



μ

μ

μ

μ

μ

μ.

.



EUROPEAN MEDICINES AGENCY
SCIENCE MEDICINES HEALTH

21 July 2011
EMA/CHMP/EWP/192217/2009
Committee for Medicinal Products for Human Use (CHMP)

Guideline on bioanalytical method validation

Draft agreed by the Efficacy Working Party	September 2009
Adoption by CHMP for release for consultation	19 November 2009
End of consultation (deadline for comments)	31 May 2010
Agreed by Pharmacokinetics Working Party (PKWP)	June 2011
Adoption by CHMP	21 July 2011
Date for coming into effect	1 February 2012

Guidance for Industry

Bioanalytical Method Validation

DRAFT GUIDANCE

This guidance document is being distributed for comment purposes only.

Comments and suggestions regarding this draft document should be submitted within 90 days of publication in the *Federal Register* of the notice announcing the availability of the draft guidance. Submit electronic comments to <http://www.regulations.gov>. Submit written comments to the Division of Dockets Management (HFA-305), Food and Drug Administration, 5630 Fishers Lane, rm. 1061, Rockville, MD 20852. All comments should be identified with the docket number listed in the notice of availability that publishes in the *Federal Register*.

For questions regarding this draft document contact (CDER) Brian Booth, 301-796-1508 or (CVM) John Kadavil, John.Kadavil@fda.hhs.gov

U.S. Department of Health and Human Services
Food and Drug Administration
Center for Drug Evaluation and Research (CDER)
Center for Veterinary Medicine (CVM)

September 2013
Biopharmaceutics

Revision 1

(validation)

(validation)

μ

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(selectivity)

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$\mu\mu$

, μ

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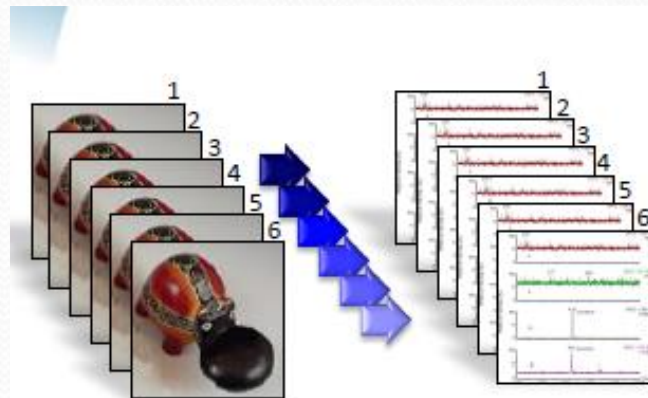
μ

6

μ

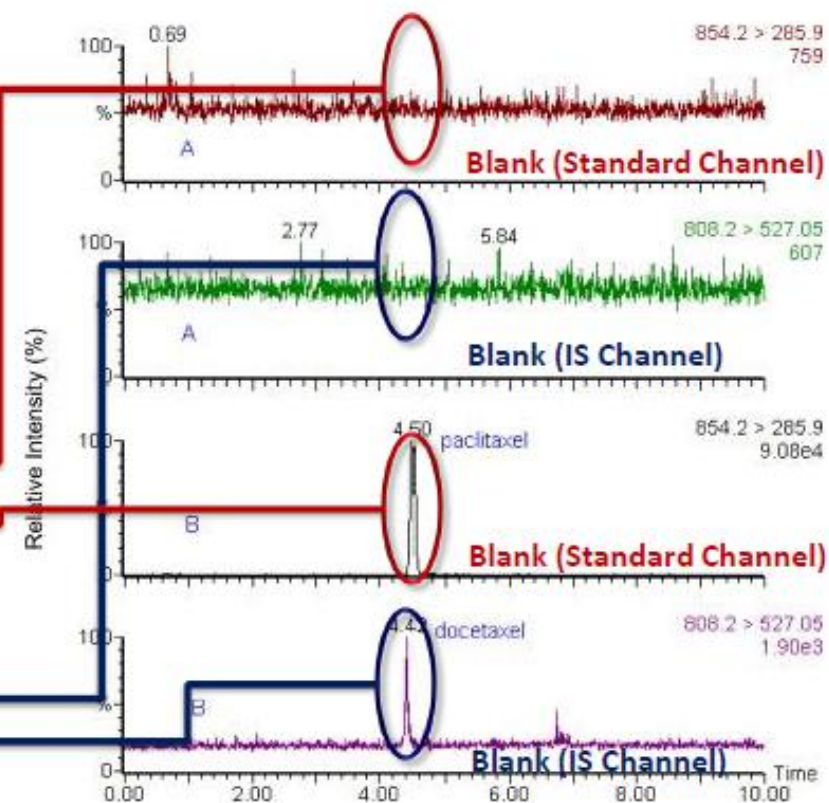
(
(pooling)

),



$$\frac{\text{Area Blank}}{\text{Mean LLOQ Area}} \times 100 \leq 20\%$$

$$\frac{\text{Area Blank}}{\text{Mean LLOQ Area}} \times 100 \leq 5\%$$

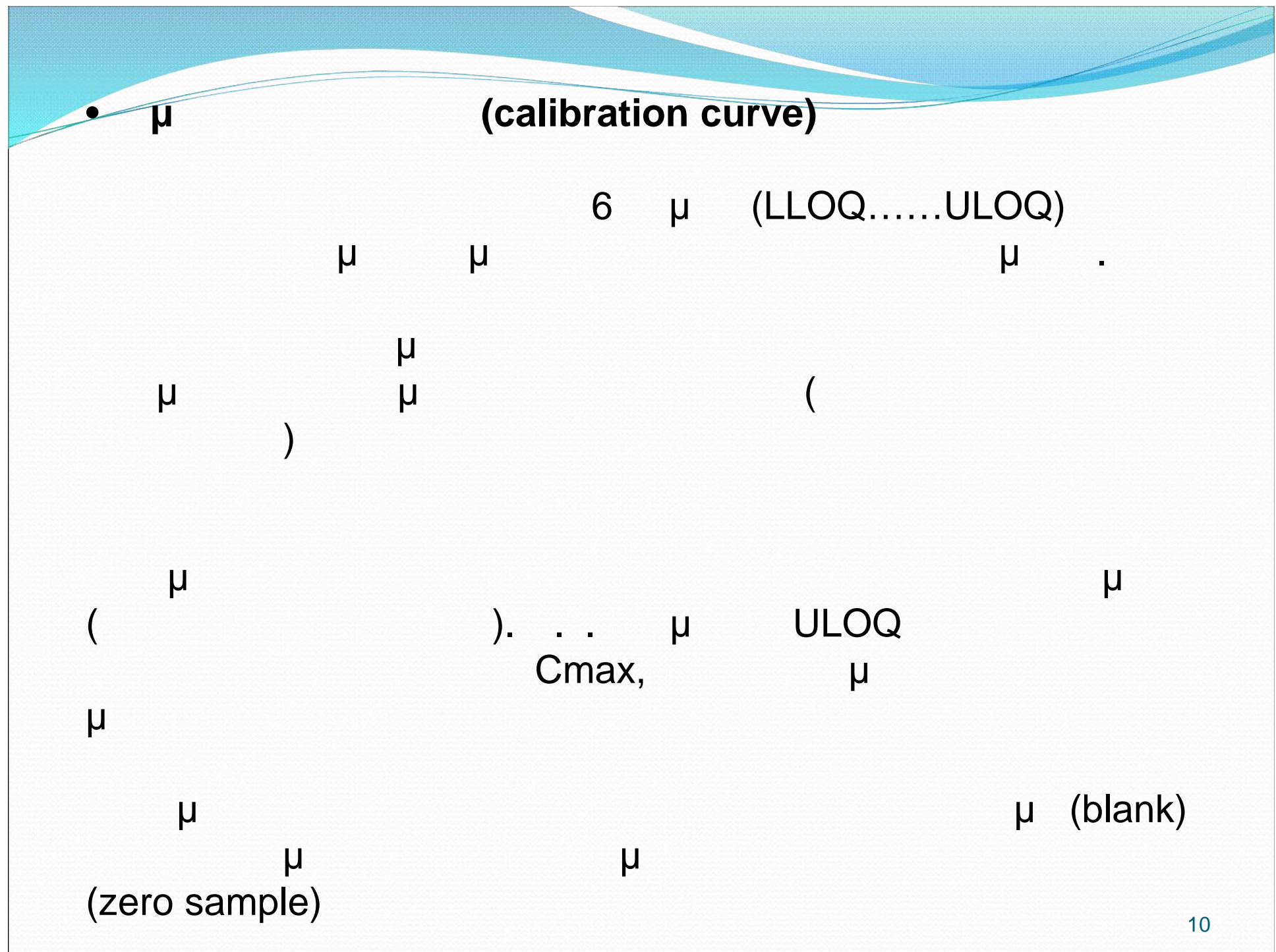


• μ (carry-over)

μ , μ μ μ .
 (ULOQ). standard μ
 μ < 5% LLOQ (μ standard) μ < 20%
 μ .

• μ μ (Lower Limit of Quantitation)

S/N > 10). μ LOQ (μ ,
 LLOQ < 5% μ Cmax. μ



- μ

(calibration curve)

(μ μ)
(back calculated)
 μ μ ,

<15%
LLOQ (<20%).

μ LLOQ & ULOQ,

μ ,
 μ . ,
50% μ .

μ r > 0.98

μ $\mu\mu$

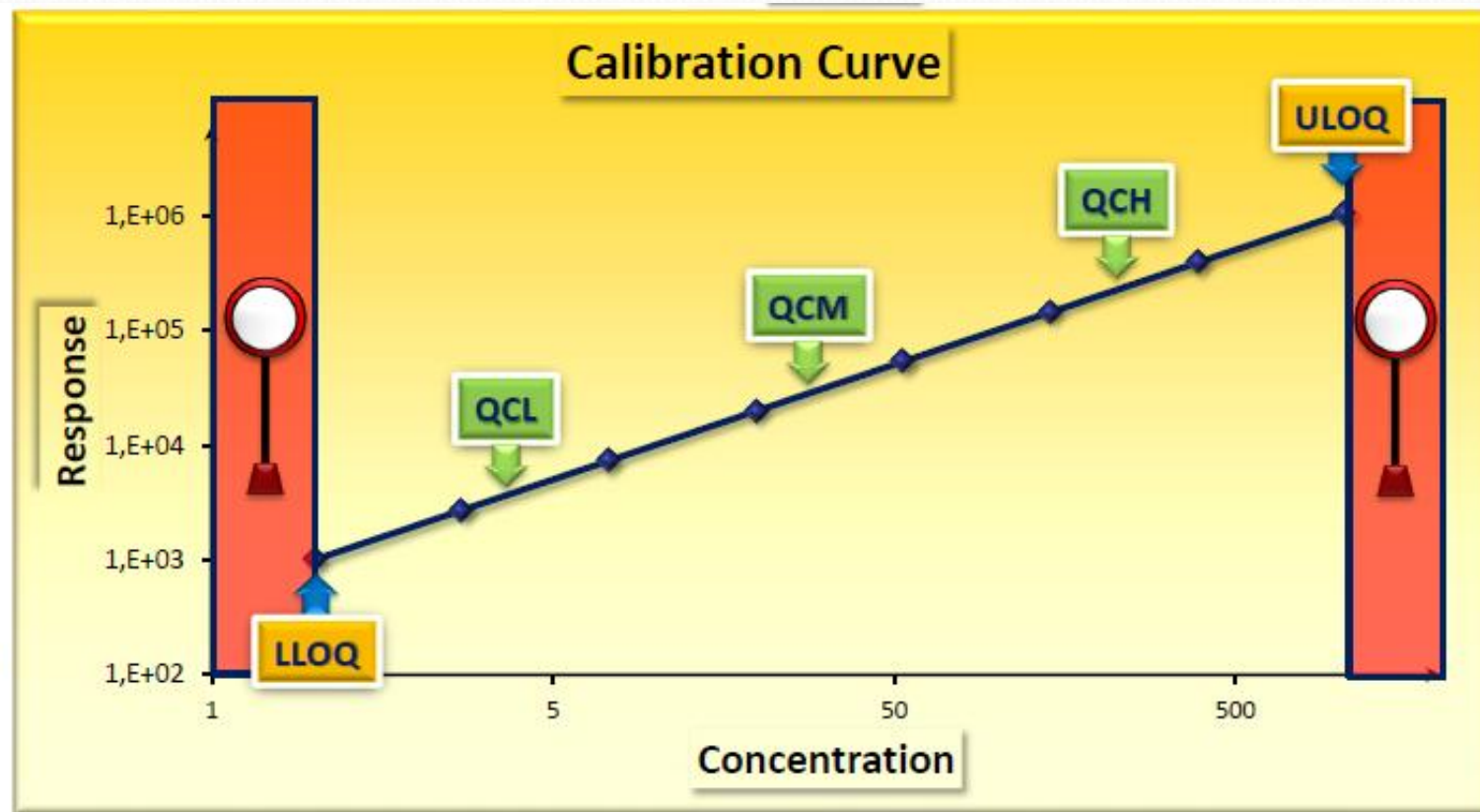
LLOQ=Lower limit
of quantification

QCL=Low Quality
Control

QCM=Medium
Quality Control

QCH=High Quality
Control

ULOQ=Upper Limit
of quantification



(accuracy)

•

μ
 μ

μ

(stock solution) 4 3
Control, QC samples)

μ

(Quality

.

$QC_L = LLOQ$

$QC_1 = 3 \times LLOQ$

$QC_2 = \sim 50\% ULOQ$

$QC_3 = > 75\% ULOQ$

μ

%

(recovery %)

μ

μ

(% bias, % RE).

(accuracy)

μ (run)

2/3

*

:

85-115%
80-120%

1-3
L

assay)

μ

μ

μ (intra-
 μ (inter-assay)

*

6

μ

μ

μ

3

μ

• (precision)

Deviation, SD)
(%RSD)

μ

μ

%

(Standard

μ

(run)

:

15%
20%

1-3
L

μ

μ

assay)

μ (intra-

μ

(inter-assay)

(dilution integrity)

μ

μ

μ

$\mu > \text{ULOQ}$

‘ ’

μ

μ

:

Accuracy 85-115%
Precision <15%

μ

(Extraction Recovery)

•

•

μ

μ

μ

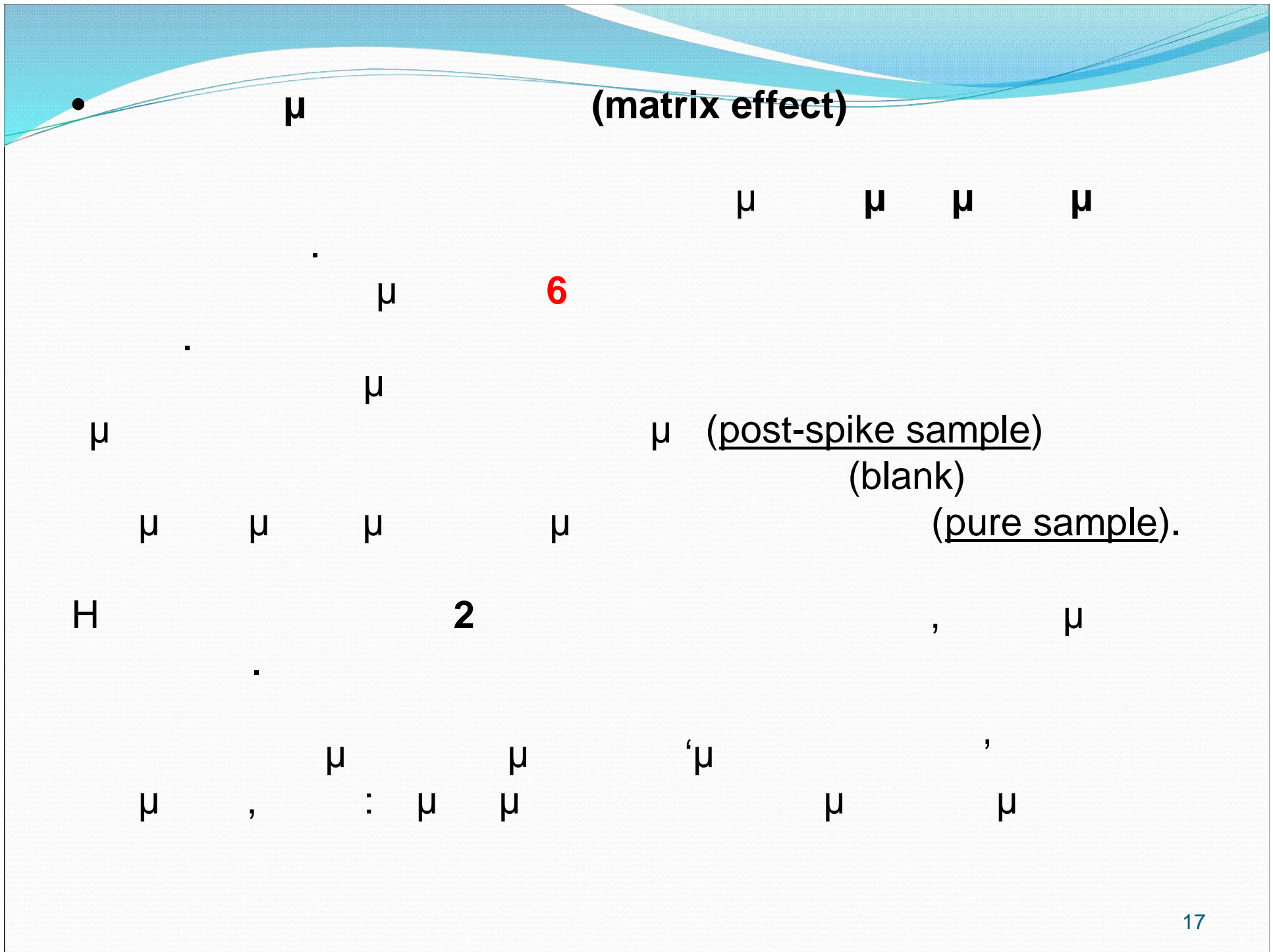
(3

μ

)

μ

μ



**Post-spike
Samples**

- Spike **after** extraction
- **In presence** of matrix

**Pure
Samples**

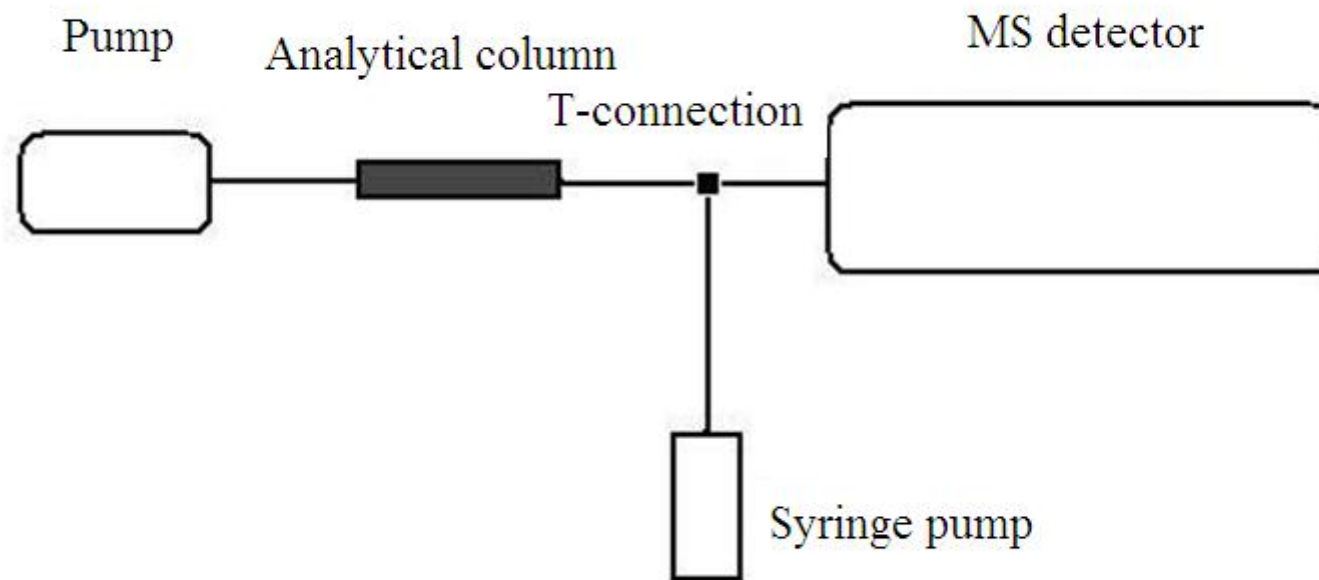
- Pure Solvent
- **In absence** of matrix

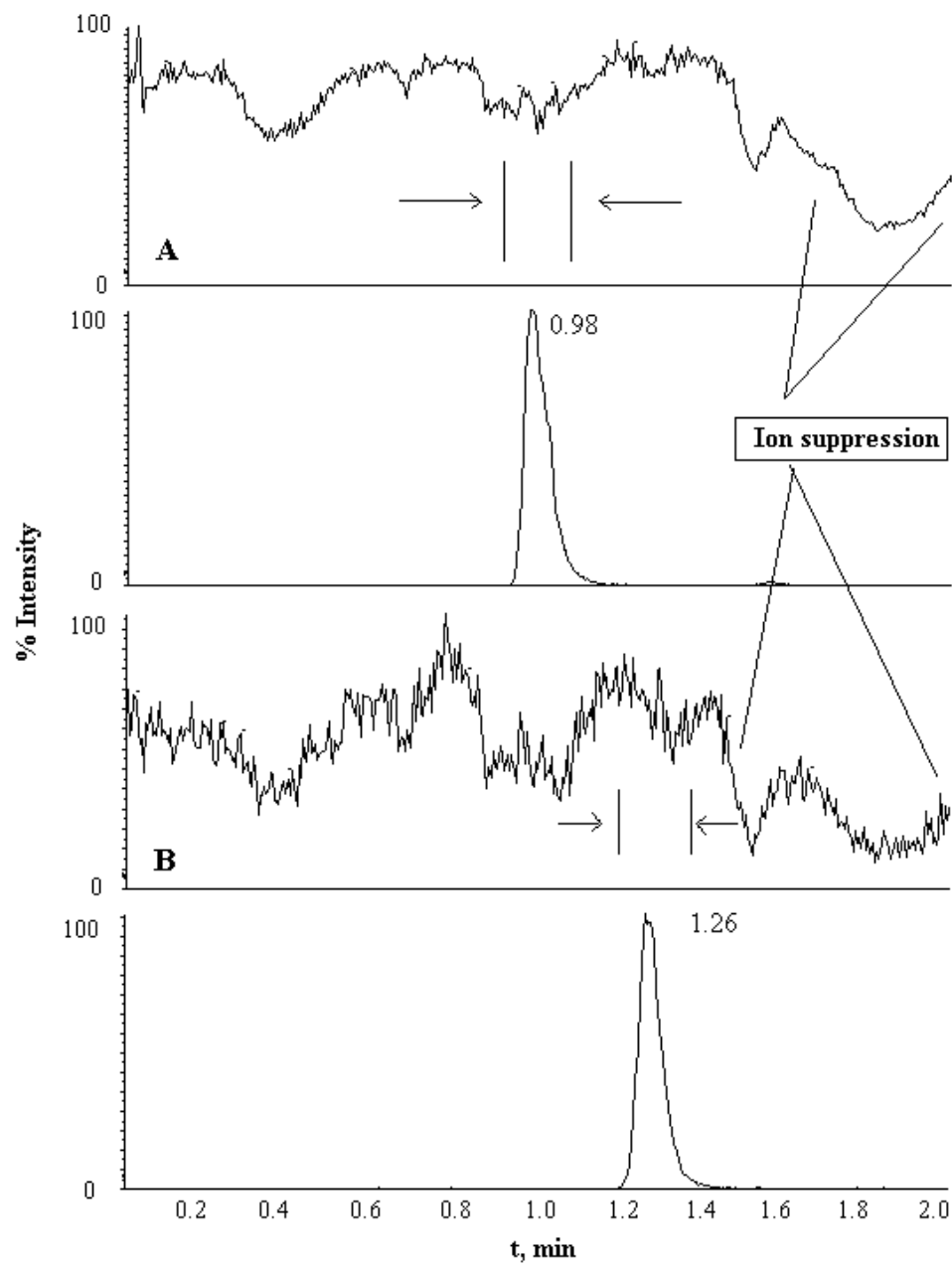
$$\text{Matrix Factor}(MF) = \frac{\text{Area}_{\text{Post-Spike}}}{\text{Area}_{\text{pure}}}$$

MF , 2 μ (Normalized MF)

% RSD Normalized MF 6 μ < **15%**

μ





2

accuracy 85-115%

1)

μ

μ

$$(1-2 \mu)$$

(3 μ) &

 μ

< 5%

2)

μ

(6 h)

μ

 μ

< 15%

3)

μ

(. . 4 μ)

μ

< 15%

4)

μ

3

-

μ

< 15%

5)

μ

μ

μ

)

μ

(

(partial validation)

μ

μ

μ

μ

, . .

-
-
-
-
-
-

μ ,

,

μ

μ

(μ)

μ

μ

μ

,

.

μ

(sample reanalysis)

μ :

- μ , μ

- μ

- μ μ μ

- μ μ μ μ

- μ μ μ μ μ

$> \text{ULOQ}$

(incurred

μ

μ

μ

>

1000

10%

μ

 μ

> 1000

μ

5 %

μ

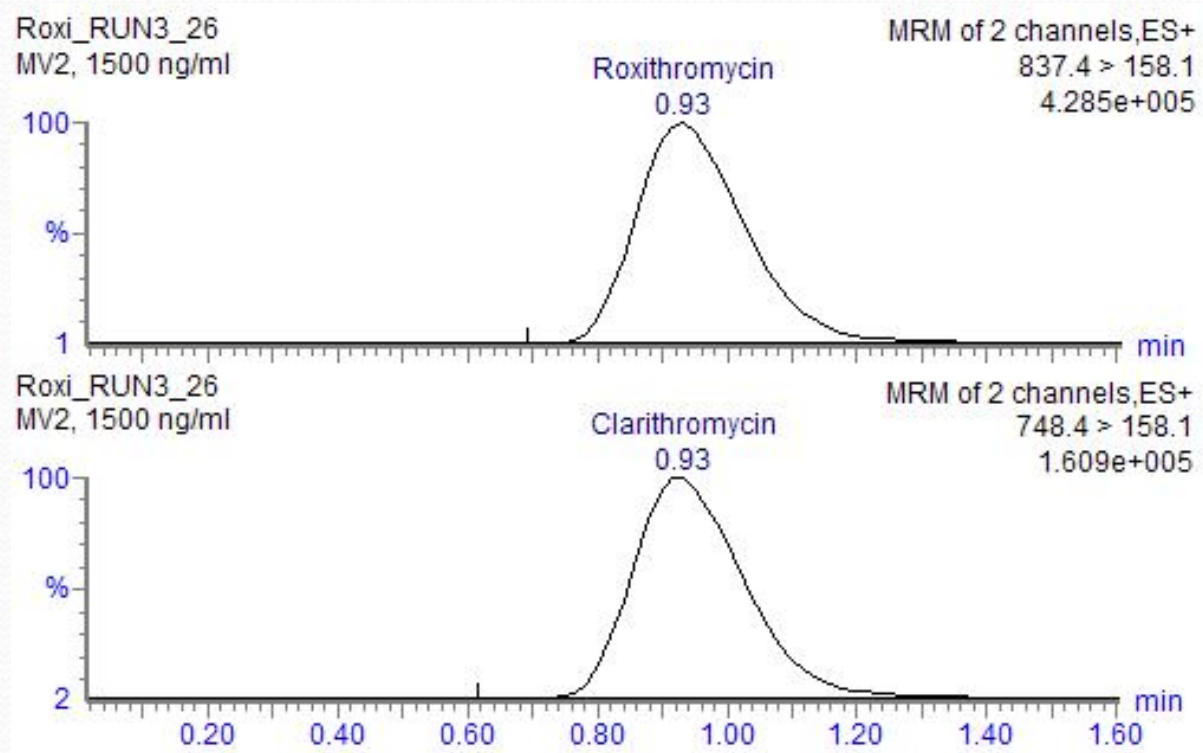
μ
67%

 μ

-
-

< 20%

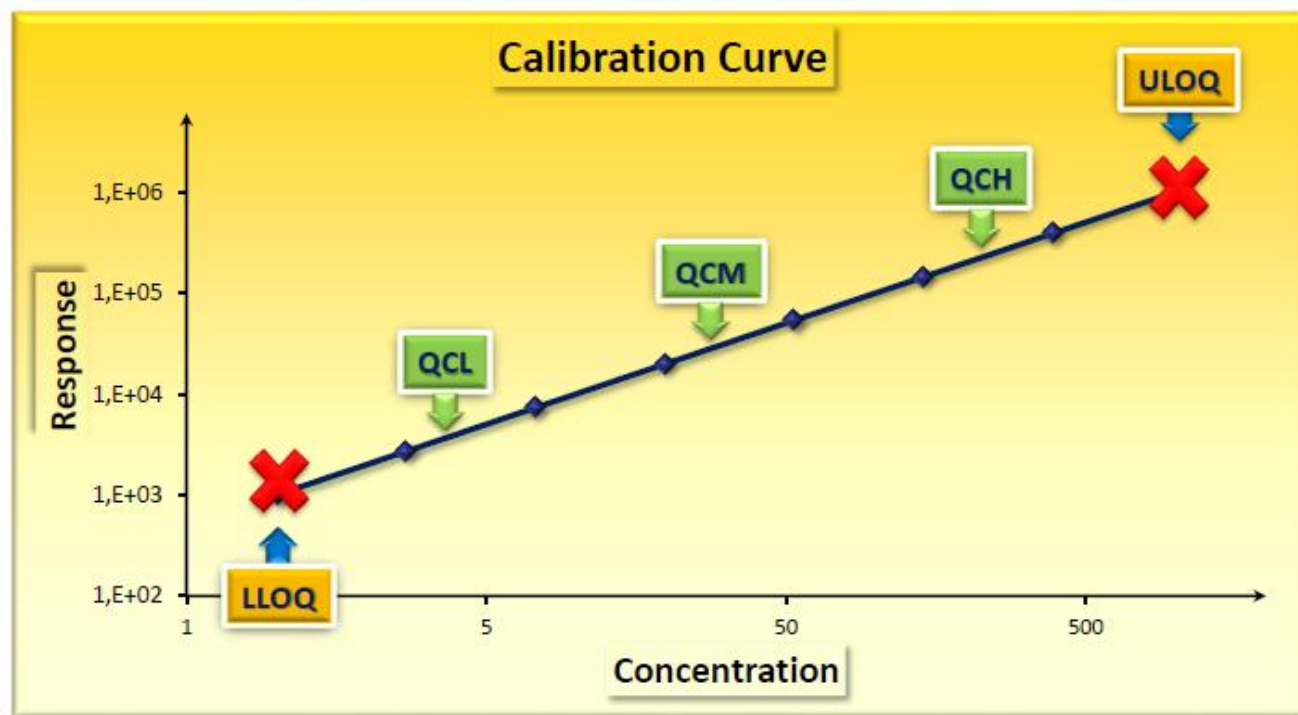
MS/MS



μ (analytical runs)

1. μ \cdot μ μ $:$ μ
(system suitability)
2. μ (blank) μ
(zero)
3. μ
4. μ μ (carry-over)
5. 2-3 μ QCs, 3 (QC₁, QC₂,
QC₃) μ μ

μ :
 - 100 μ μ μ
 - μ
 μ /QCs, μ μ μ

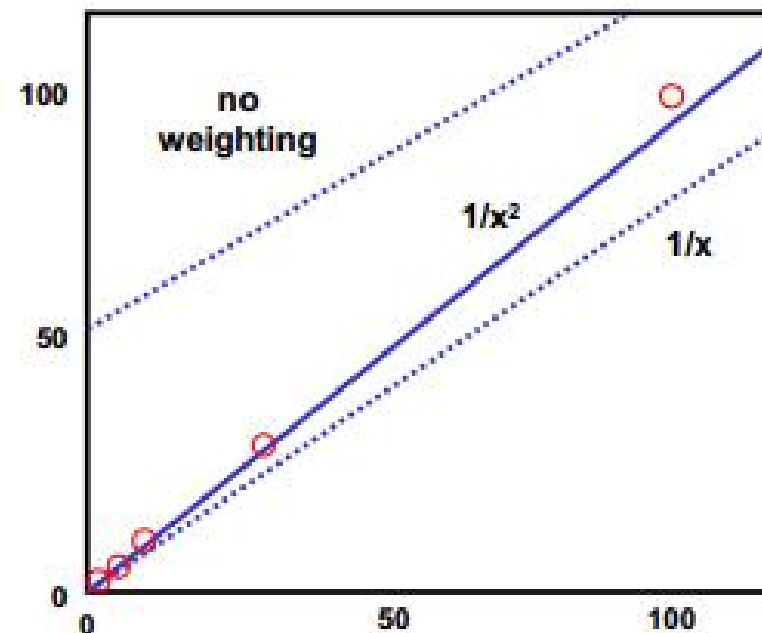
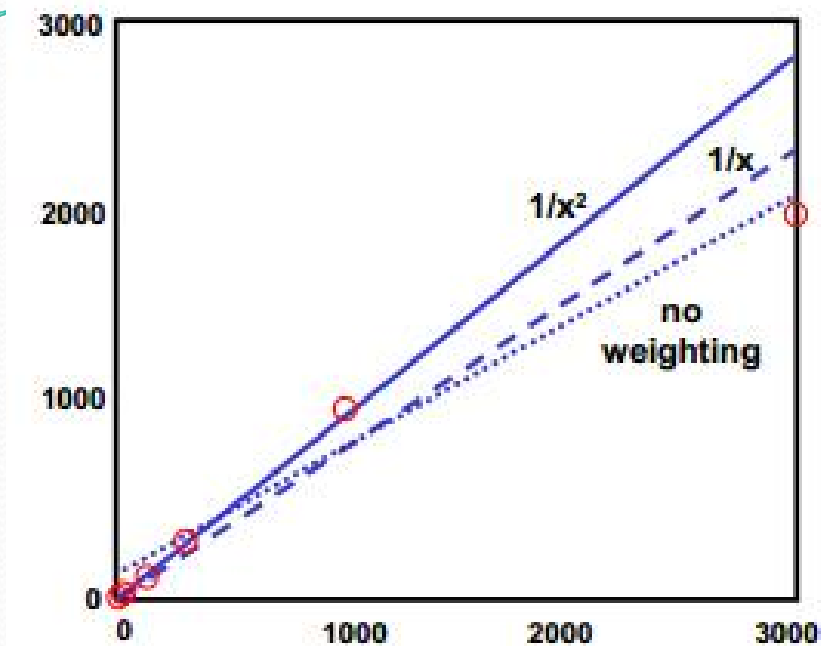


μ
 -
 :
 μ
 -
 QCs
 QCs,
 50%
 μ μ μ
 (85-115%)

1) $\mu\mu$ ()

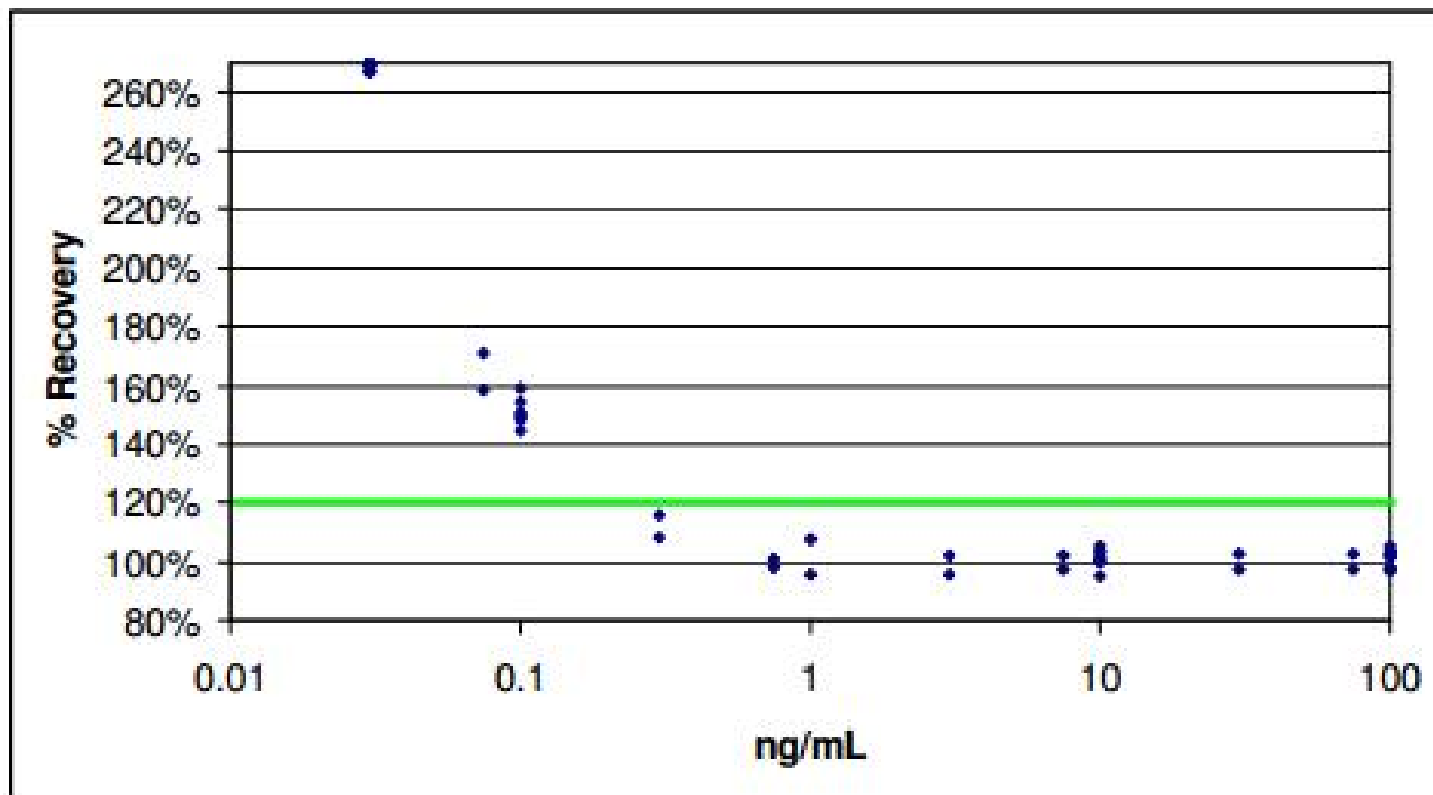
2) F -test ()

2

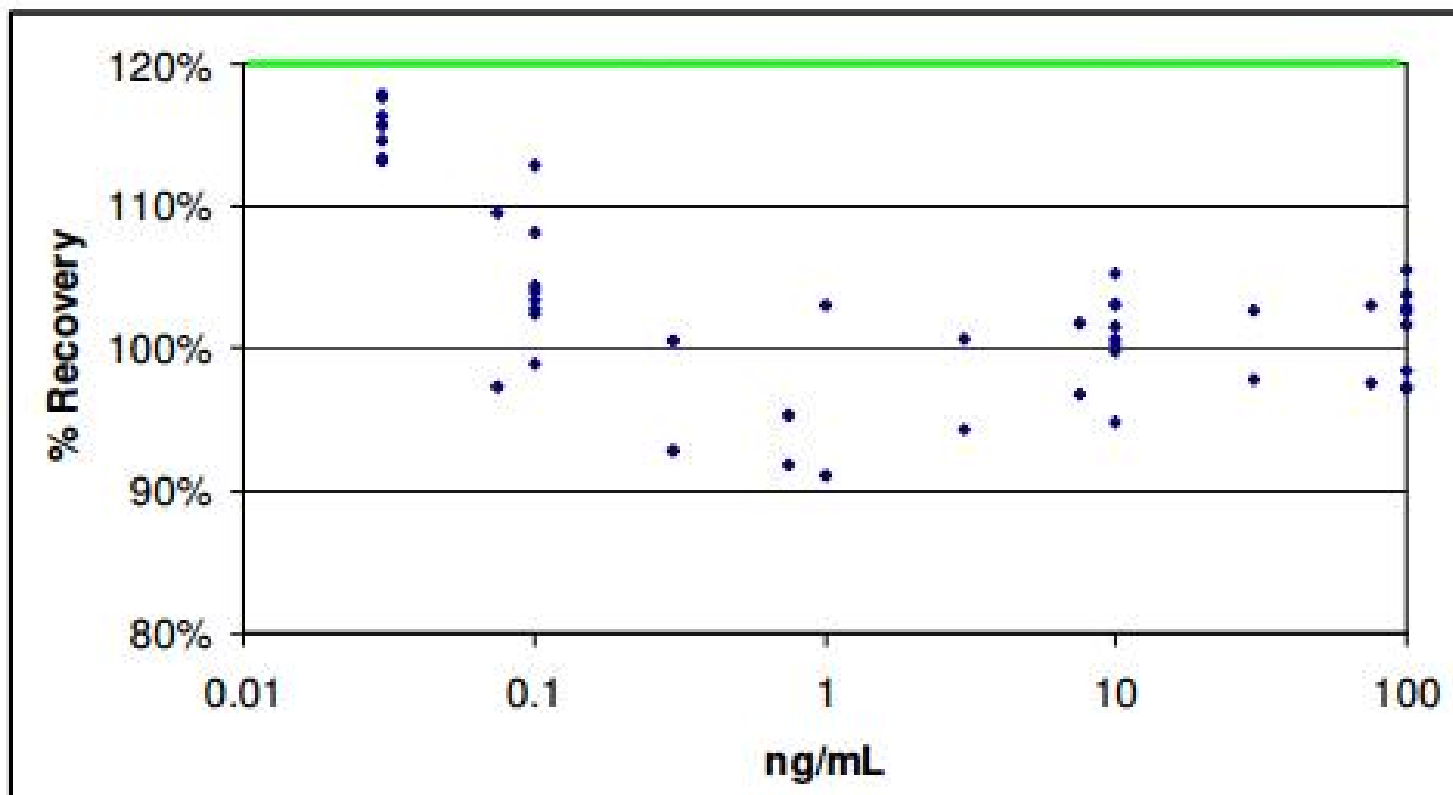


μ μ μ
 μ μ μ
 .
 (residual plots) $\mu\mu$

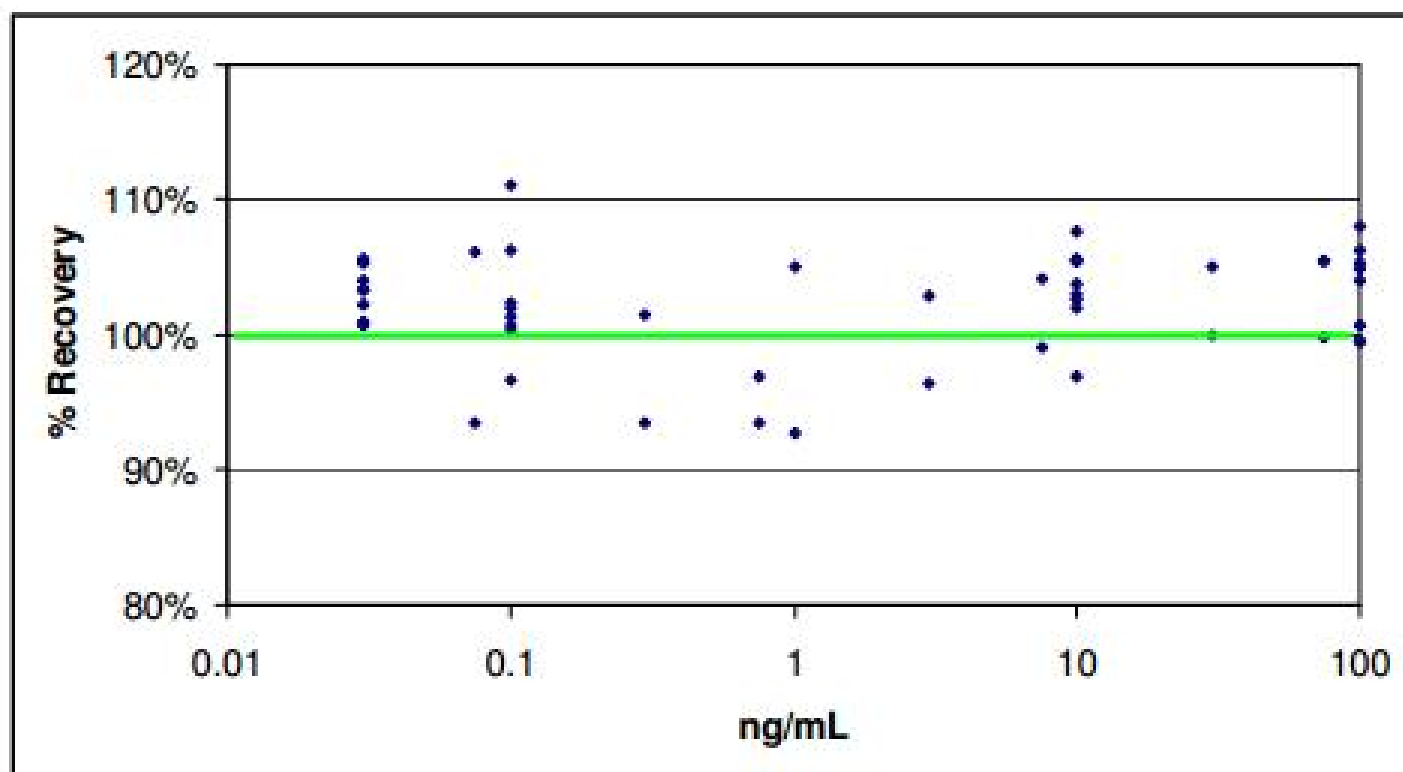
Residuals (no weighting)



Residuals (1/x weighting)



Residuals ($1/x^2$ weighting)



[illegible]