#### Formulation of Filgrastim Influences Protein Dynamics.

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#### CASSS Washington Discussion Group 19 April 2022





## **The People**

#### Dr. Houman Ghasriani

From Samples to Structures: NMR data collection and analysis, resonance assignment, structure determination, relaxation parameter extraction and calculations of protein dynamics from NMR data.

#### Geneviève Gingras

From Genes to Magnet: Molecular biology, construction of expression vectors for the production of labeled proteins (*E. coli* and *Pichia Pastoris*): rhGM-CSF (*E.coli* and *P. Pastoris*)

#### Sara Ahmadi

Construction of the NIST-mAb-scFv and initial expression-purification protocol development

#### Derek Hodgson

Protein expression, (Intereron- $\alpha$ 2a and  $\alpha$ 2b; hGH; **Met-G-CSF** and mutants; NIST-mAb-scFv), NMR data collection including all collaborative studies with WHO and USP.

Grant Frahm and Dr. Michael Johnston All thermal unfolding studies by CD

#### Dr. Donald Gagné and Dr. Muzaddid Sarker

Production of isotopically labelled (<sup>2</sup>H,<sup>13</sup>C,<sup>15</sup>N) cleavable single chain Fab fragments of NIST-mAb, adalimumab, bevacizumab, infliximab, rituximab and trastuzumab for the expression in *E. coli*.



#### Neupogen® (Met-GCSF, filgrastim)

sample: concentration of 20 vials, 1 mM protein (volume: 0.4 mL)



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## **Formulation of Neupogen®**

Component	Amount /0.5 mL	Concentration
GCSF	300 µg	$32~\mu M$
Acetate	0.295 mg	10 mM
Sorbitol	25.0 mg	274  mM
Polysorbate 80	0.02 mg	0.03 mM
Sodium	0.0175  mg	1.52 mM
Water	0.5 mL	

#### Resulting pH is 4.0



#### A bit of NMR Concepts









## **NMR Time Scale of Protein Dynamics**





Effects of Solution conditions on the NMR spectra of Filgrastim

# pН

# Sorbitol

# Polysorbate-80 and Polysorbate-20



#### Thermal unfolding by CD and NMR Measurements carried out on <sup>15</sup>N-Filgrastim

Relaxation parameters T<sub>1</sub>, T<sub>2</sub> and het-NOE:

sorbitol (0 mM, 274 mM, 749 mM) Polysorbate-80 (0, 30, 100, 300 uM) Polysorbate-20 (0, 30, 100, 300 uM) pH: 4, 5, 6

#### Monitoring thermal unfolding by circular dichroism:

sorbitol (0 mM, 274 mM, 749 mM) Polysorbate-80 (0, 30, 100, 300 uM) Polysorbate-20 (0, 30, 100, 300 uM) pH: 4, 5, 6



## **Effects of pH on chemical shifts**





#### **Lowering pH: Cation-**π **Interaction**



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#### **Lowering pH: Cation-**π Interaction



#### **Lowering pH: Cation-** $\pi$ **Interaction**



#### H156 W58 H52

H79 W118



## **Effects of pH on Filgrastim Stability**

GCSF - Thermal Denaturation at Varying pH Values



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## **Effects of pH on Protein Dynamics**







Sequence

## **Effects of pH on Protein Dynamics**

#### Order Parameter (S<sup>2</sup>) as a Function of pH



#### Average of Order Parameters for Helices and Loops



Structural Elements



## **Amplitudes of Motions of Helices and Loops**





Helices with low amplitudes of motions allow loop motions with larger amplitudes Helices with large amplitudes of motions restrict loop motions; lower motion amplitudes









#### **Effects of Excipients on Protein Dynamics**





#### **Effects of sorbitol on Protein Dynamics**





Sorbitol-induced chemical shift changes (spectra acquired at 45 °C) are predominantly affecting Trp<sup>58</sup>. Sorbitol concentrations were at 0, 274, or 749 mM. CCSDs of shifting resonances were between 8-20ppb for 274mM sorbitol, and 20-50ppb for 749mM sorbitol. G-CSF concentration was kept at ~30uM

Sorbitol-induced chemical shift changes color-coded onto G-CSF, where red represents large, green moderate, and blue small chemical shift changes. Sorbitol concentration was 749 mM



### **Effects of sorbitol on Protein Dynamics**

T<sub>1</sub>, final sorbitol study (600 MHz, 0 vs. 793 mM)



NOE for final sorbitol study (600 MHz, 0 vs. 793 mM)





#### Effects of Excipients (pH) on Filgrastim Dynamics



Effect of sorbitol on S<sup>2</sup>. S<sup>2</sup> for G-CSF in presence and absence of sorbitol as a function of residue number, using ellipsoid diffusion tensor and a model that accounts for exchange dynamics in model-free analysis. High sorbitol concentration (793 mM) results in enhanced flexibility (increased entropy, decreased S<sup>2</sup>), for helix B, loop BC, and helix C.



#### Average of Order Parameters for Helices and Loops



Structural Elements







#### Diffusion Tensors Reflect a Change of Protein Shape in the Presence of Sorbitol





#### From Filgrastim to Therapeutic Monoclonal Antibodies







## Pushing the Limit: NMR of Therapeutic mAbs

Arbogast, Brinson and Marino demonstrated the application of NMR spectroscopy to obtain high-resolution 2D spectra of the NIST-mAb fragments (Fab and Fc)

Arbogast, LW, Marino, JP, Brinson, RG (2015) *Analytical Chemistry*, 87: 3556-3561
Arbogast, LW, Brinson, RG, Formolo, T, Hoopes JT, Marino, JP (2016) *Pharmaceutical Research*, 33:462-475



#### Enabling adoption of 2D-NMR for the higher order structure assessment of monoclonal antibody therapeutics, MABS (2019) 11: 94–105

Robert G. Brinson,a John P. Marino,a Frank Delaglio,a Luke W. Arbogast,a Ryan M. Evans,b Anthony Kearsley,b Geneviève Gingras,c Houman Ghasriani,c Yves Aubin,c Gregory K. Pierens,d Xinying Jia,d Mehdi Mobli,d Hamish G. Grant,eDavid W. Keizer,e Kristian Schweimer,f Jonas Ståhle,g Göran Widmalm,gEdward R. Zartler,h Chad W. Lawrence,i Patrick N. Reardon,†,i John R. Cort,iPing Xu,j Feng Ni,j Saeko Yanaka,k Koichi Kato,k Stuart R. Parnham,I Desiree Tsao,m Andreas Blomgren,n Torgny Rundlöf,n Nils Trieloff,o Peter Schmieder,oAlfred Ross,p Ken Skidmore,q Kang Chen,r David Keire,r Darón I. Freedberg,sThea Suter-Stahel,t Gerhard Wider,t Gregor Ilc,u,v Janez Plavec,u,v Scott A. Bradley,w Donna M. Baldisseri,x Mauricio Luis Sforça,y Ana Carolina de Mattos Zeri,z Julie Yu Wei,aa Christina M. Szabo,bb Carlos A. Amezcua,bb John B. Jordan,cc and Mats Wikströmdd

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#### Approved Therapeutic mAbs in US or EU (as of November 2014)

1. Abthrax (raxibacumab)	IgG1-lambda	25. Nplatep (romiplostim)	IgG1-Fc + peptide (trombopoeitin receptor)
2. Actemra (tocilizumab)	lgG1-kappa	26. Nulojixq (belatacept)	lgG1-Fc + CTLA-4
3. Adcetrisc (brentuximab vedotin)	lgG1- ADC	27. Orenciar (abatacept)	lgG1-Fc + CTLA-4
4. AlprolIXd (Factor IX Fc fusion protein)	lgG1-Fc + Factor IX	28. Perjeta (pertuzumab)	IgG1-kappa
5. Arcalystf (rilonacept)	lgG1-Fc + IL1R	29. Prolias (denosumab)	IgG2-kappa
6. Arzerra (ofatumumab)	lgG1-kappa	30. <mark>Remicade (infliximab)</mark>	lgG1-kappa
7. Avastin (bevacizumab)	lgG1-kappa	31. Removabt (catumaxomab)	IgG2ab (rat-mouse hybrid)
8. Benlysta (belimumab)	lgG1-lambda	32. Remsimak l (infliximab [biosimil	ar]) IgG1-kappa
9. Cimziag (certolizumab pegol)	Fab'-PEG2MAL 40K	33. ReoProu (abciximab)	Fab fragment
10. Cyramza (ramucirumab)	lgG1-kappa	34. <mark>Rituxan (rituximab)</mark>	lgG1-kappa
11. Eloctateh (Factor VIII Fc fusion protein)	IgG1-Fc + Factor VIII	35. Simponi/ Simponi Aria (golimun	nab) IgG1-kappa
12. Enbrel (etanercept)	lgG1-Fc + TNFR	36. Simulect (basiliximab)	IgG1-kappa
13. Entyvio (vedolizumab)	lgG1-kappa	37. Soliris (eculizumab)	IgG2/4-kappa
14. Erbitux (cetuximab)	lgG1-kappa	38. Stelara (ustekinumab)	IgG1-kappa
15. Eyleaj (aflibercept)	lgG1-Fc + VEGF	39. Sylvant (siltuximab)	lgG1-kappa
16. Gazyva (obinutuzumab)	lgG1-kappa	40. Synagis (palivizumab)	lgG1-kappa
17 <mark>. Herceptin (trastuzumab)</mark>	lgG1-kappa	41. Tysabri (natalizumab)	IgG4-kappa
18. <mark>Humira (adalimumab)</mark>	lgG1-kappa	42. Vectibix (panitumumab)	IgG2-kappa
19. Ilaris (canakinumab)	lgG1-kappa	43. Xgevas (denosumab)	IgG2-kappa
20. Inflectrak l (infliximab [biosimilar])	lgG1-kappa	44. Xolair (omalizumab)	lgG1-kappa
21. Kadcylan (ado-trastuzumab emtansine)	lgG1-kappa + emtansine (ADC)	45. Yervoy (ipilimumab)	lgG1-kappa
22. Keytruda (pembrolizumab)	IgG4-kappa	46. Zaltrapw (ziv-aflibercept)	lgG1-Fc + VEGF
23. Lemtrada (alemtuzumab)	IgG1-kappa	47. Zevalinx (ibritumomab tiuxetan	) IgG1-kappa + linker + Yttrium-90
24. Lucentiso (ranibizumab)	Fab from IgG1-kappa		

Dawn M Ecker, Susan Dana Jones, and Howard L Levine (2015) *The therapeutic monoclonal antibody market*, mAbs 7:1, 9—14



# **Therapeutic mAbs**



Enbrel® (etanercept)

IgG1-Fc + TNFR



# Papain cleaves after His between Fab and Fc





# **Sample Preparation**



#### **2D-NMR of Rituximab-Fab 600 MHz**



## 2D-<sup>1</sup>H,<sup>15</sup>N-NMR of four Fab 700 MHz



#### 2D-<sup>1</sup>H<sup>13</sup>C-NMR of four Fab 700 MHz



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### Current Methods QA 2D-NMR

Electrospray ionization time-of-flight mass spectroscopy (ESI-TOF-MS)

Reduced and nonreduced tryptic peptide mapping LC-MS

Far-UV and Near-UV CD, FT-IR, Fluorescence etc.

Bioassays (Binding and Potency)

**Primary Sequence** 

#### **Primary Sequence**

Secondary and Tertiary structure

3D structure





# A Deeper Understanding via Assignment of NMR Resonances

A complete or near complete assignment can be:

A powerful tool to understand the significance (or lack of) of spectral changes with regard to the conformation or the dynamics of the drug substance.

A mean to monitor various perturbations (pH, solution conditions, excipients) at the amino acid level.



## Isotopic labeling of NISTmAb Fragments in *Pichia Pastoris*

#### Fab

Construction of a bis-cistronic vector inserted in the methylotropic *Pichia Pastoris* Polypeptide is secreted in the culture media after removal of the signal peptide.

**Signal Peptide-EKR**EAEA – N-ter(Heavy [V<sub>H</sub>-C<sub>H</sub>1])

**Signal Peptide-EKR**EAEA – N-ter(Light [V<sub>L</sub>-C<sub>L</sub>])

#### Fc

Signal Peptide-EKREAEA – N-ter(Heavy [C<sub>H</sub>2-C<sub>H</sub>3])

The final polypeptide is glycosylated with a high-mannose glycan that is further hyper mannosylated (Glycan MW is ~5000 Da by SDS-PAGE).



## **Isotopic labeling of NISTmAb Fragments in Pichia Pastoris**



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## **NMR Time Scale of Protein Dynamics**









## <sup>15</sup>N-Adalimumab-Fab prepared from E.coli



#### Humira®-Fab over <sup>15</sup>N-Adalimumab-Fab



## <sup>15</sup>N-Rituximab-Fab prepared from E.coli



#### **Rituxan®-Fab over <sup>15</sup>N-Rituximab-Fab**



#### Herceptin®-Fab over <sup>15</sup>N-Trastuzumab-Fab





#### NISTmAb-Fab (900) over <sup>15</sup>N-NISTmAb-Fab





# Thank you

