Table GMO

Matrix	Parameter	Method	Accreditatie
Soybeans and derived, processed solid products	Detection and quantification of GMO soybean events (*RRS*)	Construct-specific methods; literature	Yes
Seeds of maize and corn and derived, processed products	Detection and quantification of GMO maize events (*Bt11*, *Bt176*, *Mon810*, *GA21*, *T25*)	Construct-specific methods; literature	Yes
Pure raw materials and derived, processed solid products	Plants	EURL official methods	Yes
Pure raw materials and derived, processed solid products	Screening elements (*p-35S, t-NOS, p-FMV*)	EURL official methods; literature	Yes
Pure raw materials and derived, processed solid products	Detection of GMO events (all in the EU-authorised events)	EURL official methods	Yes
Pure raw materials and derived, processed solid products	Quantification of GMO events (all in the EU-authorised events)	EURL official methods	No

GMO analyses are divided in three groups:

1. In a screening PCR, we search for common, regulatory DNA sequences in GMOs, such as the *Cauliflower Mosaic Virus* promotor 35S (p-35S), the *Agrobacterium tumefaciens* nopaline synthase terminator (t-NOS), and the *Figwort Mosaic Virus* promotor 35S (p-FMV). This is done in combination with a detection of one or more plant species (species-specific PCR).
2. If one or more of the species-specific DNA targets and/or GMO-screening elements are positive, then qualitative analysis is done to look for the presence of EU-authorised GMOs, depending on the crop that was detected (identification PCR).
3. Finally, the individually identified GMO events are quantified (quantitative PCR) in order to determine whether or not the sample conforms with the regulations (mandatory labeling treshold of 0.9% GMO per crop for EU authorised events).