into the GMOs, EUginius commercialised organisms as well as about published ones which present market-relevant traits. Please note that EUginius exhaustive list of organisms developed with NGTs and presence of a market-relevant trait does not necessarily imply address.

Free-text search

Here you can perform any free-text keyword search on GMOs and literature. Use * as wildcard if necessary. Search for 'gene registered organisms developed using NGTs'.

Please also notice the advanced search options which are available below the respective search buttons for both GMOs and:

Search term: Search GMO Search Literature

[advanced GMO search](#) [advanced Literature search](#)

About the partners

- The Federal Office of Consumer Protection and Food Safety (BVL) fulfills many tasks in the
- Wageningen Food Safety Research (VFSR) is an independent research institute in the

[about the partners](#)

we also the organisations below:



GMO Database www.EUginius.eu

The **European GMO initiative** for a **unified database system**

- A cooperation of



- In partnership with



- Shared standards with EURL GMFF (GMOMETHODS) and BCH (GMOGET)

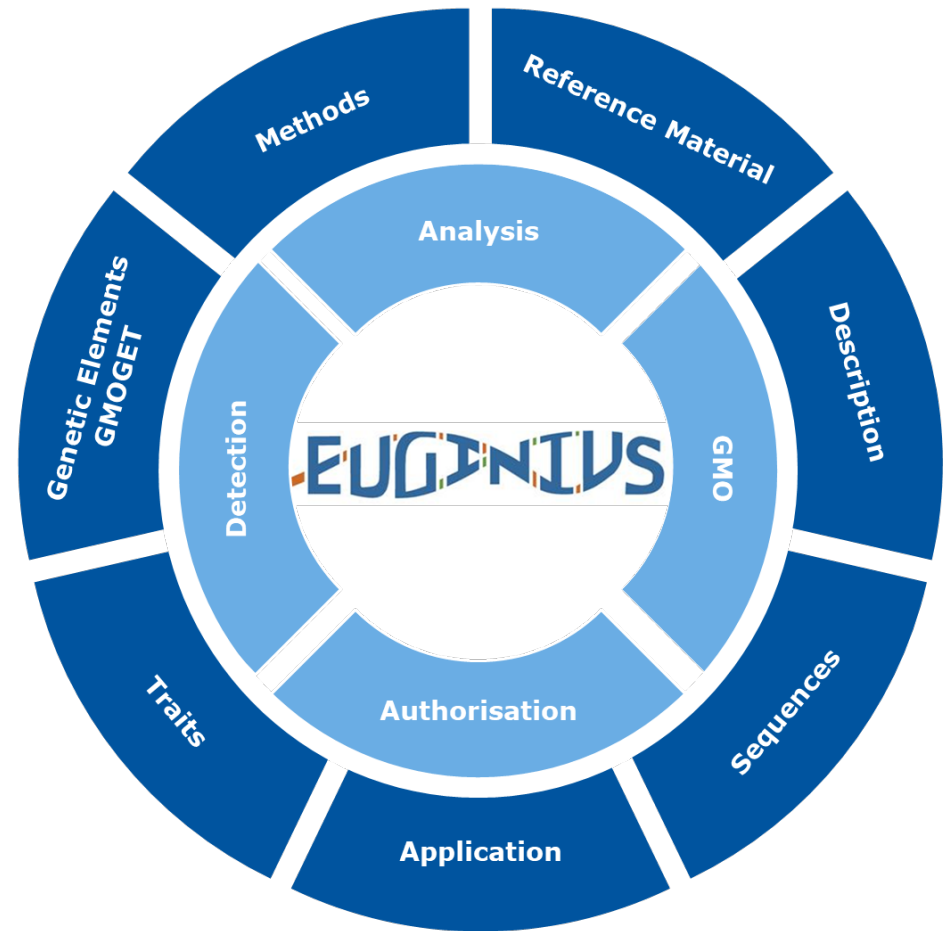
Sharing information

- Reliable information for GMO detection and identification
 - GMOs authorised in the EU (Reg. 1829/2003, 258/97; Dir. 2001/18/EC; 90/220/EEC)
 - GMOs non-authorised in the EU that are market relevant (incl. authorised elsewhere)

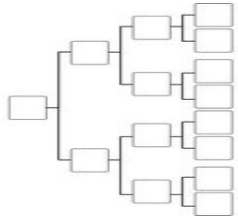
- Stakeholders
 - (official) GMO analysis laboratories
 - (EU-MS) enforcement institutions

Features of the EUginius database

- 4 modules to explore data
- Manifold information crosslinked supporting GMO analysis



Genetic Element Thesaurus GMOGET



- Standardised naming developed together with BCH
- Elements linked to GMOs as well as to detection methods

Genetic element	Donor	Trait	Definition	BCH record
Promoter				
➤ P-Cauliflower mosaic virus				
➤ P-e35S-CaMV	Cauliflower mosaic virus		35S promoter with duplicated enhancer region; inserted element length can vary between 307 – 615 bp. Kay R, et al. (1987)	100366
Coding sequence				
➤ CS-phosphinothricin N-acetyltransferase				
➤ CS-bar-STRHY	<i>Streptomyces hygroscopicus</i>	Herbicide tolerance > Glufosinate tolerance	Phosphinothricin acetyltransferase gene a.k.a. bar gene shares 85 % homology at the amino acid level with the pat gene. Thompson et al. (1987)	14972
Terminator				
➤ T-nopaline synthase				
➤ T-nos-RHIRD	<i>Agrobacterium tumefaciens</i>		3' untranslated region of the nopaline synthase gene . Bevan et al. (1983); Fraley et al. (1983)	100269

Genetic Element Thesaurus GMOGET

Adamse et al. *BMC Bioinformatics* (2021) 22:48
<https://doi.org/10.1186/s12859-020-03880-0>


BMC Bioinformatics

DATABASE

Open Access



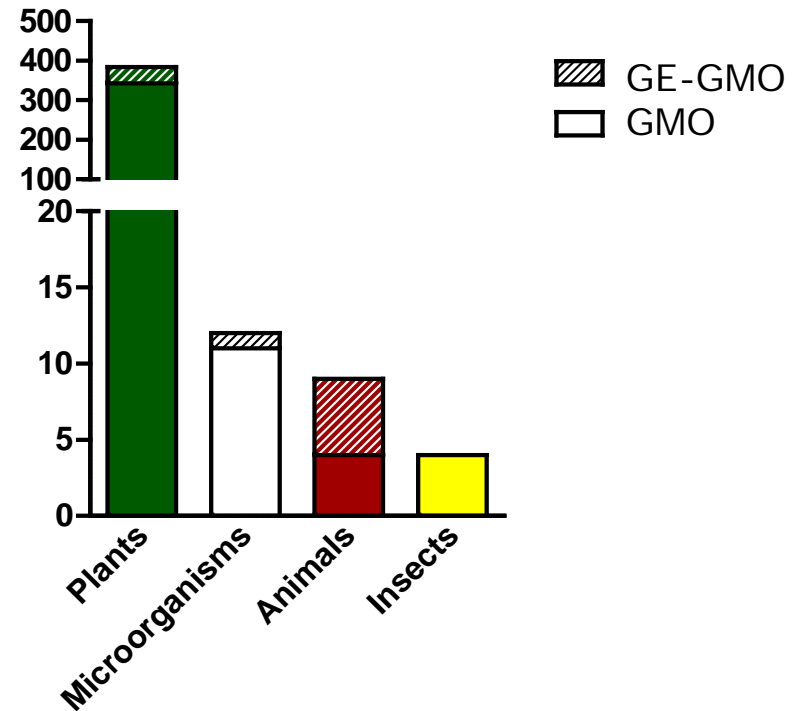
GMO Genetic Elements Thesaurus (GMO-GET): a controlled vocabulary for the consensus designation of introduced or modified genetic elements in genetically modified organisms

Paulien Adamse^{1*} , Emilie Dagand², Karen Bohmert-Tatarev^{2,3}, Daniela Wahler², Manoela Miranda^{4,5},
Esther J. Kok¹ and Joachim Bendiek^{2,6}

GMOs in EUginius

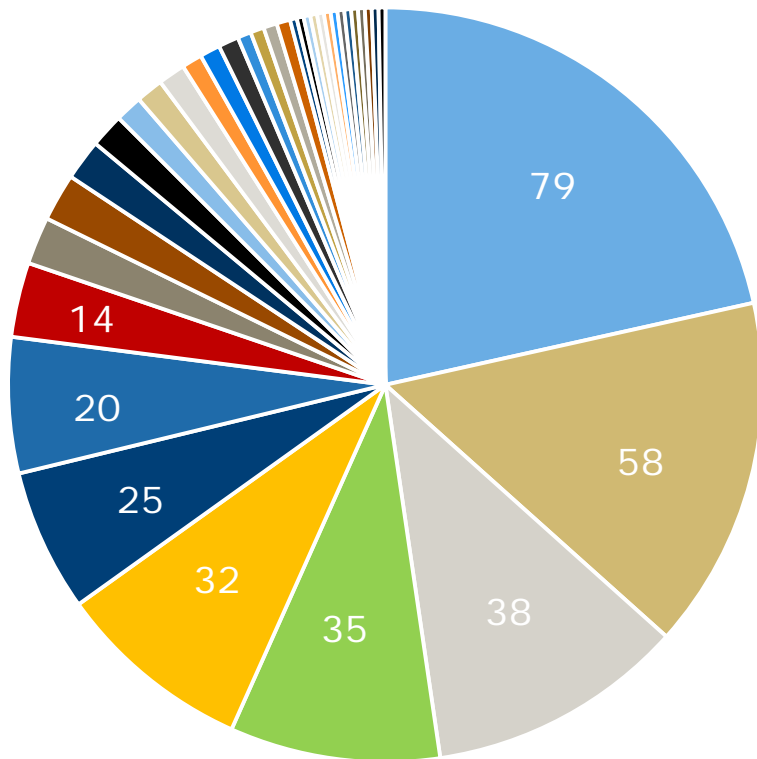
- 873 GMO entries (incl. stacks)
- 409 single events

GMO entries
- single events -



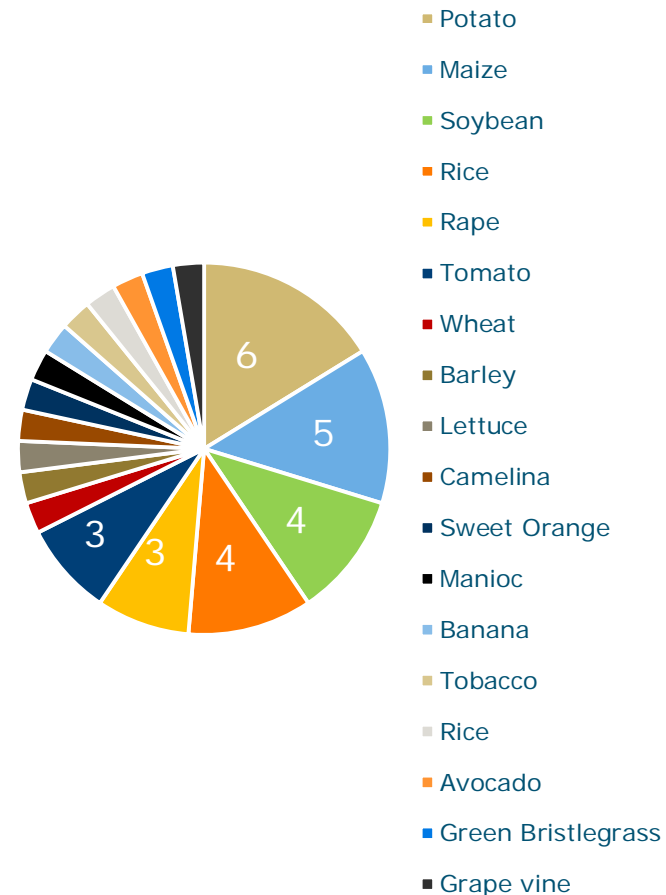
GMO plants in EUginius

GMO plants
- 344 single events -

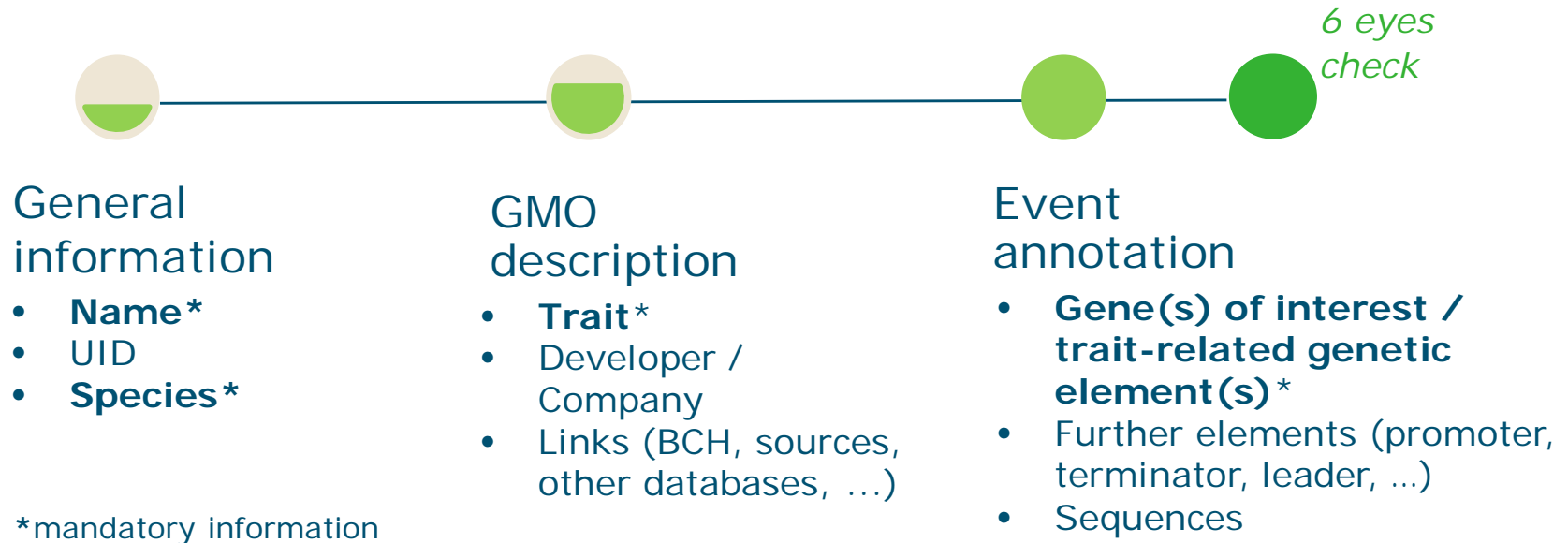


- Maize
- Potato
- Cotton
- Soybean
- Rape
- Rice
- Pumpkin
- Tomato
- Wheat
- Sugar Cane
- Papaya
- Beetroot
- Safflower
- Apple
- Petunia
- Brassica rapa
- Chicory
- Alfalfa
- Melon
- Cucurbita pepo
- Common Bean
- Rose
- Barley
- Lettuce
- Creeping Bentgrass
- Pineapple
- Thale Cress
- Brassica oleracea
- American Chestnut
- Eucalyptus
- Common Gypsophila
- Flax
- Moth Orchid
- Plum
- Eggplant
- Cowpea

GE-GMO plants (NGT)
- 37 single events -



Information for GMO entries



+ **broad data set** (data from EU-applications, ww-applications, publications, patents...)

+ **fast reaction**

+ **reliable data**

Examples of GE-GMOs in EUgenius

■ High-oleic soybean

NGT: modifications of the *FAD2* gene; oil commercialised in the USA



Source: Genetic Literacy Project, 2019/03/01

■ GABA tomato

NGT: modifications of the *Slgad3* gene; Tomatoes commercialised in Japan



Source: sanatech-seed.com

■ Heat tolerant cattle

NGT: modification of the prolactin receptor gene (*prlr*) PRLR-SLICK cattle



Source: Realimage / Alamy Stock Photo

Examples of GMOs in EUgenius

■ MON95275 maize

Insect resistant maize; *Agrobacterium*-mediated transformation



Source: BVL picture archive

■ PinkGlow pineapple EF2-114

Altered color of the fruit through accumulation of lycopene; *Agrobacterium*-mediated transformation (RNAi)



Source: USDA/ARS, Peggy Greb

■ PBR cowpea 709A

Insect resistant; *Agrobacterium*-mediated transformation



Source: NDLink.org

GMOs detailed page



- [Inserts / Modification](#)
- [Detection Methods](#)

GMO: MON95379
 Alias:
 UID: MON-95379-3
 Tradename:
 Company: [Bayer Crop Science \(formerly Monsanto\)](#)
 Developer: Bayer Crop Science (formerly Monsanto)
 Species: *Zea mays* (maize, corn)
 Traits: Pest/Disease resistance > Insect res
 EU authorisation:

14 results

Name	Type	Target	Description	Validation	Standardisation	Verification
QL-ELE-AINT 2-5/AINT 2-3'	element-specific	I-actin	Qualitative real-time PCR (TaqMan) method for detection of rice actin 1 intron (I-ract1) (Mano et al. 2009).	in-house validation	none	1
QL-ELE-P-Ubi-F/P-Ubi-R	element-specific	P-ubi1-MAIZE	Qualitative real-time PCR (TaqMan) method for detection of ubiquitin promoter of <i>Zea mays</i> (Debode et al., 2013)	in-house validation	none	1
QL-ELE-00-010	element-specific	E-FMV, P-34S FMV	Qualitative conventional PCR method for detection of Figwort mosaic virus 34S promoter (Pan et al., 2007)	ring trial validation	ISO standard	2
QL-ELE-00-015	element-specific	E-FMV, P-34S FMV	Qualitative real-time PCR (TaqMan) method for detection of Figwort mosaic virus 34S promoter (ISO/TS 21569-5).	ring trial validation	ISO standard	2
QL-TAX-ZM-002	taxon-specific	Zea mays	Qualitative real-time PCR (SYBRGreen) method for detection of maize alcoholdehydrogenase 1 gene (Barbau-Piednoir et al., 2014)	ring trial validation	unknown	1
QL-TAX-ZM-003	taxon-specific	Zea mays	Qualitative conventional PCR method for detection of the maize invertase gene (ISO 21569)	ring trial validation	ISO standard	1
QT-TAX-ZM-001	taxon-specific	Zea mays	Quantitative real-time PCR (TaqMan) method for detection of maize alcohol dehydrogenase 1 (adh1) gene. Estimated number of target copies per haploid genome (Jacchia et al. 2018): 1	ring trial validation	ISO standard	1

- [General Information](#)
- [Inserts / Modification](#)
- [Transformation Vectors](#)
- [Detection Methods](#)
- [Reference Materials](#)

- [Authorisation](#)
- [Literature reference](#)

1 result

Catalogue number	Source	Value	Type	Certified
AOCS 0521-A	AOCS	≥99.6 %	dried powder	yes

Information for GMO detection

- Ring-trial and in-house validated PCR based detection methods
- **ISO-, EU-RL GMFF verified, CEN-, national standards**
 - Element specific (62)
 - Construct specific (30)
 - Event specific (111)
 - Taxon specific (59)
- Methods with targets from element thesaurus are **automatically linked to appropriate GMOs** (verification level 1)
- **Additional verification data** (verification level 2 and 3) confirm or deny automatically assigned methods

GMO/method matrix

The screenshot shows the EUGENIUS web application interface for generating a GMO/method matrix. The header includes the EUGENIUS logo and navigation links: Home, GMO, Detection, Analysis, BLAST, Authorisation, Safety literature, Search, Help, and Data entry. Below the header, the page title is "GMO/method matrix".

The main content area is titled "GMO/method matrix" and contains the following sections:

- Generate a verification matrix that shows the ability of the selected methods to detect specific GMOs.**
- The ability of detection is verified experimentally using reference material (+/-3), by sequence alignment (in silico) (+/-2) or theoretically according to available information (from application documents, publications, etc.) about potential presence/absence of targets (+/-1).**
- Select methods for the GMO/method matrix**
- Entire pool of methods:** ALL
- or select method set:** SCREENING, ABC
- SCREENING:** set restricted to methods for GMO screening (methods for the detection of elements and constructs).
- ABC:** set of ring-trial validated screening methods (national or ISO standard) methods that is constantly checked and adjusted by the German National Reference Laboratory (NRL) in collaboration with the national network of GMO laboratories (Waiblinger et al. 2010. Anal. Bioanal. Chem. 398: 2065-2072).
- Restrict method list by:**
- Target:** selecting more than one target broadens your results
- Events:**
- Constructs:**
- Elements:**
- Species:**
- Target type:**
- Validation:**
- Standardisation:**
- Add specific method to the selected set* of methods:**
- *when no set selected (all), results are restricted to the methods selected here**
- Method:**
- Select GMOs for the GMO/method matrix:** Combining GMOs and species broadens your results
- GMO:**
- Species:**
- Exclude stacked events:**
- Restrict GMO list by: Authorisation status**
- | | | | | | |
|-------------|--|---|---------------------------------------|---------------------------------------|---------------------------------------|
| food | <input checked="" type="checkbox"/> approved | <input checked="" type="checkbox"/> approved with restrictions or phasing out | <input type="checkbox"/> not approved | <input checked="" type="checkbox"/> X | <input checked="" type="checkbox"/> X |
| feed | <input checked="" type="checkbox"/> approved | <input checked="" type="checkbox"/> approved with restrictions or phasing out | <input type="checkbox"/> not approved | <input checked="" type="checkbox"/> X | <input checked="" type="checkbox"/> X |
| cultivation | <input checked="" type="checkbox"/> approved | <input checked="" type="checkbox"/> approved with restrictions or phasing out | <input type="checkbox"/> not approved | <input checked="" type="checkbox"/> X | <input checked="" type="checkbox"/> X |
| other uses | <input checked="" type="checkbox"/> approved | <input checked="" type="checkbox"/> approved with restrictions or phasing out | <input type="checkbox"/> not approved | <input checked="" type="checkbox"/> X | <input checked="" type="checkbox"/> X |
- Search** **Reset**

* Bonfini, L., "In Silico Proposal of Screening Strategies for Detecting EU Authorised GMOs." European Commission, Ispra, JRC131782, 2023.

GMO/method matrix

Matrix assists screening

GMOs detected by selected methods

59 Results

GMO	Authorisation	Species	RM available	T-nos-RHIRD (QL-ELE-00-013)	E-FMV, P-34S FMV (QL-ELE-00-015)	CS-pat-STRVR (QT-ELE-00-002)	E-35S-CaMV, P-Cauliflower mosaic virus, P-scp1-SYNTH (QT-ELE-00-004)	DAS40278 (QT-EVE-ZM-004)
		Zea mays (maize, corn)	no	1	-1	1	1	-1
		Zea mays (maize, corn)	yes	2	-3	2	3	-1
		Zea mays (maize, corn)	yes	-2	-3	-2	3	-1
		Zea mays (maize, corn)	no	-1	-1	-1	1	-1
		Zea mays (maize, corn)	yes	1	-1	-1	3	-1
		Zea mays (maize, corn)	yes	-2	-3	2	3	-1
DAS40278		Zea mays (maize, corn)	yes	-2	-3	-2	-3	3

GMOs not detected by selected methods

20 Results

ARGOS8 Maize		Zea mays (maize, corn)	no	-1	-1	-1	-1	-1
BHB Hi-Yield Maize		Zea mays (maize, corn)	no	-1	-1	-1	-1	-1
BVLA430101		Zea mays (maize, corn)	no	-2	-2	-2	-2	-1

Verification levels

- descriptive, based on element (+/-1)
- *in silico*, Sequence-based (+/-2)
- experimental (+/-3)

Tools to assist monitoring: Analysis tool



GMO analysis tool

This tool is designed to support labs that analyse samples for the presence of GMOs. Based on data you found in your GMO analysis you can use the search module on this page to find additional information on possible GMO targets.

Step 1: select detected targets. The chosen method becomes relevant in case the output needs to be filtered for GMOs that have a verified detection method (+3).

Step 2: select target that has been analysed, but not positively detected (= select confirmed negative targets).

If detected targets can be explained by detected events, no further action will be necessary.

If targets are not explained by the detected events, the table **Suggested output** will list GMOs that could explain these targets.

Step 1:

Select species, GMOs and elements that have been detected in a laboratory analysis:

Species:	<input type="text" value="any (select to restrict options)"/>
GMO:	<input type="text" value="any (select to restrict options)"/>
Promoter:	<input type="text" value="any (select to restrict options)"/>
Terminator:	<input type="text" value="any (select to restrict options)"/>
Coding Sequence:	<input type="text" value="any (select to restrict options)"/>
Other elements:	<input type="text" value="any (select to restrict options)"/>
Construct:	<input type="text" value="any (select to restrict options)"/>

Step 2:

Select species, GMOs and elements that have been searched for in a laboratory analysis, but were **NOT** detected:

Species:	<input type="text" value="any (select to restrict options)"/>
GMO:	<input type="text" value="any (select to restrict options)"/>
Promoter:	<input type="text" value="any (select to restrict options)"/>
Terminator:	<input type="text" value="any (select to restrict options)"/>
Coding Sequence:	<input type="text" value="any (select to restrict options)"/>
Other elements:	<input type="text" value="any (select to restrict options)"/>
Construct:	<input type="text" value="any (select to restrict options)"/>

Analyse

Reset

Import result file (xlsx, see Help-file)

Select file No file chosen

Enter results detected/not detected

Step 1:

Select species, GMOs and elements that have been detected in a laboratory analysis:

Species:

GMO:

Promoter:

Terminator:

Coding Sequence:

Other elements:

Construct:

Step 2:

Select species, GMOs and elements that have been searched for in a laboratory analysis, but were **NOT** detected:

Species:

GMO:

Promoter:

Terminator:

Coding Sequence:

Other elements:


Construct:


Analyse


Reset





Everything explained? NO!

Confirmed output

Red : detected target not present in the identified GMOs





Green : detected target present in at least one identified GMO

Yellow : target tested but not detected

Analysis report: The detected GMO is: Ms11. It can explain the presence of CS-bar-STRHY , CS-barnase , T-nos-RHIRD  but not T-rbcS_E9-PEA .

[Refine Search](#)

The identified GMOs and their elements

Species	GMO	Promoter	Terminator	Coding Sequence	Construct	EU authorisation
<i>Brassica napus</i> (canola, oilseed rape, rapeseed)	Ms11	P-nos-RHIRD P-rbcS-ARATH P-ta29-TOBAC	T-barnase-BACAM <u>T-nos-RHIRD</u>  T-tr7-RHIRD	<u>CS-bar-STRHY</u>  <u>CS-barnase-BACAM</u>  CS-barstar-BACAM	P-SSU/bar	

But what about T-rbcS_E9-PEA. How can this be explained??

> 100 candidates

GMO prediction view

- Restrict list to GMOs from detected species
- Restrict list to GMOs that are linked to methods with a +3 verification value (verified detection methods)
- Exclude GMOs from the list that contain targets that were not detected

Importance sorting (x/y): GMOs sorted first by (x) = number of detected target not present in the identified GMOs (unexplained), then by (y) = number of detected target present in the identified GMOs (explained)

GMOs that can explain one or more detected targets

Species	GMO	Importance sorting <input checked="" type="checkbox"/>	Promoter	Terminator	Coding Sequence	Construct	EU authorisation
<i>Gossypium hirsutum</i> (cotton)	MON1076	1 / 1	P-34S FMV P-35S-CaMV	T-nos-RHIRD T-rbcS_E9-PEA	CS-cry1Ac-BACTU CS-nptII-ECOLX	P-35S/nptII	
<i>Gossypium hirsutum</i> (cotton)	MON1445	1 / 1	P-34S FMV P-35S-CaMV	T-nos-RHIRD T-rbcS_E9-PEA	CS-aadA-ECOLX CS-CP4epsps-RHIRD CS-nptII-ECOLX	ctp2/cp4-epsps P-35S/nptII P-FMV/cp4-epsps	
<i>Gossypium hirsutum</i> (cotton)	MON1698	1 / 1	P-34S FMV P-35S-CaMV	T-nos-RHIRD T-rbcS_E9-PEA	CS-CP4epsps-RHIRD CS-nptII-ECOLX	ctp2/cp4-epsps P-35S/nptII P-FMV/cp4-epsps	
<i>Oryza sativa</i> (rice)	LLRICE601	1 / 1	P-35S-CaMV	T-nos-RHIRD	CS-bar-STRHY	P-35S/bar	
<i>Phaseolus vulgaris</i> (bean)	INI-FMAPDF	1 / 1	P-35S-CaMV P-nos-RHIRD	T-nos-RHIRD T-rbcS_E9-PEA	CS-nptII-ECOLX CS-pdf1.2-ARATH	P-nos/nptII	
<i>Solanum tuberosum</i> (potato)	1210_amk	1 / 1	P-34S FMV P-rbcS-ARATH	T-nos-RHIRD T-rbcS_E9-PEA	CS-CP4epsps-RHIRD CS-cry3A-BACTT		
<i>Solanum tuberosum</i> (potato)	2904/1_kgs	1 / 1	P-34S FMV P-rbcS-ARATH	T-nos-RHIRD T-rbcS_E9-PEA	CS-CP4epsps-RHIRD CS-cry3A-BACTT	ctp2/cp4-epsps	
<i>Solanum tuberosum</i> (potato)	ATBT04-06	1 / 1	P-35S-CaMV P-rbcS-ARATH	T-nos-RHIRD T-rbcS_E9-PEA	CS-cry3A-BACTT CS-nptII-ECOLX	P-35S/nptII	
<i>Solanum tuberosum</i> (potato)	ATBT04-27	1 / 1	P-35S-CaMV P-rbcS-ARATH	T-nos-RHIRD T-rbcS_E9-PEA	CS-aadA-ECOLX CS-cry3A-BACTT CS-nptII-ECOLX	P-35S/nptII	
<i>Solanum tuberosum</i> (potato)	ATBT04-30	1 / 1	P-35S-CaMV P-rbcS-ARATH	T-nos-RHIRD T-rbcS_E9-PEA	CS-cry3A-BACTT CS-nptII-ECOLX	P-35S/nptII	

















Reduce possible outcome (assumptions)

GMO prediction view

- Restrict list to GMOs from detected species
- Restrict list to GMOs that are linked to methods with a +3 verification value (verified detection methods)
- Exclude GMOs from the list that contain targets that were not detected

Importance sorting (x/y): GMOs sorted first by (x) = number of detected target not present in the identified GMOs (unexplained), then by (y) = number of detected target present in the identified GMOs (explained)

GMOs that can explain one or more detected targets

Species	GMO	Importance sorting <input checked="" type="checkbox"/>	Promoter	Terminator	Coding Sequence	Construct	EU authorisation
<i>Brassica napus</i> (canola, oilseed rape, rapeseed)	GT200	1 / 0	<u>P-34S FMV</u> 	<u>T-rbcS_E9-PEA</u> 	CS-CP4epsps-RHIRD CS-gox-OCHAN	ctp2/cp4-epsps P-FMV/cp4-epsps	
<i>Brassica napus</i> (canola, oilseed rape, rapeseed)	GT73	1 / 0	<u>P-34S FMV</u> 	<u>T-rbcS_E9-PEA</u> 	CS-CP4epsps-RHIRD CS-gox-OCHAN	ctp2/cp4-epsps P-FMV/cp4-epsps	
<i>Brassica napus</i> (canola, oilseed rape, rapeseed)	LBFLEK	1 / 0	P-arc5a-PHAVU P-cni1-LINUS P-fae1-BRANA P-napA-BRANA P-pxr-LINUS P-sbp-VICFA P-set1-BRANA P-ubi4-PETCR P-usp-VICFA	T-35S-CaMV T-ahas-ARATH T-arc5a-PHAVU T-CDI-SOLTU T-fae1-ARATH <u>T-ocs-RHIRD</u>  T-pxr-ARATH <u>T-rbcS_E9-PEA</u> 	CS-ahas-ARATH CS-delta12D-PHYSP CS-delta4D-DIALT CS-delta4D-THRSP CS-delta5D-THRSP CS-delta5E-OSTTA CS-delta6D-OSTTA CS-delta6E-THAPS CS-delta6E-PHYPA CS-omega3D-PHYIT CS-omega3D-PYTIR		
<i>Brassica napus</i> (canola, oilseed rape, rapeseed)	MON88302	1 / 0	P-EF1alpha-ARATH	<u>T-rbcS_E9-PEA</u> 	CS-CP4epsps-RHIRD	ctp2/cp4-epsps P-FMV/cp4-epsps	
<i>Brassica napus</i> (canola, oilseed rape, rapeseed)	Ms1	0 / 3	P-nos-RHIRD P-rbcS-ARATH P-ta29-TOBAC	<u>T-nos-RHIRD</u>  <u>T-ocs-RHIRD</u>  T-tr7-RHIRD	<u>CS-bar-STRHY</u>  <u>CS-barnase-BACAM</u>  CS-nptII-ECOLX	P-nos/nptII P-SSU/bar	
















Remove GMOs w.o. not-detected elements

GMO prediction view

- Restrict list to GMOs from detected species
- Restrict list to GMOs that are linked to methods with a +3 verification value (verified detection methods)
- Exclude GMOs from the list that contain targets that were not detected

Importance sorting (x/y): GMOs sorted first by (x) = number of detected target not present in the identified GMOs (unexplained), then by (y) = number of detected target present in the identified GMOs (explained)

GMOs that can explain one or more detected targets

Species	GMO	Importance sorting <input checked="" type="checkbox"/>	Promoter	Terminator	Coding Sequence	Construct	EU authorisation
<i>Brassica napus</i> (canola, oilseed rape, rapeseed)	MON88302	1 / 0	P-EF1alpha-ARATH	<u>T-<i>rbcS_E9</i>-PEA</u> 	CS-CP4epsps-RHIRD	ctp2/cp4-epsps P-FMV/cp4-epsps	
<i>Brassica napus</i> (canola, oilseed rape, rapeseed)	Ms11	0 / 3	P-nos-RHIRD P- <i>rbcS</i> -ARATH P-ta29-TOBAC	T-barnase-BACAM <u>T-nos-RHIRD</u>  T-tr7-RHIRD	<u>CS-bar-STRHY</u>  <u>CS-barnase-BACAM</u>  CS-barstar-BACAM	P-SSU/bar	
<i>Brassica napus</i> (canola, oilseed rape, rapeseed)	Ms8	0 / 3	P- <i>rbcS</i> -ARATH P-ta29-TOBAC	T-barnase-BACAM <u>T-nos-RHIRD</u>  T-tr7-RHIRD	<u>CS-bar-STRHY</u>  <u>CS-barnase-BACAM</u> 	P-SSU/bar	
<i>Brassica napus</i> (canola, oilseed rape, rapeseed)	Rf3	0 / 2	P- <i>rbcS</i> -ARATH P-ta29-TOBAC	T-barstar-BACAM <u>T-nos-RHIRD</u>  T-tr7-RHIRD	<u>CS-bar-STRHY</u>  CS-barstar-BACAM	P-SSU/bar	
<i>Brassica napus</i> (canola, oilseed rape, rapeseed)	DHA	0 / 1	P-35S-CaMV P-cni1-LINUS P-cni2-LINUS P-fae1-ARATH P-FP1-BRANA	T-cni1-LINUS T-cni2-LINUS T-le1-SOYBN <u>T-nos-RHIRD</u> 	CS-delta12D-LACKL CS-delta4D-REBSA CS-delta5D-REBSA CS-delta5E-PYRCR CS-delta6D-MICPC CS-delta6E-PYRCR CS-omega3D-KOMPG CS-pat-STRVR	P-35S/pat	

Check for MON88302 canola presence

GMO prediction view

- Restrict list to GMOs from detected species
- Restrict list to GMOs that are linked to methods with a +3 verification value (verified detection methods)
- Exclude GMOs from the list that contain targets that were not detected

Importance sorting (x/y): GMOs sorted first by (x) = number of detected target not present in the identified GMOs (unexplained), then by (y) = number of detected target present in the identified GMOs (explained)

GMOs that can explain one or more detected targets

Species	GMO	Importance sorting <input checked="" type="checkbox"/>	Promoter	Terminator	Coding Sequence	Construct	EU authorisation
<i>Brassica napus</i> (canola, oilseed rape, rapeseed)	MON88302	1 / 0	P-EF1alpha-ARATH	<u>T-rbcS_E9-PEA</u> 	CS-CP4epsps-RHIRD	ctp2/cp4-epsps P-FMV/cp4-epsps	

Search options



European GMO Initiative for a Unified Database System

Search for GMO



Get to the searches you can performed on the EUginus database.

Type in keyword(s) for **free-text search** on GMOs or literature. Click on **advanced GMO search** or **advanced Literature search** to define respective search domain. Use * before/after search item for wildcard search if necessary. Click on Help for more details on free-text search modality.

Access to the theme-specific search by clicking on the respective link.

Search term


Search GMO

Search Literature


[advanced GMO search](#)


[advanced Literature search](#)

GMO

 [List with GMOs and their identifiers](#)

 [List with GMOs and traits](#)


 [List with GMOs and genetic elements](#)

 [Element search](#)

Detection

 [Detection method](#)

 [GMO/method matrix](#)


 [Reference material](#)


Search term

Search

Analysis

Authorisation

 [Search for generic approval](#)

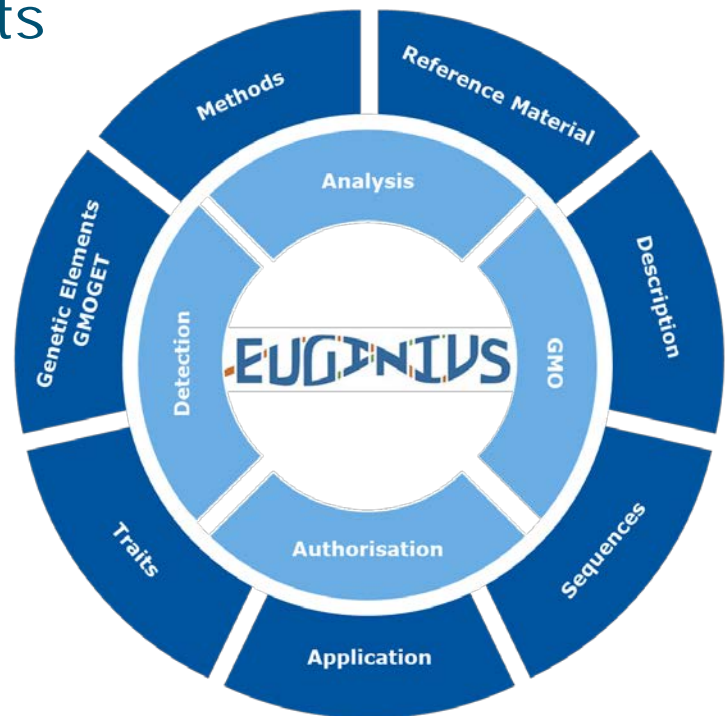
 [Traffic light search](#)

Search term

Search

EUginius support in GMO analysis

- Reliable data
- Broad method and GMO datasets
- Clear quality level
- Combined information



Thank you for your attention

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The logo for EUGENIUS features the word in a bold, blue, sans-serif font. The letters are stylized with vertical bars of varying colors (orange, green, blue) integrated into the letterforms. A large orange diagonal line is positioned to the left of the 'E'.

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