lifeprint Analysis – High-Quality Laboratory

Partner for analyses in food and feed

Service Description

Content

We gladly help and advice you with any specific questions and further parameters you need. You can place your enquiry by phone 07303 95195-0 or by email office@lifeprint.de.

GMO analysis: screening

GMO screening	Method
In the following you will find different testing strategies, although no analysis strategy can guarantee a complete detection of all GMOs. Depending on the risk assessment different testing packages can be ideal.	The Real Time-PCR (Polymerase Chain Reaction) detects sections of genetic material often used in genetically modified organisms (GMOs). The analytic statement shows whether certain DNA-sequences were detected (yes/no). Our analyses are done according to the protocols of the Joint Research Centre belonging to the EU Commission (JRC) and DIN standards. For several testing systems no suitable JRC-protocol exists, in these cases we work according to peer-reviewed publications.

Limit of detection	The limit of detection (LOD) in raw material is 5 to 20 target DNA copies depending on the system.

Screening	What it provides…	… and what it doesn´t
2-parameter-screening	The worldwide most relevant GM-plants contain either the 35S-promoter (p35S) or NOS-terminator (tNOS) or both (like the Roundup Ready®-Soya-1 MON-Ø4Ø32-6 with the worldwide largest market presence at the moment). Depending on origin and kind of product, different 2-parameter-screenings are reasonable.	Increasingly, a 2-parameter-screening is not enough for detecting relevant GMOs. Additional screening parameters are necessary.
3-parameter-screening	For soya, canola, mustard, rice, grain and mixed products we recommend a 3-parameter-screening. This way the GMO-canola GT73/RT73 (MON-ØØØ73-7) and the Roundup Ready®-Soya-2 (MON89788) amongst others will be detected. Depending on origin and kind of product, different 3-parameter-screenings are reasonable. We would be happy to advise you!	For some GMOs, a 3-parameter-screening does not suffice anymore. Therefore an additional identification test is necessary for such GMOs.
5-parameter-screening	This testing package is especially suitable for mixed and processed products (e.g. convenience food, spices, compound feed). The 5-parameter-screening convinces by it´s high information density: a lot of GMOs can be detected and this way you also have a higher detection reliability concerning GMOs without an EU market approval. Based on this pattern, we often can narrow it down to a few possible candidates before doing an identification of a variety.	If a GMO does not contain any of the screening-parameters, it can not be found by the screening (only by a direct event-specific analysis).
6-parameter-screening	You want a very high density of information? Then you are well equipped with a 6-parameter-screening. Depending on your type of question different 6-parameter-screenings can be reasonable. In comparison to the stepwise procedure you have a significant time advantage.	We gladly advise you with any specific questions you might have!
7-parameter-screening	In addition to the 6-parameter-screening the Cauliflower Mosaic Virus (CaMV) will be tested, which provides a significant time advantage in comparison to the stepwise procedure.	

GMO analysis: identification and quantification

Variety-ID	Method and what it provides
For identifications, specific gene sections are detected, using Real Time-PCR. The statement shows whether a certain GM variety (or a kind of plant or virus) was detected.	Depending on the positive screening parameters of the initial analysis, possible GMOs can be identified, assigned and excluded. To find the right decision for follow-up tests, amongst others we consult the current market situation, global amounts of cultivation and our vast experience. Our analyses are done according to the protocols of the Joint Research Centre belonging to the EU Commission (JRC) and DIN standards. For several testing systems no JRC-protocol exists, in these cases we work according to peer-reviewed publications.
Limit of detection	The limit of detection (LOD) in raw materials is < 5 to 40 target DNA copies (~ 0,01 % – 0,05 %) depending on the system.

GMO quantification	Method and what it provides (Method and its performance)
The relative quantification using Real Time-PCR gives a statement about the genomic relation.	Once the GMO-variety is identified, quantification offers you information about the compliance with the threshold value (relevant for EU approved varieties). Should the variety identification show an unauthorized variety you can skip the quantification (there is an exception to the “zero-tolerance” policy for feed: according to EU Regulation (EU) 619/2011 some GMOs will be tolerated up to 0,1 % under certain circumstances). For the quantitative determination of the GMO content, the calibration curve method is applied (relative quantification). Thereby separate calibration curves are established: one for the specific GMO gen and a second for the species specific reference gen. Based on the calibration curves the GMO content in relation to the reference gen is determined. This procedure does not give any statement about masses. All varieties of which reference gens and adequate detection methods are available can be quantified. Our analyses are done according to the protocols of the Joint Research Centre belonging to the EU Commission (JRC) and DIN standard. For several testing systems no JRC-protocol exists, in these cases we work according to peer-reviewed publications.
Limit of quantification	The limit of quantification (LOQ) is < 0,1 % and (amongst others) depends on the kind of matrix.

GMO analysis: screening combinations

2-parameter-screening
p35S + tNOS
p35S + *epsps*[1] gene
p35S + Roundup Ready-Soya-2 (MON89788) qualitative
pNOS-*npt*II-gene + FP967-construct
Further combinations for your specific questions available on request

3-parameter-screening
p35S + tNOS + *epsps*[1]-gene
p35S + tNOS + pFMV
tNOS + *pat*- + *epsps*[1]- gene
p35S + tNOS + cry1Ab/cry1Ac
epsps1- + *pat*- + *bar-Gen*
p35S + tNOS + *pat*- gene
Further combinations for your specific questions available on request

4-parameter-screening
p35S + tNOS + *epsps*[1]- *pNOS-nptII-gene*
Further combinations for your specific questions available on request

5-parameter-screening
p35S + tNOS + *epsps*[1]- *pat*- + *bar*-gene
Further combinations for your specific questions available on request

6-parameter-screening
p35S + tNOS + *epsps*[1]- + *pat*- + *bar*-gene + CaMV-ID
p35S + tNOS + *epsps*[1]- + *pat*- + *bar*-gene + pNOS-*npt*II-gene

7-parameter-screening
p35S + tNOS + *epsps*[1]- + *pat*- + *bar*-gene + pNOS-*npt*II-gene + CaMV-ID

[1] CTP2-CP4*epsps*-construct

GMO analysis: identification and quantification

Identification / Quantification	qual. PCR	% PCR	GMO variety
Virus	●		CaMV (Cauliflower Mosaic Virus; no GMO)
Soya	●	●	68416 (DAS-68416-4)
	●	●	A2704-12 (LibertyLink; ACS-GMØØ5-3)
	●	●	A5547-127 (LibertyLink; ACS-GMØØ6-4)
	●	●	BPS-CV127-9 (BPS-CV127-9)
	●	●	DP-305423 (DP-3Ø5423-1)
	●	●	DP-356043 (DP-356Ø43-5)
	●	●	FG72 (MST-FGØ72-2)
	●	●	MON87701-Soya ((MON877Ø5-6)
	●	●	MON87705 (MON877Ø5-6)
	●	●	MON87708 (MON-877Ø8-9)
	●	●	MON87769 (MON-87769-7)
	●	●	Roundup Ready-Soya-1 (GTS 40-3-2)
	●	●	Roundup Ready-Soya-2 (MON89788)
	●	●	DAS 44406-6 (DAS-444Ø6-6)
	●	●	DAS 81419-2 (DAS-81419-2)
Maize	●	●	3272 (SYN-E3272-5)
	●	●	5307 (SYN-Ø53Ø7-1)
	●	●	98140 (DP-Ø9814Ø-6)
	●	●	Bt11 (SYN-BTØ11-1)
	●	●	Bt176 (Maximizer; SYN-EV176-9)
	●	●	DAS59122 (Herculex; DAS-59122-7)
	●	●	DAS-40278-9 (DAS-4Ø278-9)
	●	●	GA-21 (Roundup Ready; MON-ØØØ21-9)
	●		LY038 (REN-ØØØ38-3)
	●	●	MIR162 ((SYN-IR162-4)
	●	●	MIR604 (SYN-IR6Ø4-5)
	●	●	MON810 (YieldGard; MON-ØØ81Ø-6)
	●	●	MON863 (YieldGard; MON-ØØ863-5)
	●	●	MON87460 (MON-8746Ø-4)
	●	●	MON88017 ((MON88Ø17-3)
	●	●	MON89034 (MON89Ø34-3)
	●	●	MON87427 (MON-87427-7)
	●	●	NK603 (Roundup Ready: MON-ØØ6Ø3)
	●	●	T25 (LibertyLink; ACS-ZMØØ3-2)
	●	●	TC1507 (Herculex; DAS-Ø15Ø7-1)

Identification / Quantification	qual. PCR	% PCR	GMO variety
Canola	●	●	73496 (DP-Ø73496-4)
	●	●	HCN 92 (Topas 19/2; ACS-BNØØ7-1)
	●	●	MS8 (ACS-BNØØ5-8)
	●		Oxy-235
	●	●	RF3 (ACS-BNØØ3-6)
	●	●	Roundup Ready-Canola (GT73/RT73; MON-ØØØ73-7)
	●	●	T45 (HCN 28, LibertyLink; ACS-BNØØ8-2)
	●	●	MON88302 (MON-883Ø2-9)
Flax	●		FP967 CDC „Triffid“
Rice	●		Bt63
	●		LL601 (LibertyLink)
	●	●	LL62 (LibertyLink; ACS-OSØØ2-5)
Sugar Beet	●	●	H7-1 (KM-ØØØ71-4)
Potato	●	●	Amflora (EH92-527-1)
Alfalfa	●	●	J101 (MON-ØØ1Ø1-8)
Cotton	●	●	MON531 (MON-ØØ531-6)
	●	●	15985 (MON-15985-7)
	●	●	MON1445 (MON-Ø1445-2)

As experienced specialists we are pleased to support you with your specific questions like the analytic of cotton, papaya and honey, also concerning marketability.

GMO analytical spectra for feed (VLOG)

Compound feed with soya	
Ingredient Soya:	RRS-1 % + RRS-2 % + A2704-12 + A5547-127 ID
Ingredient Maize additionally:	NK603 ID+ TC1507 ID + MON810 ID + MON89034 ID
Ingredient Canola additionally:	GT73 ID

Compound feed without Soya	
Soya is no ingredient:	Estimation of the soya-mass (ELISA)
Ingredient Maize additionally:	NK603 ID+ TC1507 ID + MON810 ID + MON89034 ID
Ingredient Canola additionally:	GT73 ID + bar-gene

Raw product	
Soya:	RRS-1 % + RRS-2 % + A2704-12 + A5547-127 ID
Maize:	p35S + tNOS
Canola:	tNOS + CTP2-CP4epsps + pat (LL-construct)

Abbreviations

RRS-1 ("Roundup Ready-Soja-1") = GTS 40-3-2
RRS-2 ("Roundup Ready-Soja-2") = MON89788
% = quantification
ID = identification

Plant and animal species analysis

Plant and animal species analysis	Method	
The analysis states whether a certain gene sequence of a plant or animal species was detected.	Using Real Time-PCR (Polymerase Chain Reaction) specific plant and animal DNA segments are detected. The analytic statement is whether certain DNA sequences were detected (yes/no). Our analyses are done according to the protocols of the Joint Research Centre belonging to the EU Commission (JRC) and DIN standards. For several testing systems no JRC-protocol exists, in these cases we work according to peer-reviewed publications or self-developed testing systems.	

Limit of detection	The limit of detection (LOD) in raw material is 10 to 20 target DNA copies depending on the system.

Plant species	
Canola (*Brassica napus* specific)	Sugar Beet
Canola (Brassicaceen)	Potato
Soya	Flax
Maize	Cotton
Rice	Lucerne
Pea	Oat
Rye	Barley
Wheat	Soft Wheat

Animal species	
animal DNA (mammals and poultry)	Turkey
Pork	Fish (multi species method)
Beef	Bonito *(Katsuwonus pelamis)*
Horse	Goat
Sheep	Barbary duck
Chicken	Water buffalo

Species analysis by means of sequencing

Species analysis by means of sequencing	Methods: Vertebrates; land plants
The use of sequencing does not only allow to identify a known vertebrate species, but also to determine if and which further unknown species is part of the sample that potentially differs from the declaration.	The application of the method is limited to mono products. After DNA extraction at least two different mitochondrial gene sequences are amplified. After purification and preparation the DNA sequence is identified by a subcontractor lab. The species is finally determined by correlation with sequences in DNA databases.

Identification of species using Next-Generation-Sequencing

Identification of species in mixtures	Methods: Vertebrates; land plants
Next Generation Sequencing (NGS) allows the simultaneous identification of the vertebrate- or land plant species in a mixed sample without having to know which species could be present	This method can be used for mixed samples and for single ingredient products. All species in the sample present with sufficient DNA will be identified. The limit of detections depends on the species and the tissue (DNA/mass ratio) and is usually between 0.5 and 5%. The method is primarily qualitative, but the sequences are listed in order of frequency.

Analysis of CMS species

Detection of CMS species	Method: Analysis on ogura sequence (occurrence: cabbage varieties)
The analysis states whether the CMS specific sequence has been detected.	The respective CMS specific sequence is detected by Real Time-PCR (Polymerase Chain Reaction). The statement shows if certain DNA sequences have been detected (yes/no). The detection of ogura sequence is done by our own method.
Limit of detection	The limit of detection (LOD) in raw material is 50 DNA copies.

Allergen analytics

Allergens	Method and what it provides
Parameters of the "EU-list of allergens" can be tested as follows: The ELISA test is based on proteins (antibodies-/antigen reactions), where the detected structures do not have to be identical with the allergens. The PCR detects DNA of the allergen, which often even works in highly processed and heat-treated food. The determination of lactose and galactose is done by UV measurement. Under some circumstances food can still cause incompatibility reactions even though it was tested with negative results. The PCR analysis provides the information, if the sample contains certain gene sequences (qualitative test). Estimation of the quantities are also possible by PCR, however, these can be strongly influenced by the Matrix. In case of a positive result of the PCR it might be thought of doing an ELISA afterwards (as far as possible).	

Limit of detection Limit of quantification	**ELISA** (Enzyme-linked Immunosorbent Assay)	LOD / LOQ: on request
	PCR (Polymerase Chain Reaction)	LOD: 5 - 40 target DNA copies
	Chemical enzymatical test	≤ 0,1 g/100 g

	ELISA	PCR	chem. enzym. test	Allergen
Different Allergens	●	●		Soya
	●	●		Lupine
	●	●		Sesame
		●		Mustard (S. alba, B. juncea, B. nigra)
	●	●		Gluten (Gliadin)
		●		Celery
Nuts: At the moment it is not possible to detect the allergen group „nuts" with only one test.	●	●		Peanut
	●	●		Hazelnut
	●	●		Almond
		●		Walnut
		●		Macadamia
		●		Cashew
		●		Pistacchio
		●		Brazil nut
		●		Pecan nut
Milk	●			Milk (β-Lactoglobulin + Casein)
	●			β-Lactoglobulin
	●			Casein
		●		Cattle-DNA (Milk)
			●	Lactose und Galactose
Fish & others		●		Fish
	●	●		Crustaceae
		●		Mollusca
Egg	●			Egg
	●			Lysozyme
Further parameters on request				

Further Food Fraud tests

Estimation of Bonito portion	Method
The statement of the ΔΔct-method using Real Time PCR shows the genomic relations.	Using Real Time Polymerase Chain Reaction (PCR), a DNA sequence specific for Bonito (*Katsuwonus pelamis)* and another one specific for fish are detected. For the estimation of the amount of Bonito in a sample, the ΔΔct-method was used. Our analyses are done according to the DIN standard as well as self-developed testing systems.
Limit of quantification	The limit of quantification (LOQ) is < 1%

Quantification of soft wheat portion	Method
The statement of the relative quantification using Real Time PCR shows the genomic relation	Using Polymerase Chain Reaction (PCR) wheat specific gene sequences are detected. For the quantitative determination of the wheat content the calibrate curve procedure is used (relative quantification). Therefore separate calibration curves are established. One for the specific wheat gene and another for the durum wheat and wheat specific gene. According to these calibration curves the portion of soft wheat content of the sample in relation to the total content of wheat is determined. Our analyses are done according to the DIN standard as well as according to peer-reviewed publications.
Limit of quantification	The limit of quantification (LOQ) is ≤ 3 %

Species identification of Barbary duck	Method
Result: Sample does or does not contain Barbary duck or Muscovy duck	Using Real Time Polymerase Chain Reaction (PCR), DNA sequences specific for Barbary / Muscovy / Mulard duck are detected. The statement depends on detection of certain DNA sequences (yes or no). Bejing and Mallard ducks cannot be identified using the detection system. Our analyses are done according to the DIN standard as well as self-developed testing systems.
Limit of detection	The limit of detection (LOD) is 5 copies

Species identification buffalo mozzarella	Method
Estimation of the amount of cow milk in mozzarella from buffalo	Using Real Time-PCR, DNA sequences specific for cow and water buffalo are detected. The amount of cow milk is assessed.
Limit of detection	The limit of detection (LOD) is < 5 target DNA copies

Cow milk in cheese from goat and / or sheep	Method: Real Time PCR of mitochondrial sequences
Estimation of the amount of cow whey or milk in whey / milk / cheese from goat and / or sheep	Using Real Time-PCR, DNA sequences specific for cow, sheep and goat are detected. The proportions of milk of the different species are assessed.
Limit of detection	The limit of detection (LOD) is < 5 target DNA copies

Whey falsification	Method: BRW-ELISA
The method is used for detection and quantification of bovine rennet whey in high-quality dairy products of other vertebrates (e.g. goat whey, sheep whey).	Using **ELISA** (Enzyme Linked Immunosorbent Assay), the concentration of an antibody or antigen is measured in a test solution. One of the reactants is enzyme labelled that lead to colorimetric detection.
Limit of quantification	The limit of quantification (LOQ) is 0,25%
Limit of detection	The limit of detection (LOD) is 0,1%

Veggie-, vegan- and ethic-Test

Veggie-, vegan- and ethic-Test
veggietest 4 PCRs: mammals + poultry, fish, mollusca and crustacean or 2 PCRs E.g. mammals + poultry, fish
vegantest 2 ELISAs: egg, milk and / or 4 PCRs: mammals + poultry, fish, mollusca and crustacean or 2 PCRs E.g. mammals + poultry, fish
ethiktest halal 1 PCR: pork and / or ethanol[1]

[1] Analysis performed by associated laboratory bilacon GmbH

Mycotoxin analytics [1,3,4]

Mycotoxins [1]	Method and what it provides
Mycotoxins are products of metabolism with toxic effects, created by molds. Up to now we know over 300 mycotoxins. At the moment, for only a few of them exist limits for the maximum amount on EU or national level. The analysis of mycotoxins is done by default using LC-MS/MS.	

Aflatoxins B1, B2, G1, G2	PV-SA-130
Ochratoxin A (OTA)	PV-SA-130
Deoxynivalenol (DON)	PV-SA-130
Zearalenon (ZEA)	PV-SA-130
Diacetoxyscirpenol	PV-SA-130
Fumonisins B1, B2, B3 [3]	ASU, L15.05-2 mod. (LC-MS/MS)
T2- and HT2-Toxin	PV-SA-130
Patulin [3]	PV-SA-E-017
Nivalenol [3]	PV-SA-086 (HPLC)
3-Acetyl-Deoxynivalenol (3-AcDON)	PV-SA-130
15-Acetyl-Deoxynivalenol (15-AcDON)	PV-SA-130

Mycotoxin screening [1,4]
Mycotoxin screening: 2 – 9 mycotoxins
Mycotoxin-analytics using other methods on request

[1] Analysis by affiliated company bilacon GmbH
[3] Cannot be chosen in the mycotoxin screening as parameter
[4] Only possible in case of ordering several mycotoxins for one sample at the same time and a combination of the above listed mycotoxins

Heavy metal analytics [1]

Heavy metals [1]	Method and what it provides
Heavy metals: are to be found everywhere in the environment and get into the food chain through the ground, the water and the atmosphere. Under the undesired contaminants are such ones which are harmful in higher concentration, e.g. lead, cadmium and mercury. The applied method for the quantitative determination of elements is the mass spectrometry with inductive combined plasma (ICP MS).	

Mercury (Hg)	PV-SA-E-322
Cadmium (Cd)	PV-SA-E-322
Lead (Pb)	PV-SA-E-322
Arsenic (As)	PV-SA-E-322

[1] Analysis by affiliated company bilacon GmbH

Special Analysis [1]	Method and what it provides
Under the undesired contaminants are such ones which are harmful in higher concentration, e.g. lead, cadmium and mercury. The applied method for the quantitative determination of elements is the mass spectrometry with inductive combined plasma (ICP MS) or OES	

Sodium (Na)	PV-SA-E-318
Cooper (Cu)	PV-SA-E-318
Iron (Fe)	PV-SA-E-318
Selenium (Se)	PV-SA-E-322
Zinc (Zn)	PV-SA-E-318
Phosphorous (P)	PV-AC-E-026
Calcium (Ca)	PV-SA-E-318
Magnesium (Mg)	PV-SA-E-318
Manganese (Mn)	PV-SA-E-318

[1] Analysis by affiliated company bilacon GmbH

Pesticides and other parameters [1,2]

Pesticides & others[1,2]	Method and what it provides
Pesticides: More than 2000 pesticide agents are known worldwide. In Germany about 650 pesticides are approved (authorized) which contain 252 agents. The authorization and use of pesticides in Europe is regulated by a number of laws. Often residues of pesticides are found which are prohibited in Germany but are applied in other countries. In March 2009 the European commission concluded a critical test of pesticides and approved a list of agents authorized by the EU. Of the approximately 1000 tested agents 26% passed the EU safety evaluation, 67% have been discarded and 7% have been taken off the market due to the high potential danger for humans and environment. For some substances apply transitional periods until the year 2018 at the latest Products of decomposition of pesticides which also remain on/in food are called pesticide residues. **Plant growth regulators:** Plant growth regulators are a sub group of pesticides. They serve among other things as a means for stem reduction, growth increase and root growth blocking. **PAKs (Polycyclic aromatic hydrocabons):** In case of incomplete combustion of organic material such as carbon, fuel oil, fuel, wood, tobacco PAKs are generated. They get through the air and the ground mainly into leavy vegetables and fruits and into the drinking water. The highest PAK levels can be found in smoked food. **Quaternary ammonium compounds (QAV):** The quaternary ammonium compounds are: BAC (benzalconium chloride) und DDAC (didecyldimethylammonium chloride). These are used in pesticides, plant strengthener and in the food production, e.g. as biocides (among others for disinfection).	
Pesticide multi-method	Determination of > 500 substances (PV-SA-085 (LC + GC)) – Pesticide list on request
Pesticide single-methods	LC-MS/MS or GC
Growth regulators	LC-MS//MS
PAKs (in food) EPA package	Analysis of 16 primary substances: Naphthalene, Acenaphthylene, Acenaphthene, Fluorines, Phenanthren, Anthracen, Fluoranthen, Pyren, Benzo(a)anthracen, Chrysen, Benzo(b)fluoranthen, Benzo(k)fluoranthen, Benzo(a)pyren, Dibenzo(ah)anthracen, Benzo(ghi)perylen and Indeno(1,2,3cd)pyren HPLC-UV/FLD
PAKs (in feed) PAK 4	Analysis of 4 EU relevant primary substances: Benzo(a)pyrene, Benz(a)anthracene, Benzo(b)fluoranthene und Chrysene (also: relevant parameters for QS system) HPLC-UV/FLD
Quaternary Ammonium Compounds	PV-SA-120 (SPE, LC-MS/MS)

[1] Analysis by affiliated company bilacon GmbH
[2] Analysis by accredited cooperation partner

Multi-method [1]
Determination of pesticides (multi-method)

Single-method [1]
Glyphosate, Glufosinate, AMPA
Phenylurea (Herbicide)
Dithiocarbamate (Fungicide)

Plant growth regulators [1]
Chlormequat and Mepiquat
Ethephon
Maleic hydrazide methyl

PAKs [1,2]
Food: EPA package [2]
Feed: PAK 4 [2]
Benzo-(a)-Pyrene [1]

Quaternary ammonium compounds [1]
Quaternary ammonium compounds (BAC-C8, BAC-C10, BAC-C12, BAC-C14, BAC-C16, BAC-C18, DDAC-C8, DDAC-C10, DDAC-C12, DDAC-C14, DDAC-C16, DDAC-C18)
Quaternary ammonium compounds (BAC-C8, BAC-C10, BAC-C12, BAC-C14, BAC-C16, BAC-C18, DDAC-C8, DDAC-C10, DDAC-C12, DDAC-C14, DDAC-C16, DDAC-C18, CPy, CTMA)
Quaternary ammonium compounds (BAC)
Quaternary ammonium compounds (DDAC)

Further parameters [1]
Carnauba wax (PV-SA-103)
Mineral oil components (MOSH/MOAH) (PV-SA-132)
Amino alcohols (PV-SA-109)
BHT (2,6-Bis(1,1-dimethylethyl)-4-methylphenol) (HPLC)

[1] Analysis by affiliated company bilacon GmbH
[2] Analysis by accredited cooperation partner

Dioxins & PCB [2]

Dioxins & PCB [2]	Method and what it provides
Dioxins Both groups of substances of the polychlorinated dibenzo-p-dioxins (PCDD) and dibenzofuranes (PCDF) are summarized under the term „dioxins“. They consist of 75 respectively 135 individual compounds (congeners). They result from chemical processes where chlorine is employed and are undesired byproducts. In the past among the relevant dioxin sources were pentachlorophenol (PCP) used as a biocide in great quantities as well as the technical PCB compositions themselves. Dioxins disperse on dust particles in the air in the environment; this leads to the adsorption and enrichment of plants, grounds and sediments. Due to their chemical structure 17 congeners of the 210 dioxins accumulate strongly in living organisms. **Polychlorinated biphenyls (PCB)** Until the 1980s PCB was implemented mainly in open applications among others as softener and flame retardants or for the impregnation and stabilization. Due to their similar physical chemical characteristics PCB have a similar environmental behavior as dioxins. Many PCB congeners have a strong ability for bio accumulation, this means there is an important concentration of harmful substances in the last links of the food chain, to which mainly humans belong, too.	
Polychlorinated dibenzo-dioxins and -furanes (PCDD/F)	Analysis using HRGC/HRMS Indication of the 17 2,3,7,8-congeners and the toxicity equivalent (TEQ) according to WHO 2005 Method (LM): §64 LFGB, ASU L 00.00-78 (HRGC/HRMS) Method (FM): DIN EN 16215 (July 2012)
dioxin-like PCB dl-PCB	Indication of the PCB-congeners 77, 81,126, 169, 105, 114, 118, 123, 156, 157, 167, 189 and the toxicity equivalent (TEQ) according to WHO 2005 excluding and including the limit of quantification. Method (LM): §64 LFGB, ASU L 00.00-78 (HRGC/HRMS) Method (FM): DIN EN 16215 (July 2012)
non dioxin-like PCB ndl-PCB	PCB Nr. 28, PCB No. 52, PCB No. 101, PCB No. 138, PCB No. 153, PCB No. 180 Method: VDLUFA Methods, Bd VII, Method 3.3.2.2 (2003)

Dioxins & PCB [2]
Package: PCDD/F and dl-PCB
Package: PCDD/F, dl-PCB and ndl-PCB

[2] Analysis by accredited cooperation partner

Microbiological analysis [1]

Microbiological analysis [1]
There are two types of micro organisms: the useful/beneficial germs and the spoilage-causing and pathogenous germs. If pathogenous germs such as Salmonella, E. coli or Listeria are detected in food ready for consumption it must not be sold. Spoilage agents do not bear any health risk for the consumer but can have influence on the durability of the food.

Microbiological analysis [1]	
Total bacterial count / aerobic bacteria	(ASU, L06.00-19)
Enterobacteriaceae	(PV-MB-014)
Yeast and mould	(PV-MB-009 + PV-MB-010)
Coliform bacteria	(PV-MB-001)
E. coli	(PV-MB-002)
Bacillus cereus	(PV-MB-007)
Sulphite reducing Clostridia	(PV-MB-025)
Lactobacillus	(PV-MB-008)
Salmonella in 25 g	(PV-MB-006)
Listeria monocytogenes in 25 g	(PV-MB-017)
Pseudomonas	(PV-MB-019)
Pseudomonas aeruginosa	(PV-MB-020)
Legionella	(PV-MB-E-013; Membrane filtration DIN EN ISO 11731-2)
Further parameters on request	

[1] Analysis by affiliated company bilacon GmbH

General Chemistry [1]

General Chemistry [1]
Food chemistry determines the composition of food and how it changes during production, storage and preparation.

Parameters
Nutritional values Big 8: dry mass, fat, proteins, ash, fiber, total sugar, sodium including extraction, fatty acid, calculations
Crude protein
Crude protein Kjehldahl
Total fat
Sucrose
Sulfite / sulphur dioxide
Dry mass
Fatty acids (incl. extraction)
Fatty acids (without extraction)
Nitrate
Inorganic bromide / Methyl bromide (calculated as bromide)
Acid value
Peroxide value
Common salt (calculated from sodium)
Common salt (calculated from chloride)
Ethanol (enzymatic)
Ethanol (pycnometrically)

[1] Analysis by affiliated company bilacon GmbH

Further Parameters [2]

Further Parameters [2]

Parameters
Antimicrobial active substances (4-plate test) [2]
Further parameters on request

[2] Analysis by accredited cooperation partner

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