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(See Table 1; page 7, program 343)

EQA schemes closed

Information on sample properties

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INSTAND External Quality Assessment Schemes – September 2018

Virus Immunology
Virus Genome Detection

Information on Sample Properties

Dear colleagues,

You have registered for one or several of the INSTAND external quality assessment (EQA) schemes in virus diagnostics in September 2018.

The INSTAND EQA schemes – September 2018 for virus immunology and virus genome detection are now closed.

For orientation, you receive information on the properties of the samples which were tested in the respective EQA scheme of June 2018.
The pre-evaluation of these EQA schemes which you usually receive, will be supplied in due time together with participation documents (certificate of successful participation, statement of participation, statement of individual results).

Please note that information on

- **target values/target value intervals for quantitative results and**
- **final evaluation of the respective samples**

will be specified in the forthcoming pre-evaluation, the participation documents as well as the reports of the corresponding EQA program.

For questions, please do not hesitate to contact us.

Prof. Dr. Heinz Zeichhardt

Dr. Martin Kammel

Table 1: EQA Schemes Virus Immunology – September 2018
Information on sample properties

Program	Group	RiliBÄK	Analyte	Sample	Sample properties		
					qualitative	dilution	sample source
Chikungunya virus[#] (Ak) serum* plasma**	402[#]	*conform to B 2*	anti-CHIKV-IgG anti-CHIKV-IgM	402010*	negative negative		serum of a healthy blood donor **without signs** of an acute, recent or past chikungunya virus infection
			anti-CHIKV-IgG anti-CHIKV-IgM	402011*,§= 402012	positive negative		**The samples 402011 and 402012 are identical. The sera derive from patient G-C5.** N.B.: The same patient G-C5 also donated the primarily derived serum, which was used for sample 402013. Samples 402011 and 402012 represent the **follow-up serum** (pool serum) of patient G-C5 with a **past** chikungunya virus infection. anamnestic details: see sample 402013; blood collected: **9 months and 16 months after onset of disease**
			anti-CHIKV-IgG anti-CHIKV-IgM	402012*,§= 402011	positive negative		
			anti-CHIKV-IgG anti-CHIKV-IgM	402013*	positive positive		**The sera for sample 402013 derive from patient G-C5.** N.B.: The same patient G-C5 also donated the follow-up serum, which was used for the identical samples 402011 and 402012. Sample 402013 (pool serum) represents the **primarily derived serum** from patient G-C5 with an **acute** chikungunya virus infection. chikungunya virus RNA negative; traveler returned from French Guiana; clinical signs at onset of disease: exanthema on the legs, heavy joint paint, limb pain, fever; blood collected **7 days, 22 days and 30 days after onset of disease**

§ The samples 402011 and 402012 are identical.

Non-marked samples derive from independent preparations.

[#] The EQA program Virus Immunology - Chikungunya Virus (402) is performed in cooperation with Bernhard-Nocht-Institut, Hamburg (Nationales Referenzzentrum für tropische Infektionserreger, Abteilung für Virologie, WHO Collaborating Centre for Arbovirus and Haemorrhagic Fever Reference and Research; Prof. Dr. Stephan Günther, Dr. Petra Emmerich und Prof. Dr. Dr. Jonas Schmidt-Chanasit).

Table 1 (contd.): EQA Schemes Virus Immunology – September 2018
Information on sample properties

Program	Group	RiliBÄK	Analyte	Sample	Sample properties		
					qualitative	dilution	sample source
Cyto-megalo-virus (Ab) serum	351	*conform to B 2*	anti-CMV-IgG anti-CMV-IgM	351067	negative avidity: no avidity/ not done negative		negative healthy blood donors (pool)
			anti-CMV-IgG anti-CMV-IgM	351068	positive avidity: high negative		past CMV infection (two healthy blood donors)
Dengue viruses* (Ab and NS1-Ag) serum	350*	anti-Dengue *conform to B 2* NS 1 Ag *conform to B 3*	anti-Dengue-IgG anti-Dengue-IgM Dengue NS1-Ag	350066	negative negative negative		serum of a healthy blood donor **without signs** of an acute, recent or past dengue virus infection
			anti-Dengue-IgG anti-Dengue-IgM Dengue NS1-Ag	350067	positive positive negative		serum from patient G-D26 with a **recent** primary dengue virus infection (DENV-3); traveller returned from Malaysia and Indonesia; clinical signs at onset of disease: diarrhea, fever; blood collected **4 weeks after onset of disease**
			anti-Dengue-IgG anti-Dengue-IgM Dengue NS1-Ag	350068	negative negative negative		serum of a healthy blood donor **without signs** of an acute, recent or past dengue virus infection
			anti-Dengue-IgG anti-Dengue-IgM Dengue NS1-Ag	350069	negative negative positive		dengue virus serum G-D28 represents an **acute** primary dengue virus infection **positive for NS1-Ag only** serum of a healthy blood donor without signs of an acute or past dengue virus infection spiked with a cell culture propagated virus (DENV-2; heat inactivated)

Non-marked samples derive from independent preparations.

* The EQA program Virus Immunology - Dengue Viruses (350) is performed in cooperation with Bernhard-Nocht-Institut, Hamburg (Nationales Referenzzentrum für tropische Infektionserreger, Abteilung für Virologie, WHO Collaborating Centre for Arbovirus and Haemorrhagic Fever Reference and Research; Prof. Dr. Stephan Günther, Dr. Petra Emmerich und Prof. Dr. Dr. Jonas Schmidt-Chanasit).

Table 1 (contd.): EQA Schemes Virus Immunology – September 2018
Information on sample properties

Program	Group	RiliBÄK	Analyte	Sample	Sample properties		
					qualitative	dilution	sample source
Hanta-viruses* (Ab) serum	355*	*conform to B 2*	anti-Dobrava-IgG anti-Dobrava-IgM	355065	positive negative		serum from **patient H13** with a **past Dobrava-Belgrade virus infection,** probably acquired in Brandenburg, Germany, anamnesis concerning a stay abroad outside Europe excluded, at onset of disease hospitalization necessary, characteristic symptoms such as elevated creatinine, flu-like symptoms and abnormal fatigue blood collected **approx. 5 years after onset of disease**
			anti-Hanta-IgG anti-Hanta-IgM	355066§= 355067	negative negative		serum of healthy blood donors (pool) **without signs** of an acute or past hanta virus infection
			anti-Hanta-IgG anti-Hanta-IgM	355067§= 355066	negative negative		
			anti-Puumala-IgG anti-Puumala-IgM	355068	positive detection of persisting anti-PUUV-IgM possible accepted results: negative/ borderline/ positive		serum from **patient G-H9** with a **past / post-acute Puumala virus infection,** probably acquired in North Rhine Westphalia, Germany, anamnesis concerning a stay abroad outside Europe excluded; at onset of disease outpatient treatment, characteristic symptoms such as elevated creatinine, increased liver test values and flu-like symptoms; Blood collected **approx. 4 months after onset of disease**

§ The samples 355066 and 355067 are identical.

Non-marked samples derive from independent preparations.

* The EQA program Virus Immunology - Hantaviruses (355) is performed in cooperation with Nationales Konsiliarlaboratorium für Hantaviren (Charité - Universitätsmedizin Berlin, Campus Mitte, Institut für Virologie: Prof. Dr. Jörg Hofmann, Prof. Dr. Christian Drosten).

Please note that information on

- **target values/target value intervals for quantitative results and**
- **final evaluation of the respective samples**

will be specified in the forthcoming pre-evaluation, the participation documents as well as the reports of the corresponding EQA program.

Table 1 (contd.): EQA Schemes Virus Immunology – September 2018
Information on sample properties

Program	Group	RiliBÄK	Analyte	Sample	Sample properties		
					qualitative	dilution	sample source
Hepatitis A virus (Ab) serum	343	mandatory: B 2	anti-HAV	343133	positive *target value will be specified*	(a) 1 : 150	anti-HAV-IgG positive healthy blood donor
			anti-HAV	343134	positive *target value will be specified*	(a) 1 : 300	
			anti-HAV-IgM	343135	negative		negative healthy blood donors (pool)
			anti-HAV-IgM	343136	positive	1 : 30	acute hepatitis A
Hepatitis B virus (prog. 1) (HBsAg anti-HBs anti-HBc) serum	344	mandatory: B 3	HBsAg	344397	positive *target value will be specified*	(b) 1 : 2 000	acute hepatitis B
			HBsAg	344398	positive *target value will be specified*	(b) 1 :4 000	
			HBsAg	344399	positive *target value will be specified*	(b) 1 : 1 000	
			HBsAg	344400	positive *target value will be specified*	(b) 1 : 8 000	
		mandatory: B 2	anti-HBs	344401	negative *target value will be specified*		negative healthy blood donors (pool)
			anti-HBs	344402	low positive (<10 IU/l) not evaluated		anti-HBs positive healthy blood donor
			anti-HBs	344403	positive *target value will be specified*	1 : 1 375	anti-HBs positive healthy blood donor
			anti-HBs	344404	positive *target value will be specified*	1 : 25	patient after acute hepatitis B (healed up with complete seroconversion)
		mandatory: B 2	anti-HBc	344405	negative		negative healthy blood donors (pool)
			anti-HBc	344406	positive	(c) 1 : 2 000	chronic hepatitis B (negative for HBeAg, anti-HBc-IgM negative)
			anti-HBc	344407	positive	(c) 1 : 500	
			anti-HBc	344408	positive	(c) 1 : 1 000	
Hepatitis B virus (prog. 2) (anti-HBc-IgM HBeAg anti-HBe) serum	345	mandatory: B 2	anti-HBc-IgM	345199	negative		negative healthy blood donors (pool)
			anti-HBc-IgM	345200	positive	1 : 160	acute hepatitis B
		mandatory: B 3	HBeAg	345201	negative		negative healthy blood donors (pool)
			HBeAg	345202	positive	1 :800	chronic hepatitis B
		mandatory: B 2	anti-HBe	345203	positive	(d) 1 : 90	chronic hepatitis B (negative for HBeAg)
			anti-HBe	345204	positive	(d) 1 : 180	

Non-marked samples derive from independent preparations.

a, b, c, d: Marked samples derive from corresponding stock materials diluted in consecutive steps.

Sample properties corrected on 29 October 2018.

Please note that information on
- **target values/target value intervals for quantitative results and**
- **final evaluation of the respective samples**

will be specified in the forthcoming pre-evaluation, the participation documents as well as the reports of the corresponding EQA program.

Table 1 (contd.): EQA Schemes Virus Immunology – September 2018
Information on sample properties

Program	Group	RiliBÄK	Analyte	Sample	Sample properties		
					qualitative	dilution	sample source
Hepatitis C virus (Ab and HCV-Ag) serum* plasma**	346	anti-HCV **mandatory: B 2** HCV Ag **mandatory: B 3**	anti-HCV HCV antigen	346133**	negative negative		negative healthy blood donors (pool)
			anti-HCV HCV antigen	346134**	positive positive	1 : 20	chronic hepatitis C (subtype 4a) **primarily derived plasma** (before therapy) from the same patient whose follow-up plasma was used for sample 346136
			anti-HCV HCV antigen	346135*	negative negative		negative healthy blood donors (pool)
			anti-HCV HCV antigen	346136**	positive$ negative	1 : 20	condition after chronic hepatitis C (subtype 4a) (successful therapy) **follow-up plasma** whose primarily derived plasma (before therapy) was used for sample 346134
HIV-1/ HIV-2 (Ab) serum	335	**mandatory: B 2**	anti-HIV-1	335133	positive	(e) 1 : 50	HIV-1 infection
			anti-HIV-1	335134	positive	(e) 1 : 100	
			anti-HIV-1	335135	positive	(e) 1 : 50	
			anti-HIV-1/2	335136	negative		negative healthy blood donors (pool)
HIV-1 p24 Ag serum	337	**mandatory: B 3**	p24 Ag	337067	positive	1 : 25 000	HIV-1 infection (spiked serum pool of negative blood donors; HIV-1 heat inactivated)
			p24 Ag	337068	negative		negative healthy blood donors (pool)
Rabies virus* serum	336*	*conform to B 2*	anti-RABV	336009	negative		negative healthy blood donor
			anti-RABV	336010	positive		recent active rabies vaccination

Non-marked samples derive from independent preparations.

e: The marked dilutions were performed with the same stock materials.

$ Sample 346136: Accepted target values for complementary tests (test category 20): positive and indeterminate.

* The EQA program Virus Immunology - Rabies Virus (336) is performed in cooperation with Nationales Konsiliarlabor für Tollwut (Rabies Virus) (Universitätsklinikum Essen, Institut für Virologie, Prof. Dr. Ulf Dittmer, Prof. Dr. Stefan Ross).

Please note that information on
- **target values/target value intervals for quantitative results and**
- **final evaluation of the respective samples**

will be specified in the forthcoming pre-evaluation, the participation documents as well as the reports of the corresponding EQA program.

Table 1 (contd.): EQA Schemes Virus Immunology – September 2018
Information on sample properties

Program	Group	RiliBÄK	Analyte	Sample	Sample properties		
					qualitative	dilution	sample source
Zika virus* (Ab) serum	338*	*conform to B 2*	anti-Zika-IgG anti-Zika-IgM	338016	positive negative		serum of patient G-Z1 (pool serum) with a **past** Zika virus infection; stay in Sao Paulo and Ponta Negara, Brazil clinical signs at onset of disease: strong headaches, nausea, intestinal disorders, skin rash (not itchy), fever to 38,5°C blood collected: **14 and 26 months after onset of disease**
			anti-Zika-IgG anti-Zika-IgM	338017	negative negative		negative healthy blood donor
			anti-Zika-IgG anti-Zika-IgM	338018	positive positive		serum of patient G-Z4 with a **post-acute** Zika virus infection (Zika virus RNA not detectable anymore); stay in the Caribbean / Martinique clinical signs: diarrhea, night sweats, exanthema, swelling of the joints, conjunctivitis blood collected: **53 days after onset of disease**

Non-marked samples derive from independent preparations.

* The EQA program Virus Immunology - Zika Virus (338) is performed in cooperation with Bernhard-Nocht-Institut, Hamburg (Nationales Referenzzentrum für tropische Infektionserreger, Abteilung für Virologie, WHO Collaborating Centre for Arbovirus and Haemorrhagic Fever Reference and Research; Prof. Dr. Stephan Günther, Dr. Petra Emmerich und Prof. Dr. Dr. Jonas Schmidt-Chanasit).

Please note that information on
- **target values/target value intervals for quantitative results and**
- **final evaluation of the respective samples**

will be specified in the forthcoming pre-evaluation, the participation documents as well as the reports of the corresponding EQA program.

Table 2: EQA Schemes Virus Genome Detection – September 2018
Information on sample properties

Program	Group	RiliBÄK	Sample	Sample properties			
				qualitative (note on geno-/*subtype*)	dilution	Target value of all methods (provisional data)	
						copies/ml	IU/ml
BK virus (DNA) suspension of urine	364	*conform to B 3*	364037	positive	1 : 50 000	*target values will be specified*	*target values will be specified*
			364038	positive	(a) 1 : 400		
			364039	negative	1 : 100		
			364040	positive	(a) 1 : 4 000		
Chikungunya virus[&] (RNA) cell lysates	392[&]	*conform to B 3*	392029	negative	-------	*target values will be specified*	*target values will be specified*
			392030	positive	(b) 1 : 1 500 (inactivated)		
			392031	positive	(b) 1 : 13 500 (inactivated)		
			392032	positive	1 : 4 500 (inactivated)		
CMV (DNA) spiked plasma	365	**manda-tory: B 3**	365133	negative	-------	*target values will be specified*	*target values will be specified*
			365134	positive	1 : 7 142.9		
			365135	positive	1 : 2 000		
			365136	positive	1 : 1 142.9		
HAV (RNA) spiked plasma	377	**manda-tory: B 3**	377133	positive	(c) 1 : 9 000	*target values will be specified*	*target values will be specified*
			377134	positive	1 : 500		
			377135	negative	-------		
			377136	positive	(c) 1 : 3 000		
HBV (DNA) plasma	361	**manda-tory: B 3**	361133	positive	(d) 1 : 2 213.6	*target values will be specified*	*target values will be specified*
			361134	positive	(d) 1 : 70 000		
			361135	positive	(d) 1 : 700		
			361136	negative	-------		
HCV (RNA) plasma	362	**manda-tory: B 3**	362133	positive (subtype 1b)	1 : 675	*target values will be specified*	*target values will be specified*
			362134	positive (genotype 3)	(e) 1 : 100		
			362135	negative	-------		
			362136	positive (genotype 3)	(e) 1 : 1 000		
HDV (RNA) plasma	400	*conform to B 3*	400029	positive	1 : 5 000	*target values will be specified*	*target values will be specified*
			400030	positive	(f) 1 : 100		
			400031	negative	-------		
			400032	positive	(f) 1 : 900		
HIV-1 (RNA) spiked plasma	360	**manda-tory: B 3**	360133	positive (group M / subtype B)	(g) 1 : 50 000	*target values will be specified*	*target values will be specified*
			360134	positive (group M / subtype B)	(g) 1 : 158 115.4		
			360135	positive (group M / subtype B)	(g) 1 : 15 811.5		
			360136	negative	-------		

Non-marked samples derive from independent preparations.

a, b, c, d, e, f, g: Marked samples derive from corresponding stock materials diluted in consecutive steps.

[&] The EQA programs Virus Genome Detection – Chikungunya virus (392), Dengue Viruses (369), West Nile Virus (391) and Zika Virus (403) are performed in cooperation with Bernhard-Nocht-Institut, Hamburg (Nationales Referenzzentrum für tropische Infektionserreger, Abteilung für Virologie und WHO Collaborating Centre for Arbovirus and Haemorrhagic Fever Reference and Research: Prof. Dr. Stephan Günther, Prof. Dr. Dr. Jonas Schmidt-Chanasit und Dr. Petra Emmerich).

Please note that information on
- **target values/target value intervals for quantitative results and**
- **final evaluation of the respective samples**

will be specified in the forthcoming pre-evaluation, the participation documents as well as the reports of the corresponding EQA program.

Table 2 (contd.): EQA Schemes Virus Genome Detection
September 2018 – Information on sample properties

Program	Group	RiliBÄK	Sample	Sample properties			
				qualitative (note on geno-/*subtype*)	dilution	Target value of all methods (provisional data)	
						copies/ml	IU/ml
JC virus (DNA) suspension of urine	394	*conform to B 3*	394029	negative	1 : 1 000	*target values will be specified*	*target values will be specified*
			394030	positive	1 : 33		
			394031	positive	1 : 66		
			394032	positive	1 : 50		
Parvovirus B19 (DNA) plasma	367	**manda-tory: B 3**	367133	positive	1 : 750 000	*target values will be specified*	*target values will be specified*
			367134	positive	(h) 1 : 30 000		
			367135	negative	-------		
			367136	positive	(h) 1 : 3 000 000		
Rabies virus* vaccine	390*	*conform to B 3*	390017	positive	(i) 1 : 1 250	*target values will be specified*	*target values will be specified*
			390018	positive	(i) 1 : 6 250		
			390019	positive	(i) 1 : 250		
			390020	negative	-------		

Non-marked samples derive from independent preparations.

h, i: Marked samples derive from corresponding stock materials diluted in consecutive steps.

* The EQA program Virus Genome Detection - Rabies Virus (390) is performed in cooperation with Nationales Konsiliarlabor für Tollwut (Rabies Virus) (Universitätsklinikum Essen, Institut für Virologie, Prof. Dr. Ulf Dittmer, Prof. Dr. Stefan Ross).

Please note that information on
- **target values/target value intervals for quantitative results and**
- **final evaluation of the respective samples**

will be specified in the forthcoming pre-evaluation, the participation documents as well as the reports of the corresponding EQA program.

Table 3: EQA Schemes Virus Genome Detection incl. Typing
September 2018 – Information on sample properties

Program	Group	RiliBÄK	Sample	Sample properties			
				qualitative	Target value of all methods copies/ml	species	type (note on dilution)
Dengue viruses[&] (RNA) cell lysates	369[&]	*conform to B 3*	369037	positive	*target values will be specified*	----	DENV-3 (inactivated) 1 : 100 diluted (j)
			369038	negative		----	----
			369039	positive		----	DENV-3 (inactivated) 1 : 900 diluted (j)
			369040	positive		----	DENV-2 (inactivated) 1 : 300 diluted
HCV-Geno-/Subtyping* serum	375*	**mandatory: B 3**	375041[#]	positive	*target values will be specified*	----	genotype 3[#] / (subtype 3a)[#] 1 : 118.8 diluted
			375042[§]	positive		----	genotype 1 / subtype 1a[§] 1 : 190 diluted
			375043[$]	positive		----	genotype 1[$] / subtype 1b[$] 1 : 52.8 diluted
			375044[#]	positive		----	genotype 2[#] / (subtype 2b)[#] 1 : 82.6 diluted
			375045[#]	positive		----	genotype 2[#] / (subtype 2a)[#] 1 : 95 diluted
Para-influenza-viruses (RNA) cell lysate	388	*conform to B 3*	388037	negative	*target values will be specified*	----	----
			388038	positive		----	PIV-3 1 : 100 000 diluted (k)
			388039	positive		----	PIV-2 1 : 1 000 diluted
			388040	positive		----	PIV-3 1 : 10 000 diluted (k)

Non-marked samples derive from independent preparations.

j, k: Marked samples derive from corresponding stock materials diluted in consecutive steps.

[&] The EQA programs Virus Genome Detection – Chikungunya virus (392), Dengue Viruses (369), West Nile Virus (391) and Zika Virus (403) are performed in cooperation with Bernhard-Nocht-Institut, Hamburg (Nationales Referenzzentrum für tropische Infektionserreger, Abteilung für Virologie und WHO Collaborating Centre for Arbovirus and Haemorrhagic Fever Reference and Research: Prof. Dr. Stephan Günther, Prof. Dr. Dr. Jonas Schmidt-Chanasit and Dr. Petra Emmerich).

* The EQA program Virus Genome Detection - HCV-Genotyping (375) is performed in cooperation with Nationales Referenzzentrum für Hepatitis C-Viren (Universitätsklinikum Essen, Institut für Virologie, Prof. Dr. Ulf Dittmer, Prof. Dr. Stefan Ross).

[#] Samples 375041 (subtype 3a), 375044 (subtype 2b) und 375045 (subtype 2a): The statement of the correct genotype will be considered for obtaining a certificate of successful participation.

[§] Samples 375042 (subtype 1a): The statement of the correct subtype is necessary for obtaining a certificate of successful participation.

[$] Sample 375043 (subtype 1b): In test category 30, some participants could not determine the subtype by using the test of one manufacturer (Abbott - RealTime HCV Genotype II). The final evaluation of these inconsistent results will be commented in the forthcoming pre-evaluation.

Please note that information on
- **target values/target value intervals for quantitative results and**
- **final evaluation of the respective samples**

will be specified in the forthcoming pre-evaluation, the participation documents as well as the reports of the corresponding EQA program.

Table 3 (contd.): EQA Schemes Virus Genome Detection incl. Typing September 2018 – Information on sample properties

Program	Group	RiliBÄK	Sample	Sample properties			
				qualitative	Target value of all methods copies/ml	species	type (note on dilution)
West Nile virus[&] (RNA) cell lysate	391[&]	*conform to B 3*	391053	positive	*target values will be specified*	----	WNV-1 (inactivated) 1 : 3 diluted (l)
			391054	positive		----	WNV-2 (inactivated) 1 : 100 000 diluted
			391055	positive		----	WNV-2 (inactivated) 1 : 30 000 diluted
			391056	positive		----	WNV-1 (inactivated) 1 : 30 diluted (l)
			391057	positive		----	WNV-1 (inactivated) 1 : 300 diluted (l)
			391058	negative		----	----
Zika virus[&] (RNA) plasma	403[&]	*conform to B 3*	403021	positive	*target values will be specified*	----	African lineage (inactivated) 1 : 200 diluted
			403022	positive		----	Asian lineage (inactivated) 1 : 5 000 diluted
			403023	positive		----	Asian lineage (inactivated) 1 : 30 diluted
			403024	negative		----	----

Non-marked samples derive from independent preparations.

l: The marked dilutions were performed with the same stock materials.

[&] The EQA programs Virus Genome Detection – Chikungunya virus (392), Dengue Viruses (369), West Nile Virus (391) and Zika Virus (403) are performed in cooperation with Bernhard-Nocht-Institut, Hamburg (Nationales Referenzzentrum für tropische Infektionserreger, Abteilung für Virologie und WHO Collaborating Centre for Arbovirus and Haemorrhagic Fever Reference and Research: Prof. Dr. Stephan Günther, Prof. Dr. Dr. Jonas Schmidt-Chanasit and Dr. Petra Emmerich).

Please note that information on

- **target values/target value intervals for quantitative results and**
- **final evaluation of the respective samples**

will be specified in the forthcoming pre-evaluation, the participation documents as well as the reports of the corresponding EQA program.