GaBI Educational Workshops

First Turkish Interactive Workshop on Regulation and Approval of SIMILAR BIOTHERAPEUTIC PRODUCTS/BIOSIMILARS



2–3 March 2016, Hacettepe University, Ankara, Turkey

Sundar Ramanan, PhD, USA

 Director, Global R & D and Regulatory Policy, Amgen Inc, USA









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Biologicals and biosimilars – the complexity of structure and function

Sundar Ramanan, PhD 3 March 2016











Biologicals and biosimilars – the complexity of structure and function

Sundar Ramanan, PhD

Director, Policy – R&D and Regulatory Affairs

Amgen Inc

GaBI Turkey SBP Workshop, March 2-3, 2016, Ankara, Turkey

Discussion Topics

- Overview of biosimilar development
- Elements and limitations of analytical studies
- Role of structure-function studies

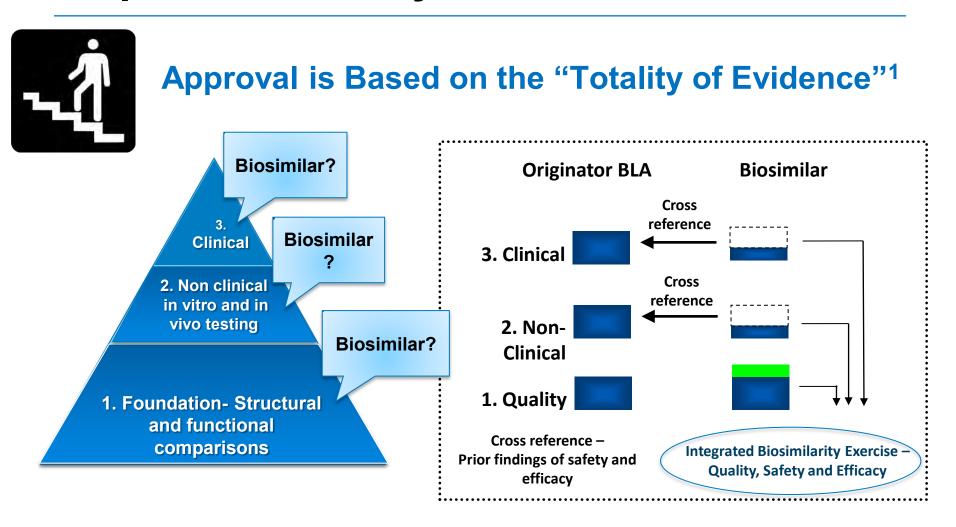


Discussion Topics

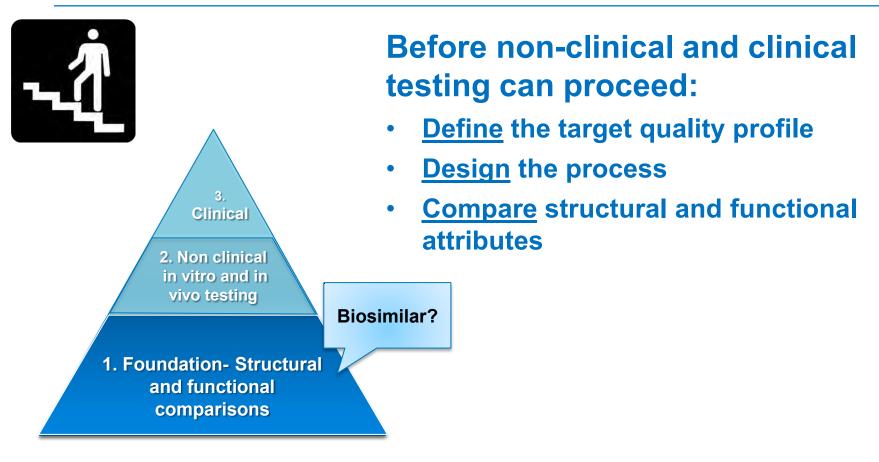
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Biosimilar development proceeds through a stepwise similarity exercise



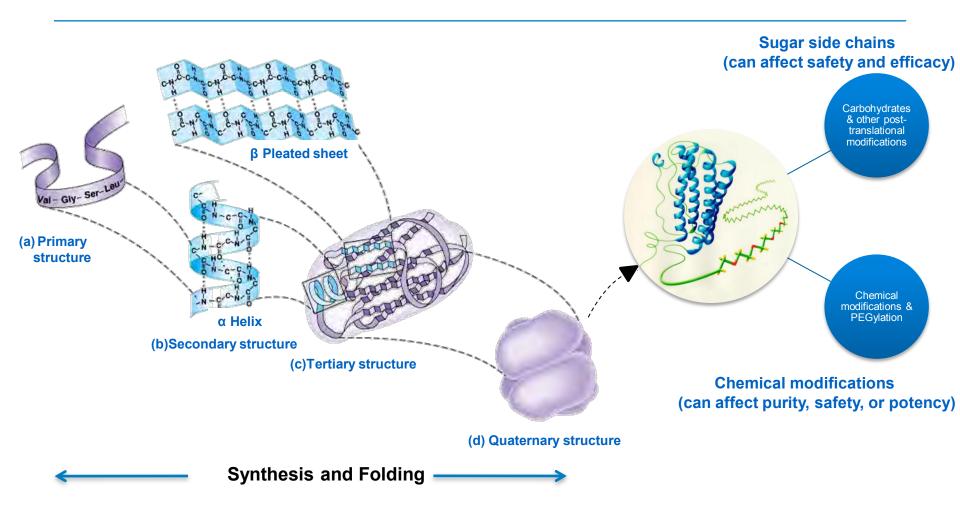
Process design and analytical studies form the foundation of biosimilar development



- Use state-of-the-art analytical characterization and functional assays to assess any structural difference
- Understand the importance and limitation of functional assays



Biologics may have 4 orders of structure plus modifications that affect in vivo characteristics

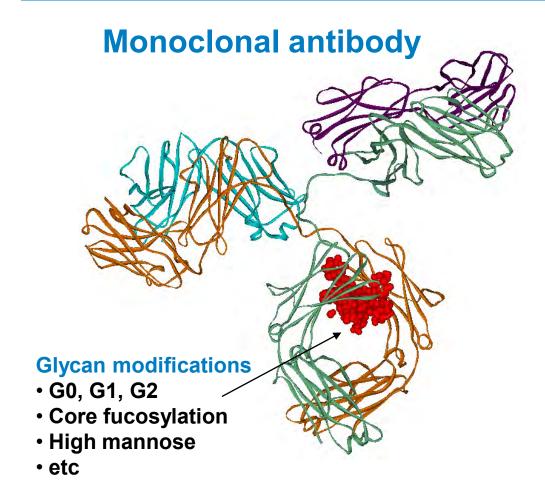


[Image Source: Tim Osslund; Amgen Usage Rights: Unlimited world-wide usage rights for an unlimited time; http://kvhs.nbed.nb.ca/gallant/biology/protein_structure.html.

Data source: USP-NF 1045. Biotechnology-derived articles: 3-20]



Biological products have very complex structures



Peptide modifications

- Deamidation
- Succinimide
- Oxidation
- N & C-terminal variants
- Amino acid substitution
- Disulfide isoforms

Folding/Size

- Truncation
- Half molecules
- Dimer
- Multimers
- Aggregates
- Particles

Figure adapted from D. Kelner (Amgen), "Comparability and Biosimilarity: Two Sides of the Same (or a Different) Coin?" presented at IBC Analytical Technologies, San Diego, CA (March 2012)



Typical analytical similarity assessment evaluates 90 to 100 unique attributes

Results from a wide breadth of assay combinations compares the analytical "footprint" of the biosimilar to the reference product.



Is it possible to "match" all attributes?

Figure adapted from J. Liu et al. (Amgen), "Analytical Similarity Assessment of Biosimilars" presented at the Spring ACS Meeting, Dallas, TX (March 2014)



Biosimilar development can use a Qualityby-Design (QbD) approach

QbD for biosimilars

- Assess criticality based on literature & experience
- Characterize reference product quality attributes
- Design biosimilar to minimize differences for high criticality attributes
- Assess potential clinical relevance of remaining differences

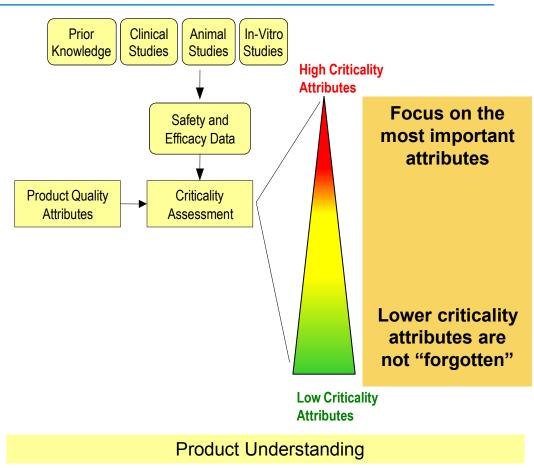


Figure adapted from G. Grampp (Amgen), "Challenges of Structure-Function Studies for Assessing Similarity" presented at the Spring ACS Meeting, New Orleans, LA (April 2013)



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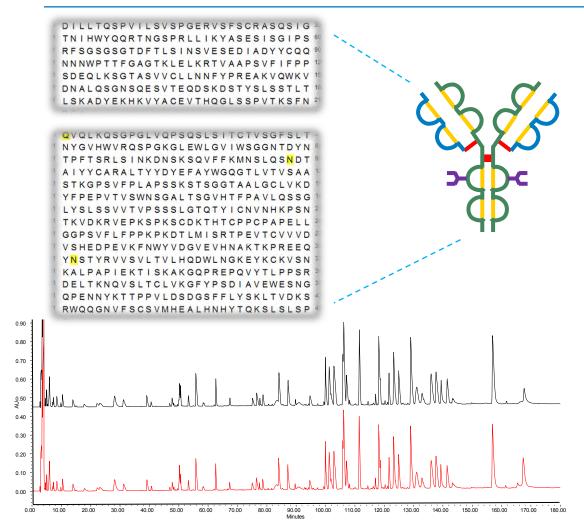


Analytical studies should assess several aspects of structure

- Primary structure (sequence and linkages)
- Higher order structures (folding, aggregates)
- Covalent modifications (glycosylation and chemical modifications)
- Impurities (product and process)
- Stability profile

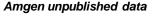


Biosimilar product should have identical amino acid sequence to the innovator



Peptide mapping

- 100% sequence confirmation
- Search for any low level amino acid substitution (sequence variant) due to translational errors, misincorporation, or mutation
- Post-translational modifications, such as glycosylation, acetylation, sulfation, phosphorylation, glycation, etc





Primary structure and covalent modifications can be assessed to high fidelity

Mass spectroscopy combined with separation based methods can address many uncertainties

- Amino acid sequences confirmed to ~100% coverage
- Covalent modifications, sequence variants and glycan structures detected to <1% resolution

Example: LC ESI MS/MS

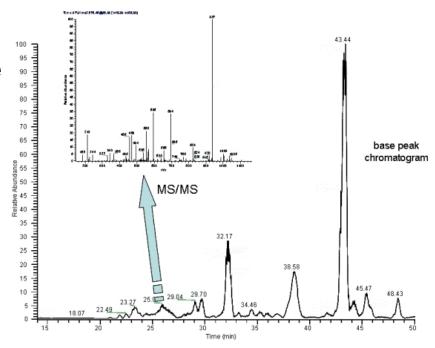


Image obtained from University of Kentucky Mass Spectrometry Facility http://www.research.uky.edu/ukmsf/example2a.html

Figure adapted from G. Grampp (Amgen), "Analytical Similarity Assessments" presented at the DIA/FDA Biosimilars Conference, Washington DC (September 2012)



Advanced mass spectroscopy methods still leave some uncertainties

Examples of some remaining challenges

 Accurate quantitation of minor species

 Identifying and quantifying disulfide bonding patterns

Accounting for combinatorial effects

Sample (14N)

Mix

Std +Sample

Proteolysis

m/z

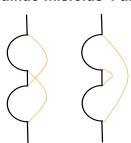
Stable Isotope Labeled Internal Standard (SILIS)

Figures courtesy of Jiang et al, PEGS 2011

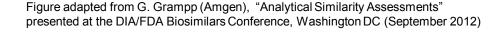


Disulfide misfolds 1 and 2



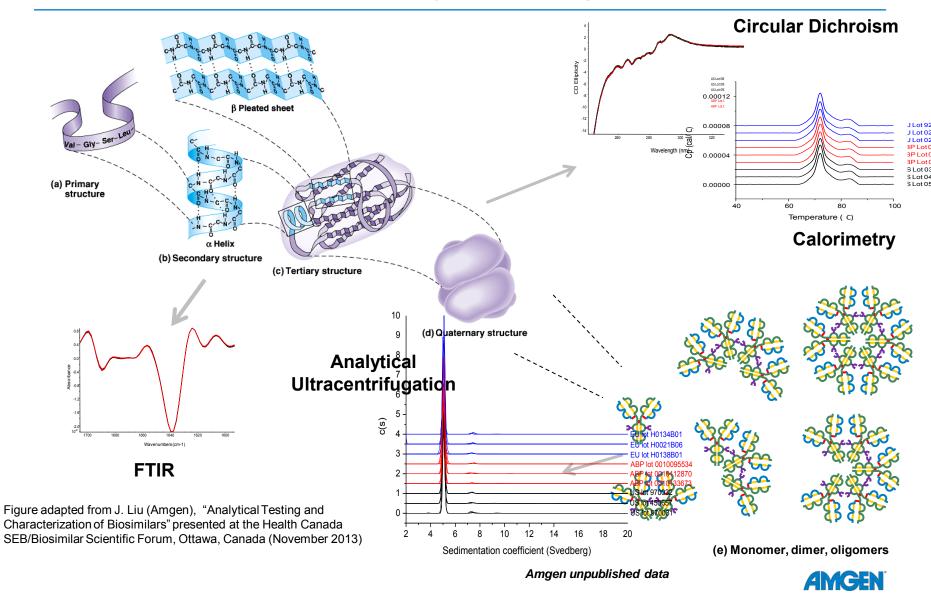








Higher order structure and size variants are characterized by orthogonal methods

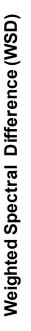


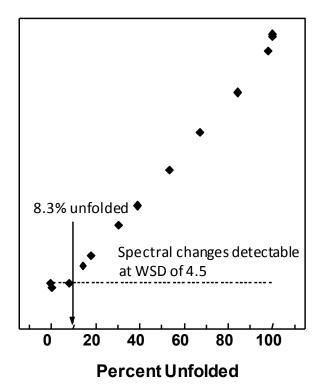
A common limitation of spectroscopic methods is sensitivity to mixtures

Eg, unfolded protein spiked into product

- Limit of detection is 8% by near UV circular dichroism
- How sensitive to partially unfolded species?

Near UV CD





Amgen unpublished data

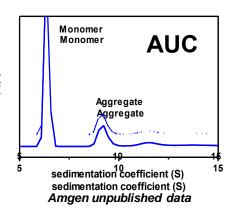


Particulate characterization technology is improving

- Focus on characterizing particles (0.1 μm to 10 μm)
 - Size, composition, quantity, structure
 - Relevance to immunogenicity
- Improving sensitivity, accuracy, and specificity
 - Protein vs. container
 - Emerging nanotechnology-based approaches for < 1 μm particles
- Quantitative and qualitative comparisons remain difficult

Aggregation (<0.1 μm)

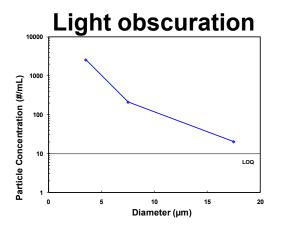




Particulation (>1 μm)

MFI

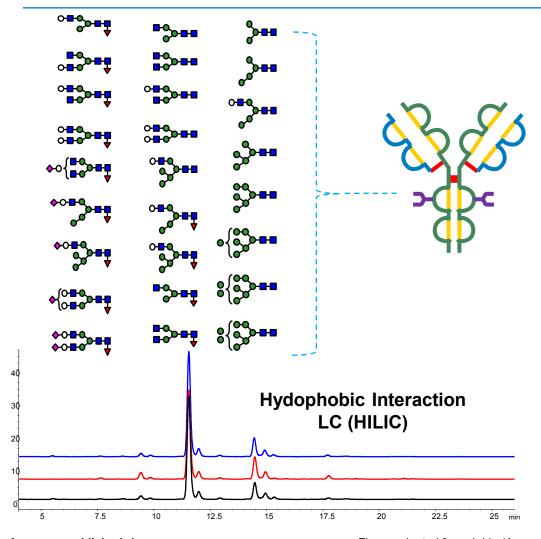




Amgen unpublished data

Figure adapted from G. Grampp (Amgen), "Analytical Similarity Assessments" presented at the DIA/FDA Biosimilars Conference, Washington DC (September 2012)

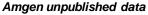
Glycosylation is a critical quality attribute that can impact biological functions



Glycan mapping by HILIC and Mass Spectrometry

- Over 25 mAb glycans identified
- Correlate glycan attributes with biological function

Glycan Type	Impact to function
No glycan	No ADCC
Bisecting GN	Increase ADCC
High mannose	Clearance and effector function
Terminal Gal	Increase CDC
NANA	Anti-inflammatory
Afucosylated	Increase ADCC





Product isoforms need to be fully characterized using separation methods

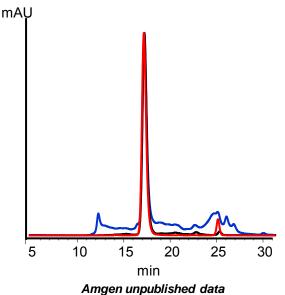
Size variants

- Truncation
- Dimer
- Multimers

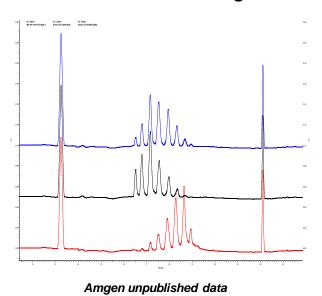
Charge and hydrophobic variants

- N-terminal modification
- C-terminal modification
- Deamidation
- Oxidation

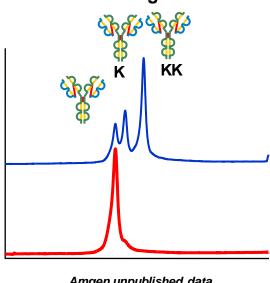
Size Exclusion HPLC



Isoelectric Focusing



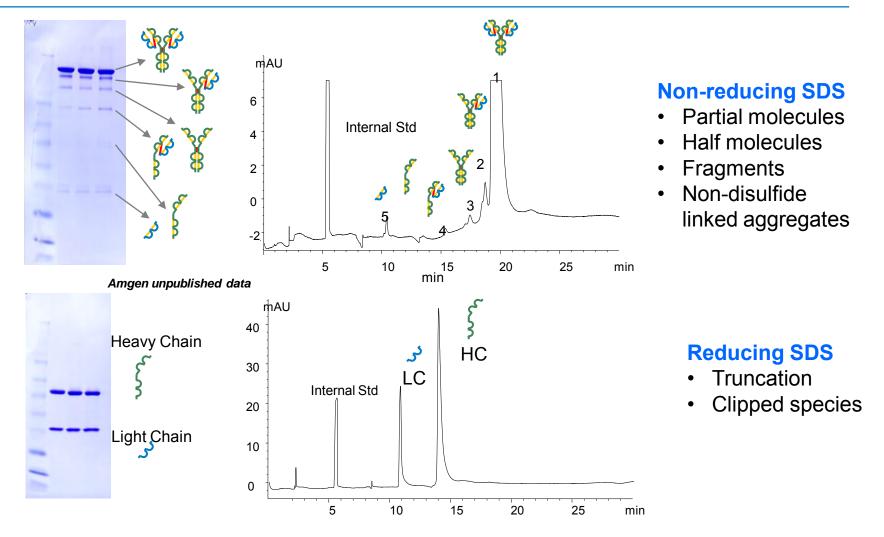
Ion Exchange HPLC



Amgen unpublished data



Separation methods also used to examine the integrity of covalent structure





Product-related and process-related impurities must be well characterized

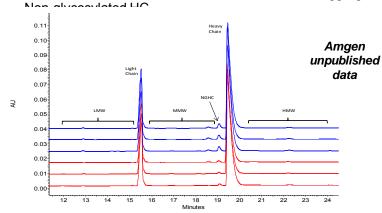
 High resolution and orthogonal methods are required to characterize product-related species.

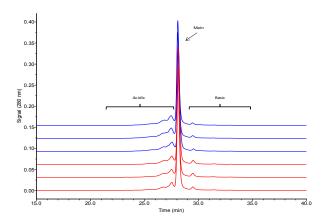
Size variants:

- Truncation
- Dimer
- Multimers
- Clipped species
- Partial molecules
- Half molecules
- Fragments
- Non-disulfide linked aggregates

Charge and Hydrophobic Variants:

- N-terminal modification
- C-terminal modification
- Deamidation
- Oxidation



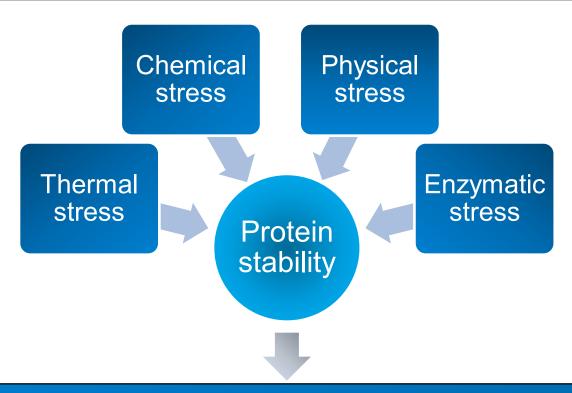


- Process-related impurities (HCP, DNA, leachables, etc) need to be characterized to ensure product quality.
- Particles and aggregates of various sizes need to be evaluated and characterized.

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Proteins undergo complex degradation and are sensitive to storage and handling

Biosimilar stability is impacted by its manufacturing process and formulation



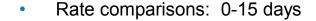
Degradation contributes to eventual loss of biological activity and/or potential immunogenicity

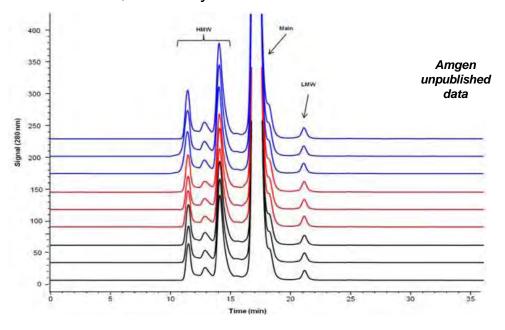


Forced degradation studies should demonstrate similar stability profiles

Multiple accelerated thermal stress conditions (25, 40, 50°C) provide a quantitative, reproducible, and sensitive comparison of degradation profiles and rates

Example: Size Exclusion Chromatography profiles
 – 50°C, T=15 days





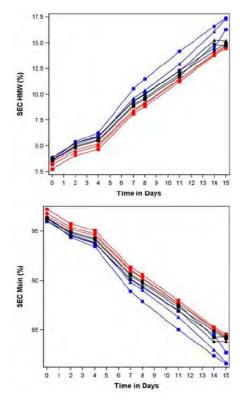


Figure adapted from J. Liu et al. (Amgen), "Analytical Similarity Assessment of Biosimilars" presented at the Spring ACS Meeting, Dallas, TX (March 2014)



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Structural comparisons leave residual uncertainties

Sources of uncertainty	Potential consequences
Assay limitations (limit of detection, specificity, etc.)	Unobserved differences could potentially impact efficacy or safety
Lot to lot variability and population statistics	Equivalence of means does not prove that individual lots are biologically equivalent
Observed differences in critical attributes	Could impact safety or efficacy if differences are large enough
Observed differences in less critical attributes	 Are assumptions about criticality correct? Could combinations of attributes become significant?

Functional studies are the first step in addressing these residual uncertainties



Why functional characterization?

Part 1: Required by regulators

- Functional characterization required
 - To confirm quality and potency of the product
 - To address limitations of structural assays
 - To confirm similar mechanism(s) of action
 - presence of expected function, absence of new function
 - specificity of target binding
- Relevant passage from FDA guidance

"Depending on the structural complexity of the protein and available analytical technology, the **physicochemical analysis may be unable to confirm the integrity of the higher order structures**. Instead, the integrity of such structures can be inferred from the product's biological activity." (Emphasis added)

FDA Draft Guidance, Quality Considerations in Demonstrating Biosimilarity to a Reference Product, February 2012



Matching all biological and functional properties is essential

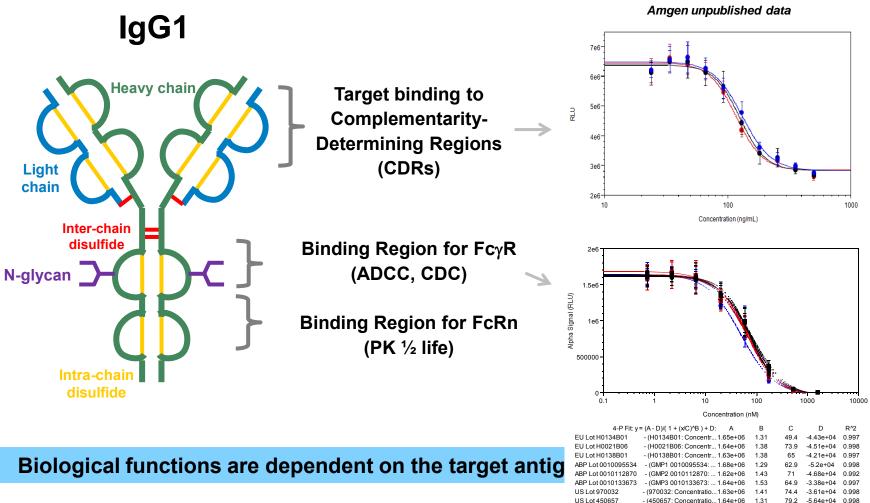


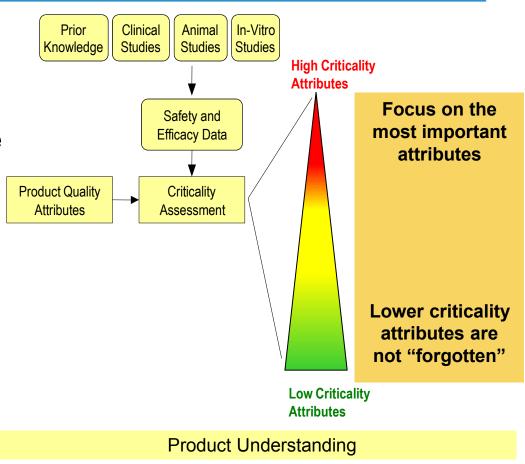
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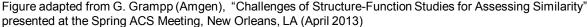
Why functional characterization?

Part 2: May be essential to justify differences

QbD for biosimilars

- Assess criticality based on literature & experience (where available)
- Minimize differences for high criticality attributes
- Perform structure-function studies to assess remaining differences
- Relate findings to potential clinical impact







Prepared samples can increase sensitivity of structure-function studies

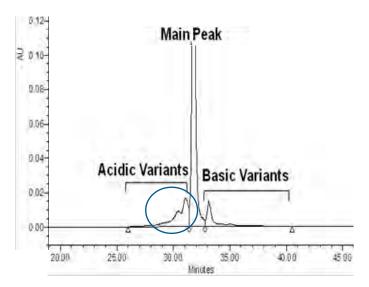
Observed range Enriched sample Slope estimate

% variant

Notional data for illustration purposes only

Figure adapted from G. Grampp (Amgen), "Challenges of Structure-Function Studies for Assessing Similarity" presented at the Spring ACS Meeting, New Orleans, LA (April 2013)

Cation exchange profile of a mAb



Charge Variants	% Relative Potency
Acidic variants	82
Main peak	101
Basic variants	84

Amgen unpublished data

Improved estimate of slope informs potential criticality and permitted magnitude of differences



Studies must provide relevant conclusions

- 1) Evaluate in vitro functional data
- Test functional equivalence of actual batches

Is a 25% difference *really* acceptable?

- Relate attribute difference to parameters from structure function studies
 - Measured difference in means
 - Estimated quantitative effect
 - Relate to clinically meaningful differences

Reference Lots **Biosimilar Lots** Potency Test for equivalence of means 80% < ∆ < 125%

Attribute Level

Notional data for illustration purposes only

Attribute Leve Reference **Biosimilar** Lots

Lots

Notional data for illustration purposes only



Studies must provide relevant conclusions

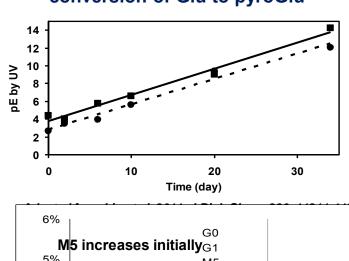
2) Evaluate PK and drug metabolism where feasible

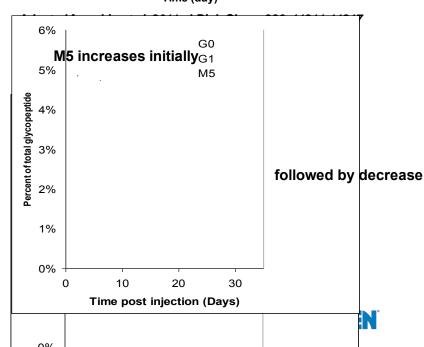
 Serum incubation in vitro: is a variant formed under physiologic conditions?

Product recovery from PK samples

Figure adapted from G. Grampp (Amgen), "Challenges of Structure-Function Studies for Assessing Similarity" presented at the Spring ACS Meeting, New Orleans, LA (April 2013)







Small effects can combine in unexpected ways

Process change case study

- Change resulted in shifts in 2 attributes (see figure)
- Bioassays predicted equivalent potency
- Equivalent PK shown in human clinical study
- Potency difference detected in clinical PD study
- Post hoc studies with prepared fractions identified additive effects on potency

In vitro potency of prepared fractions

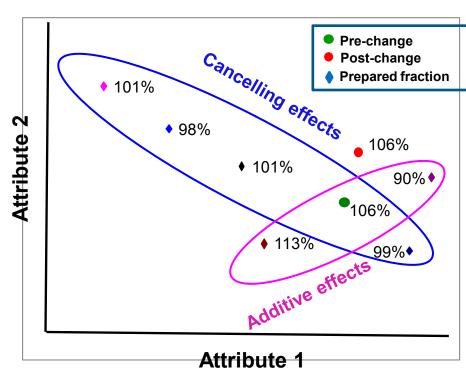


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Amgen unpublished data

Additional challenges in structurefunction studies

- Predicting human PK/PD
 - Animal studies may not account for species specific clearance mechanisms
 - Insufficient power due to small number of animals
- Predicting human immune response
 - In silico, in vitro, and in vivo methods are insufficient to rule-out clinically relevant differences



Summary and Conclusions

- Analytical advances permit high resolution similarity assessments for many attributes
 - Higher order structure and particle assessments still subject to uncertainty
 - Orthogonal approaches partially compensate for lower sensitivity
- Assessing impact of differences remains challenging
 - Not all clinically relevant effects can be evaluated preclinically (e.g., PK and immunogenicity)
 - Small effects and combinations difficult to assess



Thank you!



