

# EBF view and future perspective of free/total large molecule drug quantification

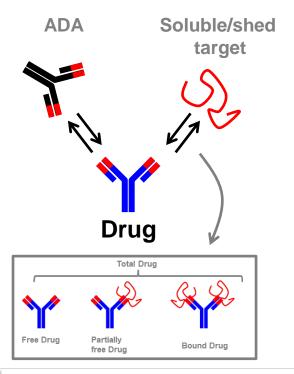
Roland Staack on behalf of the European Bioanalysis Forum (EBF)

> 9th JBF Symposium February 6-8, 2018 Tokyo

http://www.europeanbioanalysisforum.eu

## What is it all about?

#### (neutralizing) soluble binding partner(s)



### **EBF Activities:**

#### **Topic Team 20**

Daniela Stoellner (Novartis – TT lead) Margarete Brudny-Kloeppel (Bayer) Sherri Dudal (Novartis/Roche) Marianne Scheel Fjording (Novo Nordisk) Marie-Hélène Pascual (Sanofi-Aventis) Michaela Golob (Nuvisan) Roland F Staack (Roche) Eva Vieser (Amgen)

# 10th EBF Open Meeting, Barcelona 2017 ➢ Mini Workshop on "free/total" drug quantification

Daniela Stoellner, Roland Staack, Joanne Goodmann, Marianne Scheel Fjording

WS-9 Calibration concepts in LBA

To what extend do we (bioanalytical scientists) need to consider soluble binding partner(s) when defining a bioanalytica assay strategy



# Why do we need "free/active" drug data? → Literature statements

- The possible influence of plasma binding proteins and/or antibodies in plasma/serum on the assay performance should be determined!!! (ICHS6 Guideline)
- The validity of a non-clinical safety study relies upon the demonstration of active drug exposure throughout the dosing phase of the study (Ponce et al., Regul. Toxicol. Pharmacol. 54(2), 164-182 (2009))
  - by an appropriate PD marker (Ponce *et al., Regul.Toxicol.Pharmacol.* 54(2), 164-182 (2009)
  - ➢ by appropriate Bioanalytical Methods to show "active drug exposure → if an appropriate PD Marker is not available
- The interference of soluble targets, extracellular domain of the target receptors, or ADA on the PK assay need to be considered in the design of the sampling strategy by looking for free or total drug. (Chirmule et al. AAPS.J. 14(2), 296-302 (2012))
- The success of the PK–PD modeling effort depends on close communication between the PK–PD bioanalytical and clinical scientists: the PK–PD model is only as good as the data provided for modeling.(Roskos et al., Bioanalysis. 3(6), 659-675 (2011))



"Ignition" of the discussion within the bioanalytical community

## **AAPS** white paper entitled

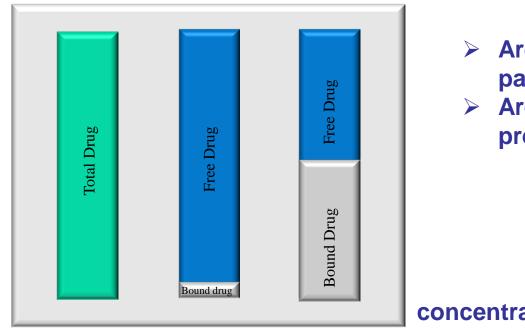
Bioanalytical approaches to quantify "total" and "free" therapeutic antibodies and their targets: technical challenges and PK/PD applications over the course o drug development.

Lee JW, Kelley M, King LE, Yang J, Salimi-Moosavi H, Tang MT, Lu JF, Kamerud J, Ahene A, Myler H, Rogers C.

APPS J. 2011 Mar;13(1):99-110.

Do we always need to differentiate between "free/active" vs "total" drug?

> Answer: NO!  $\rightarrow$  highly dependent on the project/biology!





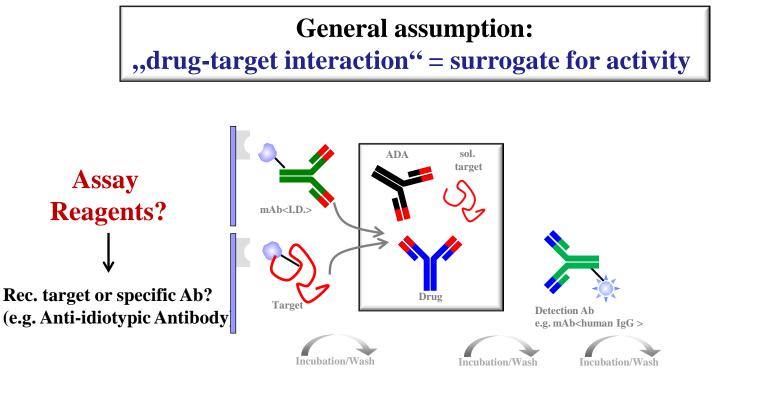
Are soluble binding partner present at "relevant" amounts?

*"relevant*" depends on concentrations of drug & binding partner

If "free/active" drug data is important → appropriate assay development is required



## What makes an assay an "free/active" drug assay?

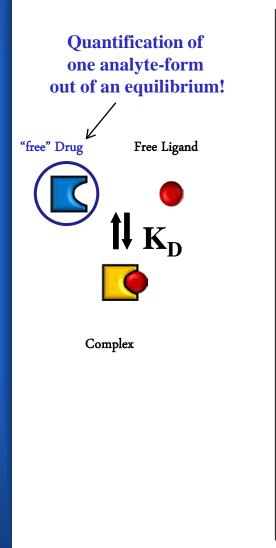


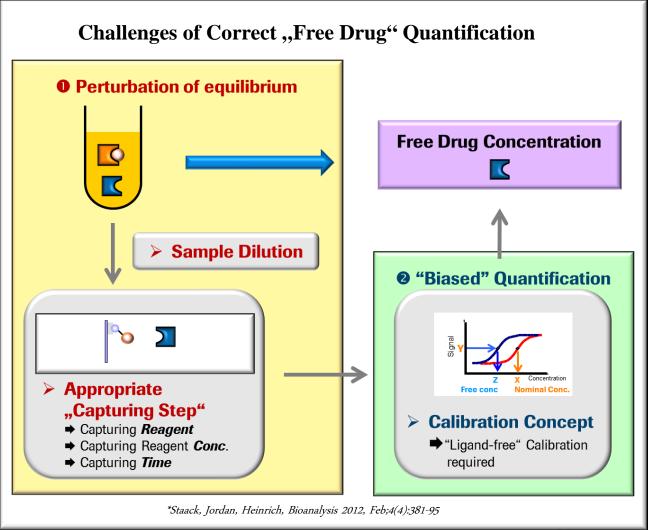
Assay Procedure?  $\rightarrow$ 

Impact of assay procedure in case of (neutralizing)soluble binding partners?

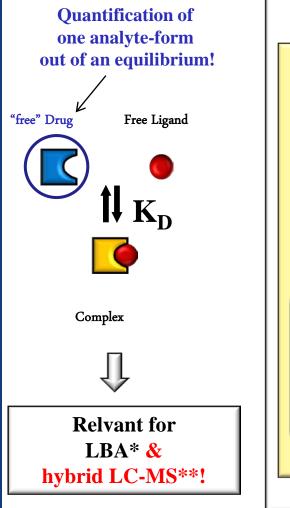


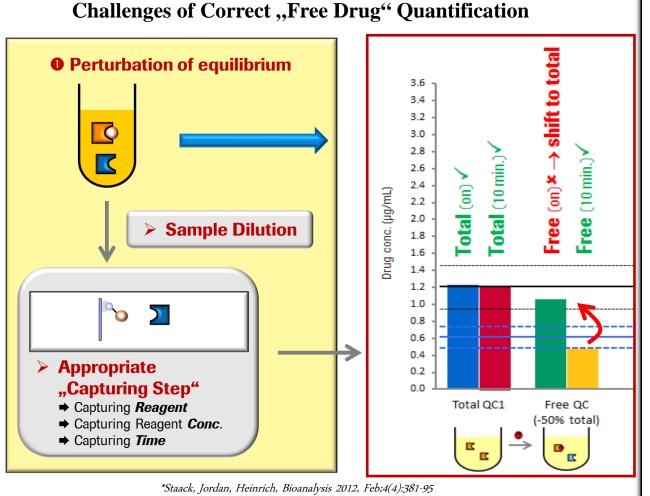
# Challenges of active drug determination in the presence of soluble binding partners





# Challenges of active drug determination in the presence of soluble binding partners

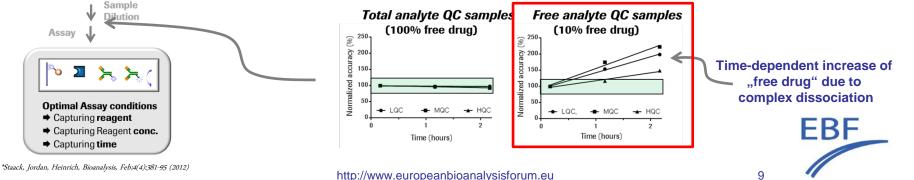




## **Bioanalytical Challenges: Sample Dilution**

#### $\succ$ Theoretical Problem $\rightarrow$ "Dilution Matrix"\*

Assay Range Target-free Dissociation **Free Drug** Complex dilution concentration  $\uparrow$ Target containing rormation **Free Drug** Complex dilution concentration  $\downarrow$ Drug concentration [ng/mL] ...which might be relevant!! a Free Ligand tl κ₀ ( Optimize Assay "timing"  $\rightarrow$  time between end of dilution and assay conduct Complex Sample Total analyte QC samples Free analyte QC samples Dilution (100% free drug) (10% free drug) 250-250 8

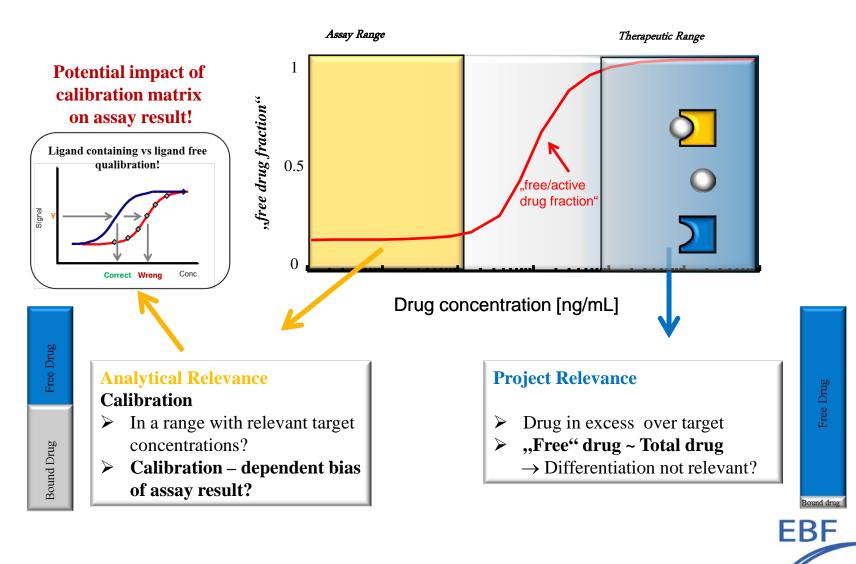


\*\*Schick, Staack, Haak, Jordan, Dahl, Heinrich, Birnboek, Papadimitriou; Bioanalysis; 8(24):2537-2549 (2016)

Assav

 $\sum$ 0

## "Project relevance"vs "analytical relevance"



## **EBF** views:

### Assay development

- Appropriate assay development technically challenging & requires:
  - o Appropriate assay reagents
  - o Understanding of drug mode of action
  - o Understanding of drug-ligand binding kinetics



Success factor: implementation of BA scientist into project team! How the bioanalytical scientist plays a key role in interdisciplinary project teams in the development of biotherapeutics – a reflection of the EBF Dudal S, Staack RF, Stoellner D, Fjording MS, Vieser E, Pascual MH, Brudny-Kloeppel M, Golob M. Bioanalysis. 2014 May;6(10):1339-48.

### Assay "characterization"

- Experiments should be performed to undertstand the result of the bioanalytical method ( $\rightarrow$  different approaches are reported)



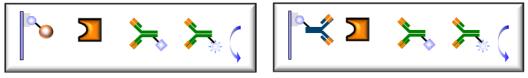
#### **Critical factor: Communication!**

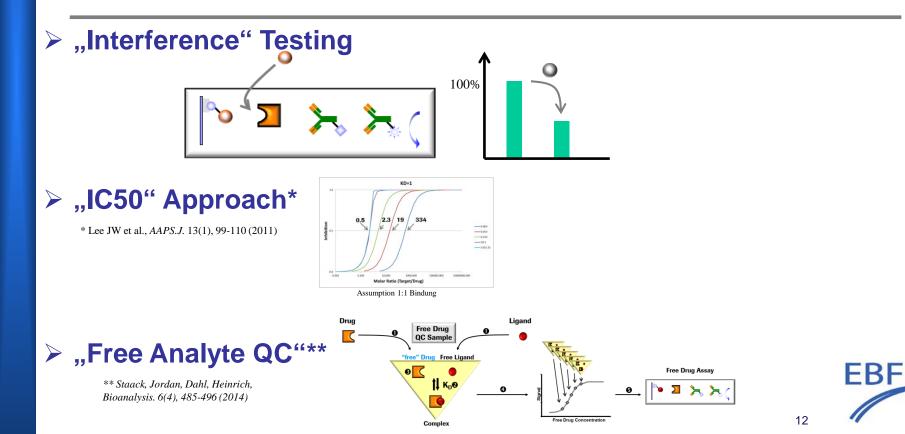
Define name of analyte species and deliver assay with short description on what it actually measures considering all interferences and factors impacting binding equilibrium



## What makes an assay a "free drug assay? Reported Approaches

➤ Assay Format → Target-Capture Assay





## EBF views.....and outlook

#### Matrix selection for calibration/QCs EBF Discussion: WS-9 Calibration concepts in LBA @ EBF 2017

- Impact of specific matrix effect (target interference) versus non-specific matrix effect needs to be evaluated
- Potential bias of the assay result due to use of "ligand-containing" matrix shoud be assessed!

### Bioanalytical Strategy

#### EBF Discussion: Mini Workshop on "free/total" drug @ EBF 2017

If multiple PK assays are required, e.g. to differentiate between "free & total" drug or to monitor different domains of multi-domain biologics,

differentiate between
 *"investigative bioanalysis"* (e.g. assays to monitor drug integrity)

#### "bioanalysis to assess drug exposure"

Pivotal studies: aim for a "lean assay panel"

#### Outlook:

Highly potent ( $\rightarrow$  low dosed) multi-domain biologics will significantly increase the complexity of large molecule bioanalysis.

EBF will address these challenges

# Acknowledgement

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- Margarete Brudny-Kloeppel
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- Philip Timmermann

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