

# In Vitro Assay to Predict Human IgG Half-Life

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Scientist, Product Discovery

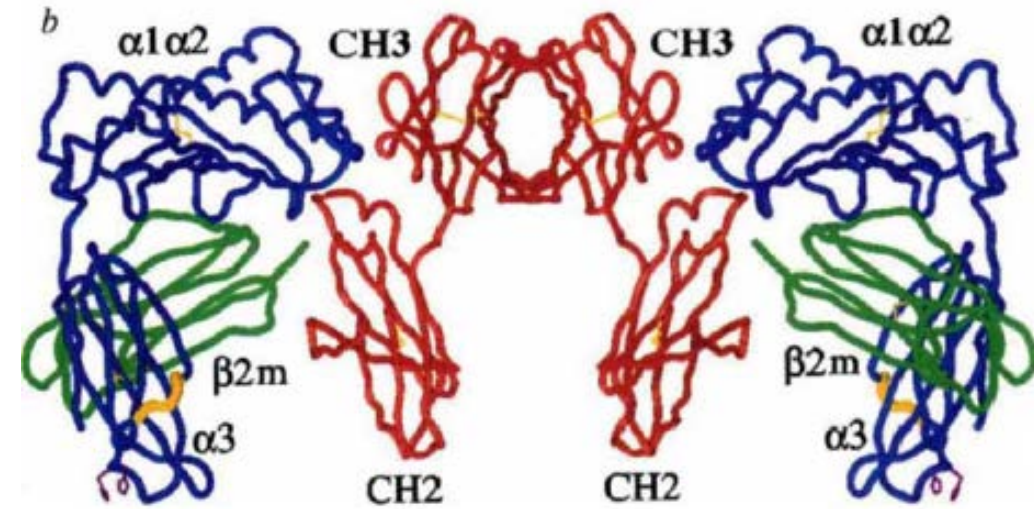
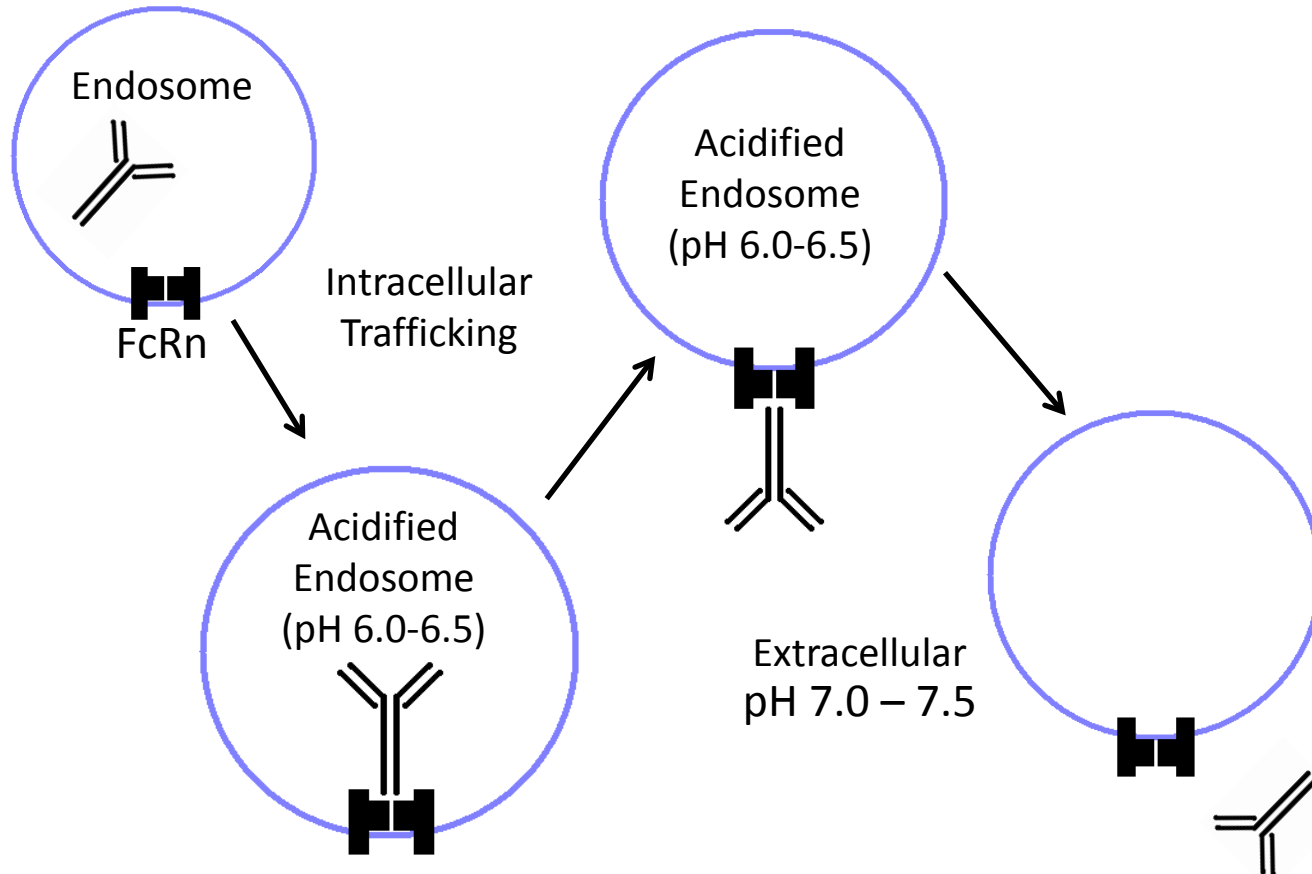
MassBiologics of University of Massachusetts Medical School

Current Affiliation: Scientist - Protein Engineering, Kanyos Bio

# Clinical Relevance of Antibody Half-Life

- For therapeutic mAbs, longer half-life enhances:
  - Safety
  - Efficacy
  - Cost
  - Convenience
- For diagnostic mAbs, shorter half-life is usually desired.
- Lack of cost effective, high-throughput assays to predict human IgG half-life
  - Implement during screening and candidate selection stages of discovery

# Mechanism IgG Half-Life



Burmeister et al, Nature 1997

# Assessing IgG-FcRn Interactions

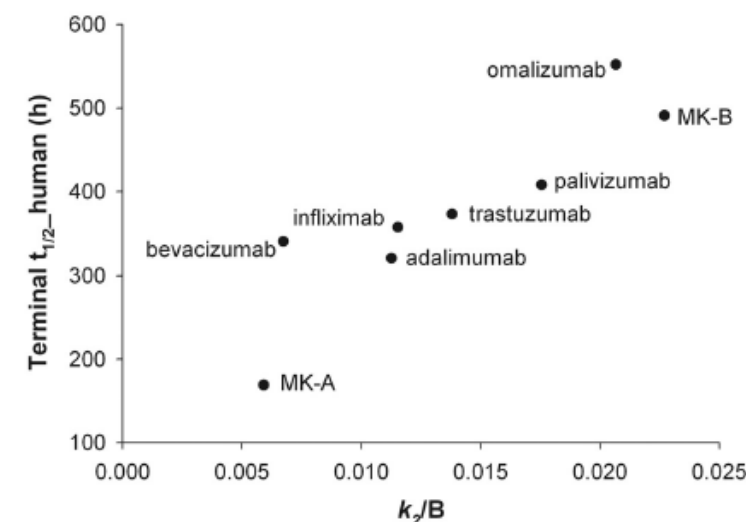
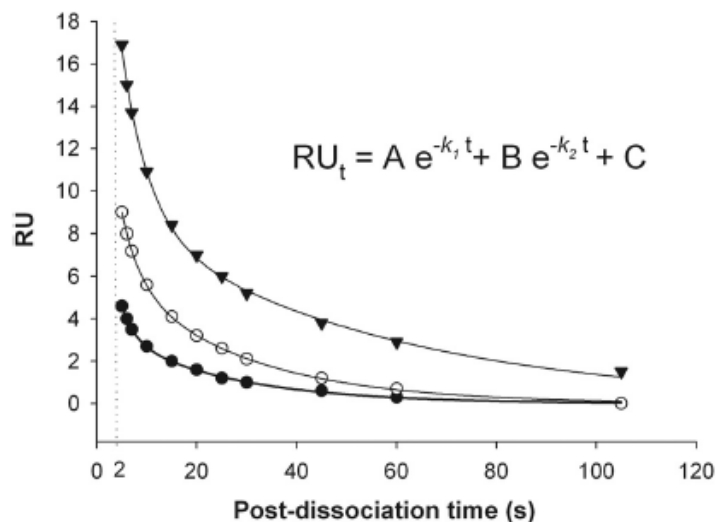
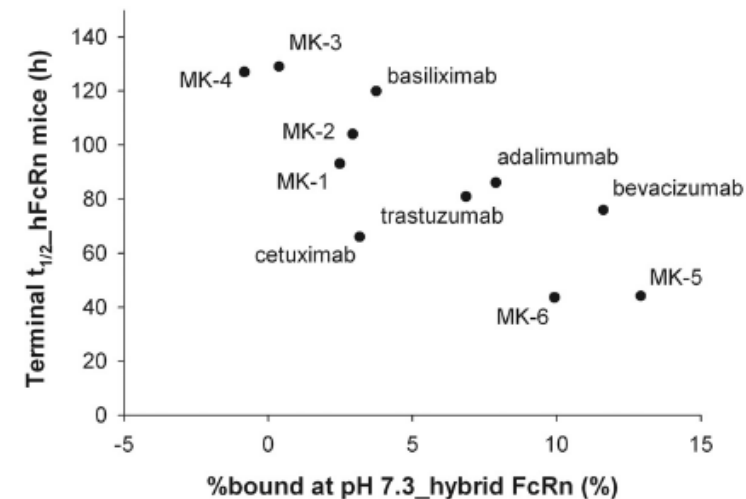
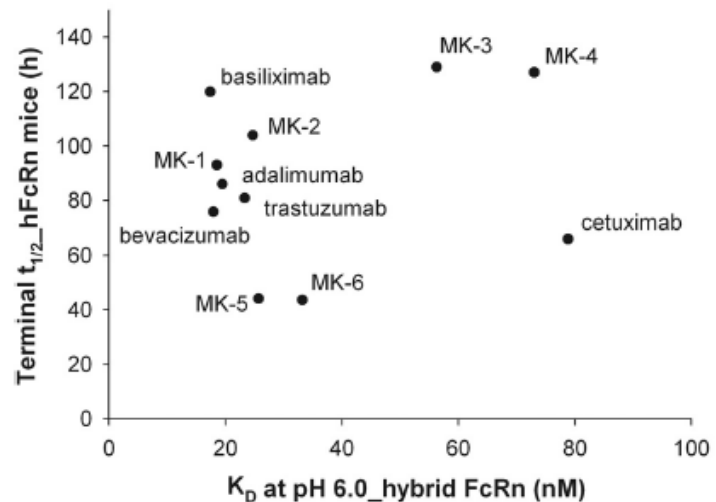
Wang et al., Drug Metab Dispos 2011

TABLE 1

*In vitro* human FcRn binding and dissociation parameters of MK-1 to MK-6

Compounds	MK-1	MK-2	MK-3	MK-4	MK-5	MK-6
Isotype Fab <sup>a</sup>	IgG1 A	IgG2 A	IgG1 B	IgG2 B	IgG1 C	IgG2 C'
K <sub>D</sub> (nM) at pH 6.0	56.3	73.0	18.5	24.7	25.7	33.2
%bound at pH 7.3 (%)	0.4	0.0	2.5	2.9	12.9	9.9

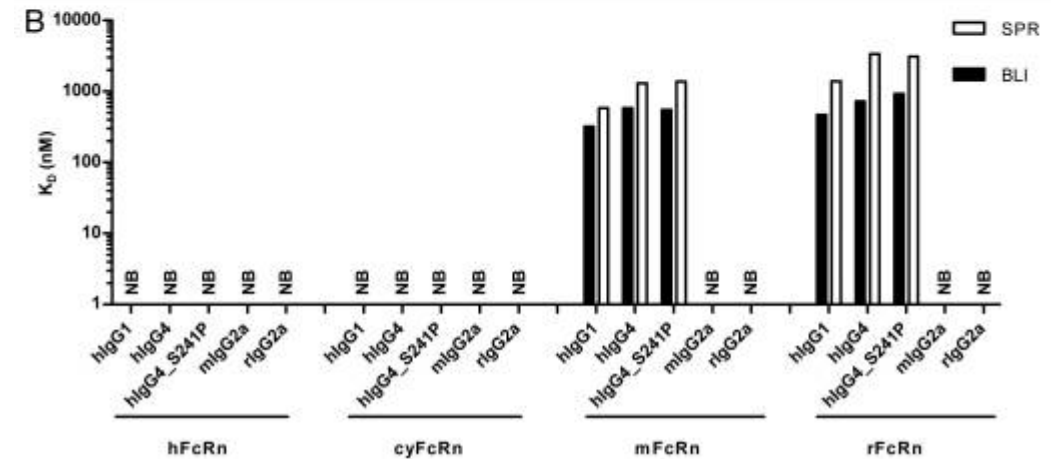
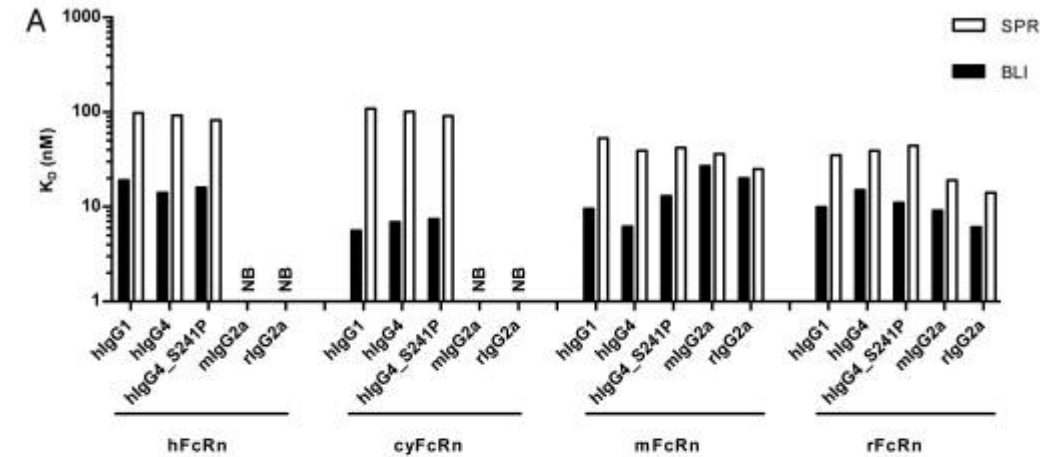
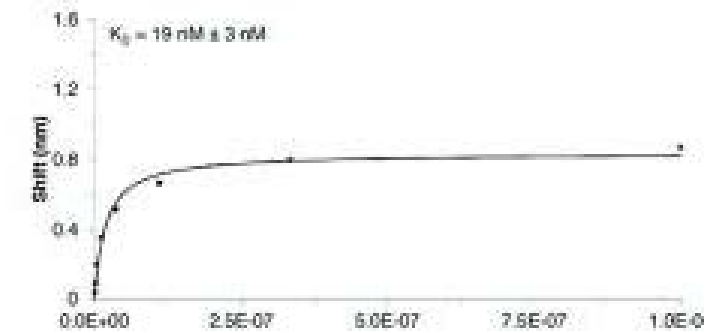
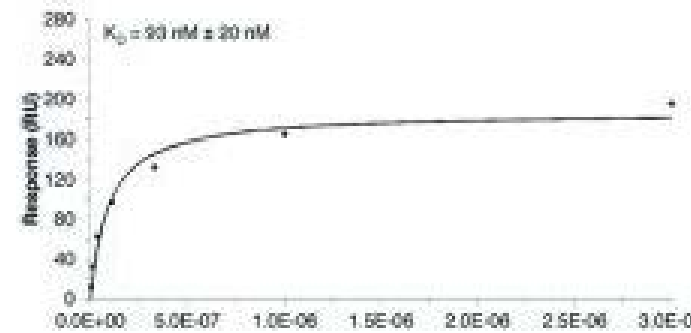
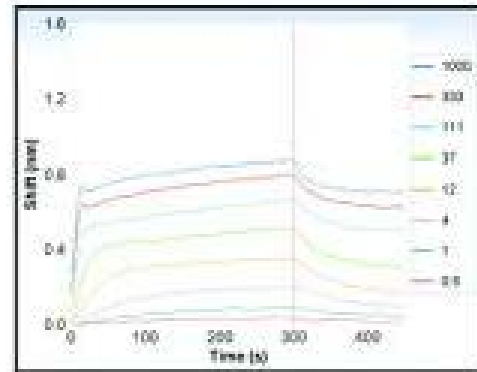
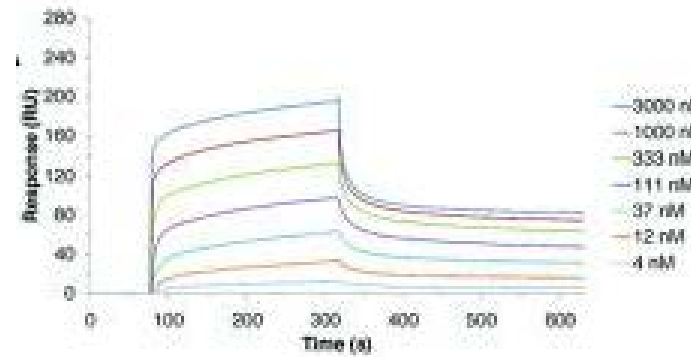
<sup>a</sup> MK-1 and MK-2 have an identical Fab domain A, MK-3 and MK-4 have an identical Fab domain B, and MK-5 and MK-6 have closely related, but slightly different, Fab domains C and C'.



# IgG-FcRn Interaction on SPR vs BLI Neuber et al., mAbs 2014

SPR

BLI



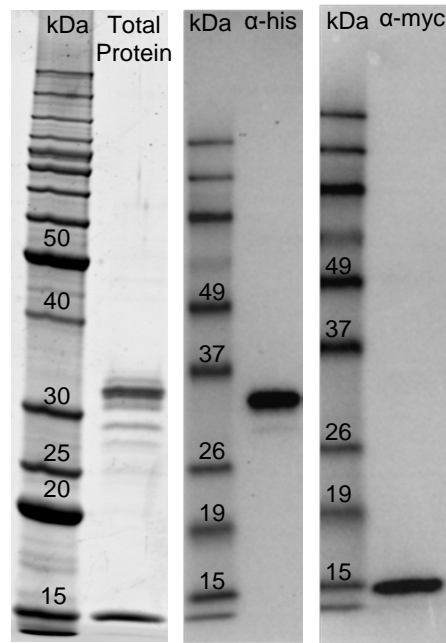
# BLI Assay for Half-Life Prediction

Souders et al., mAbs 2015

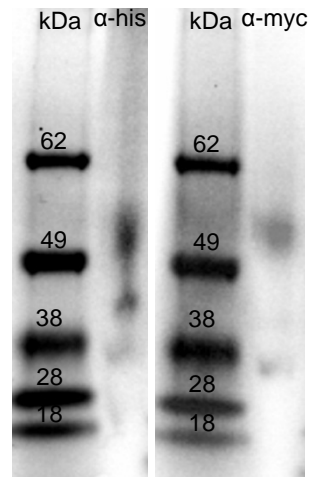
- Extend current knowledge to combine:
  - Association at acidic pH
  - Dissociation at physiological pH
  - On and off rates (rather than equilibrium constants)
- Implement assay to screen for potential therapeutic mAbs with high half-life and investigate sequence or post-translational modifications that may enhance half-life.

# Production of High-Quality Reagents

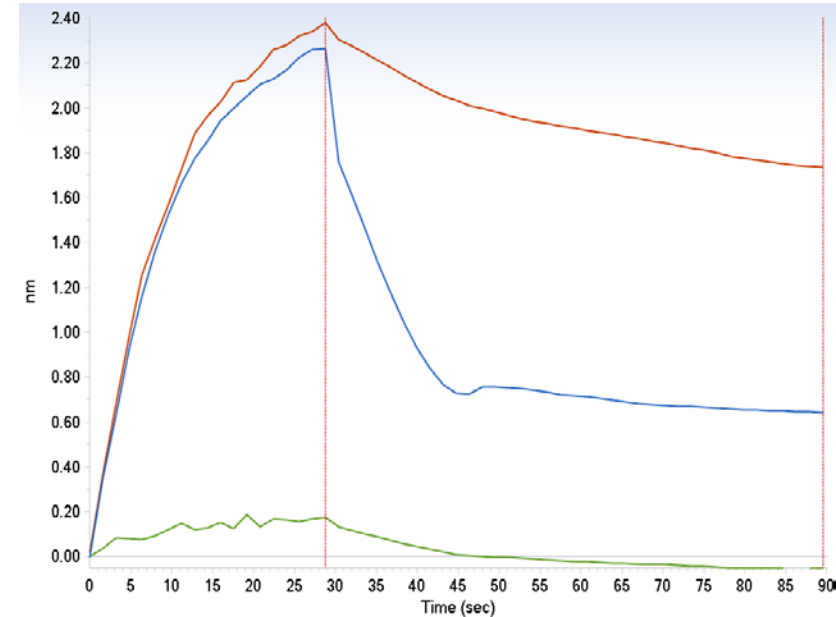
FcRn heterodimer purified from stable cell line producing  $\alpha$ FcRn-His and  $\beta_2$ M-Myc



Reduced, denatured



Native

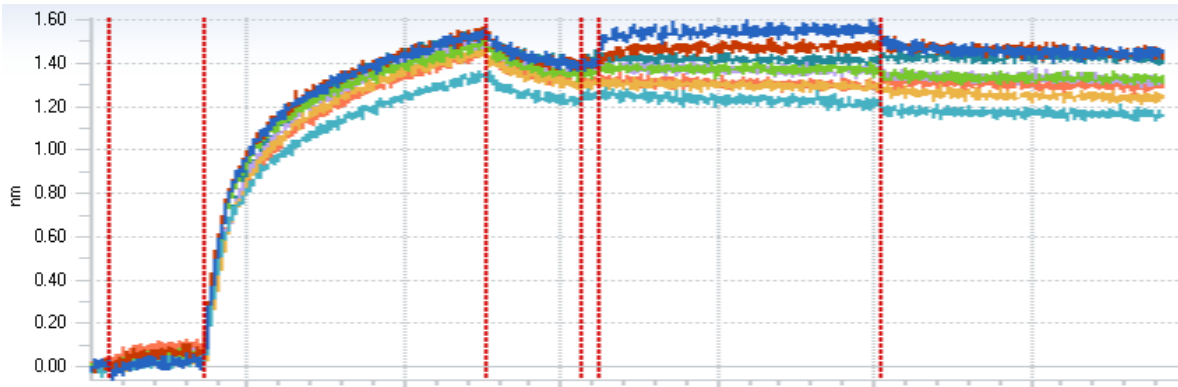


Condition			
Association pH	6.0	6.0	7.5
Dissociation pH	7.5	6.0	7.5
$K_{on}$ (1/s)	0.110	0.105	negligible
$K_{off}$ (1/s)	0.101	0.020	N/A

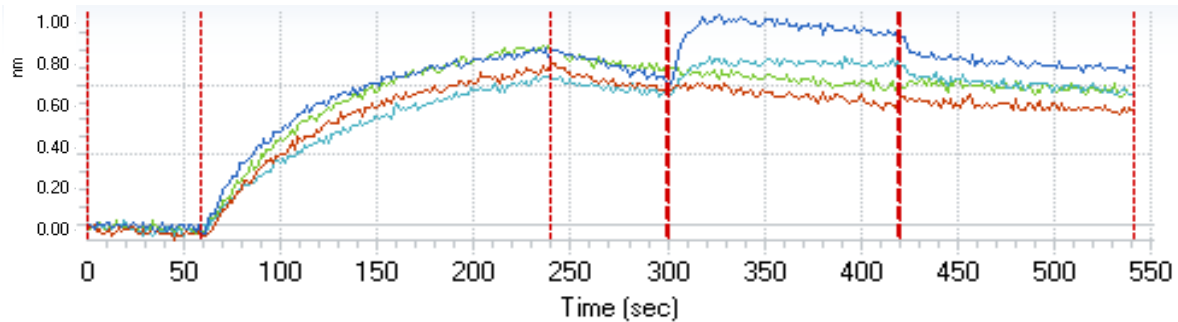
# Assay Development

Biosensor Selection

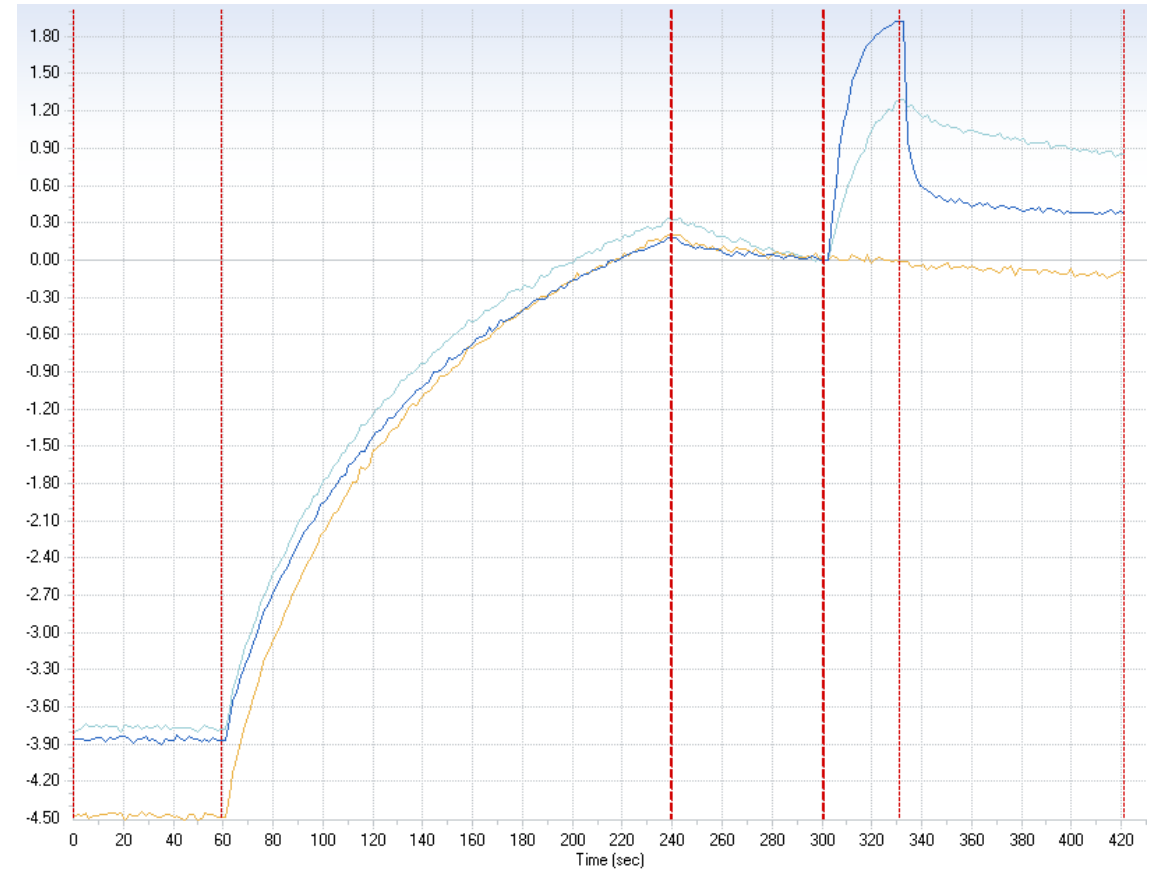
### Amine Reactive Biosensors



### Anti-Penta-His Biosensors



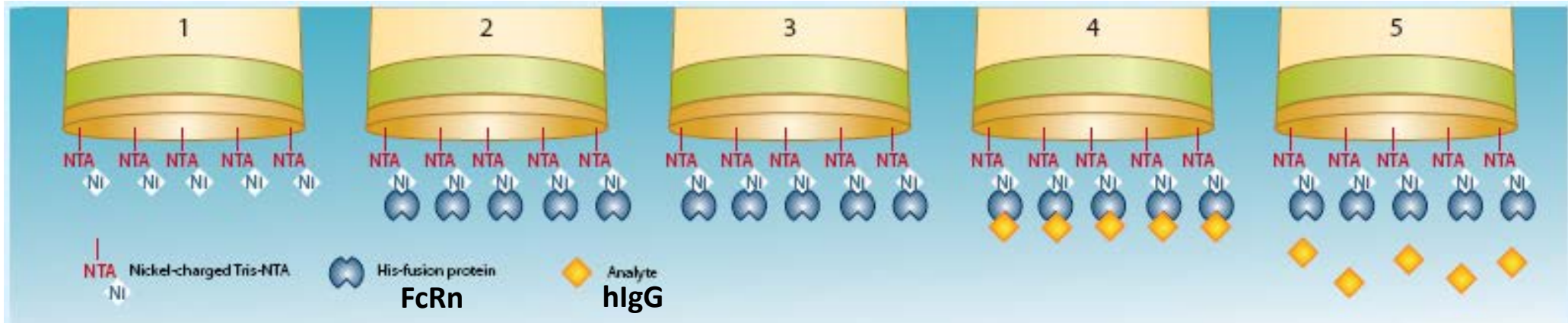
### Ni-NTA Biosensors



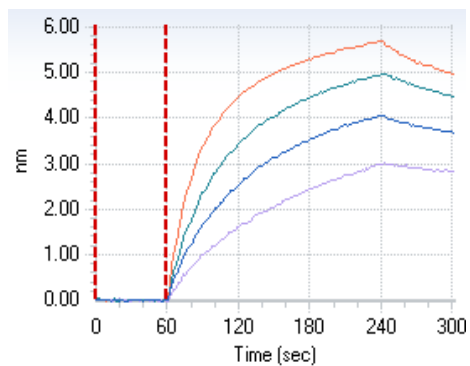


# Assay Development

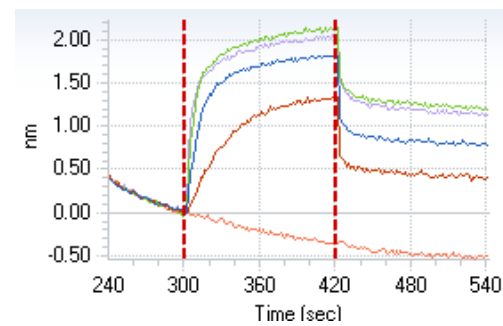
## Concentration Scouting



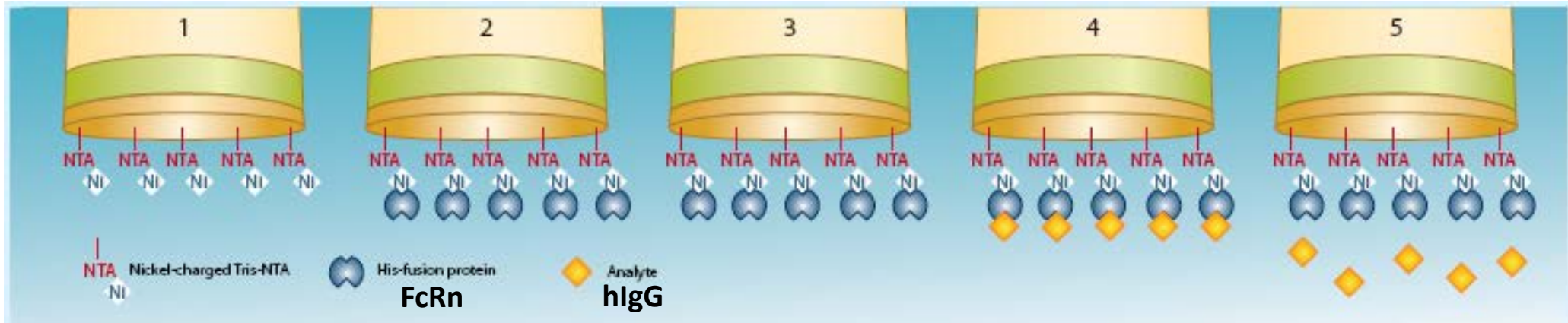
### Loading Concentration



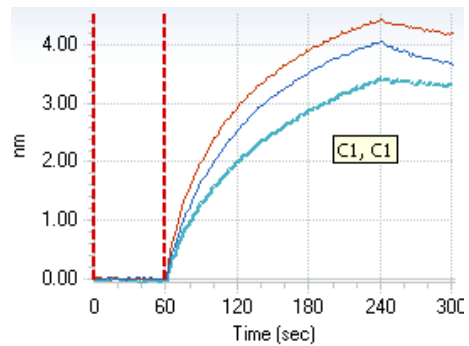
### Association Concentration



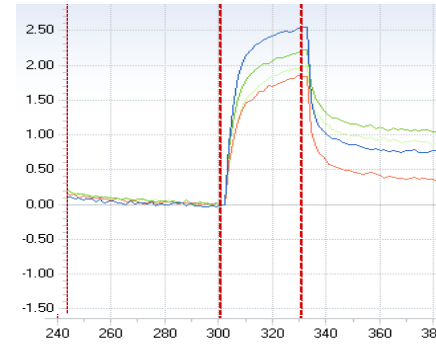
# Assay Development pH Scouting



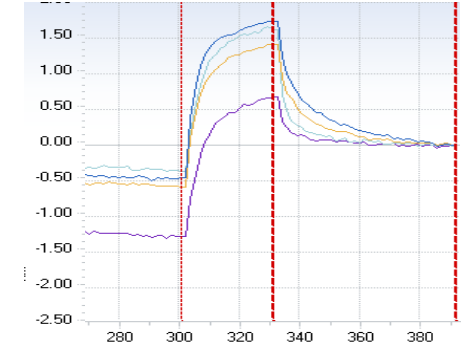
Loading pH



Association pH

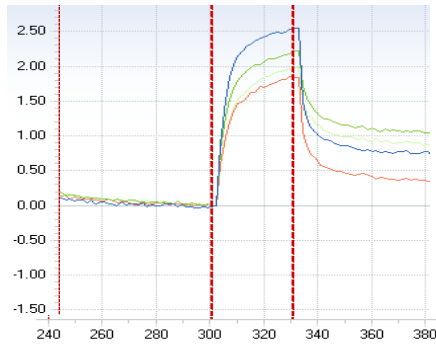


Dissociation pH

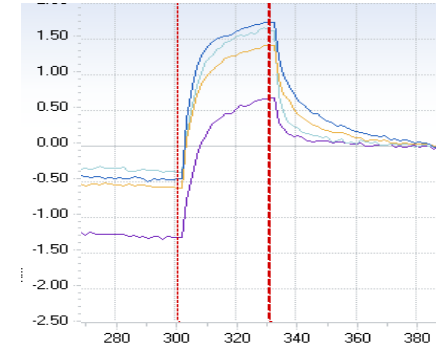


# Assay Development pH Scouting

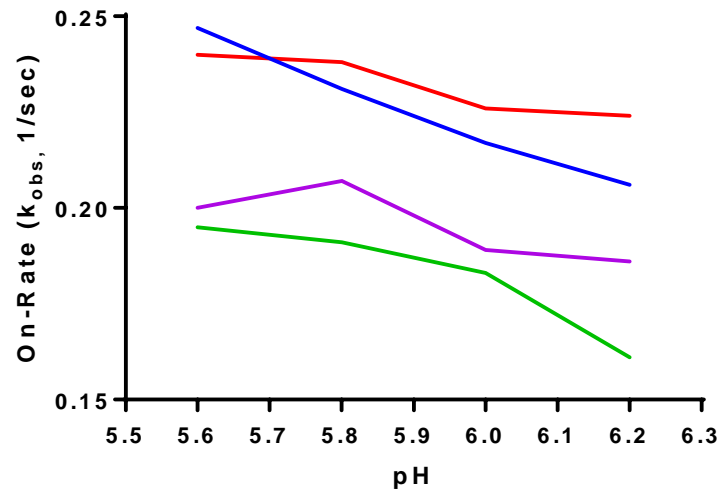
### Association pH



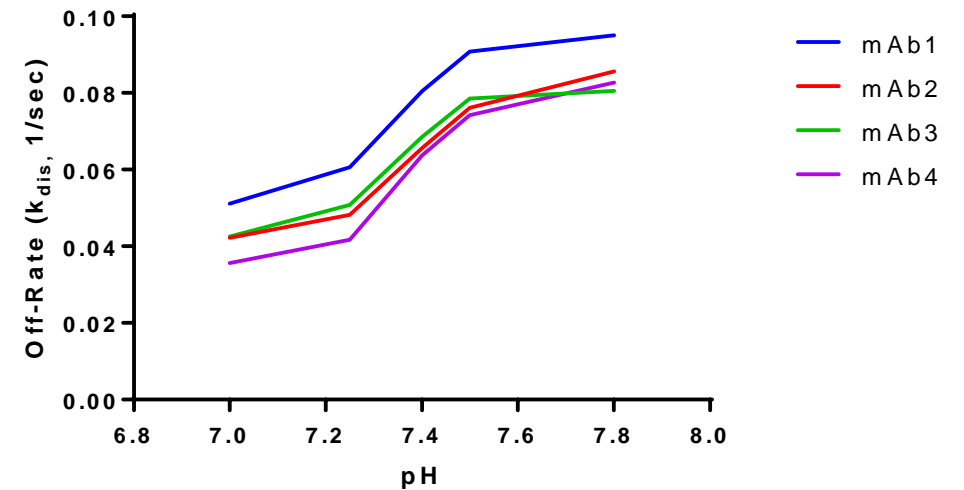
### Dissociation pH



### Association Rate - pH Scouting



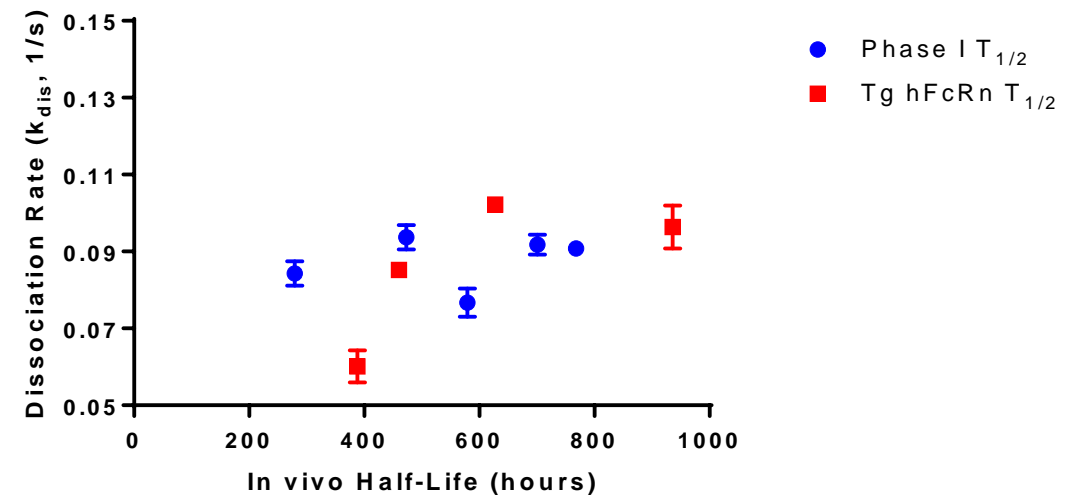
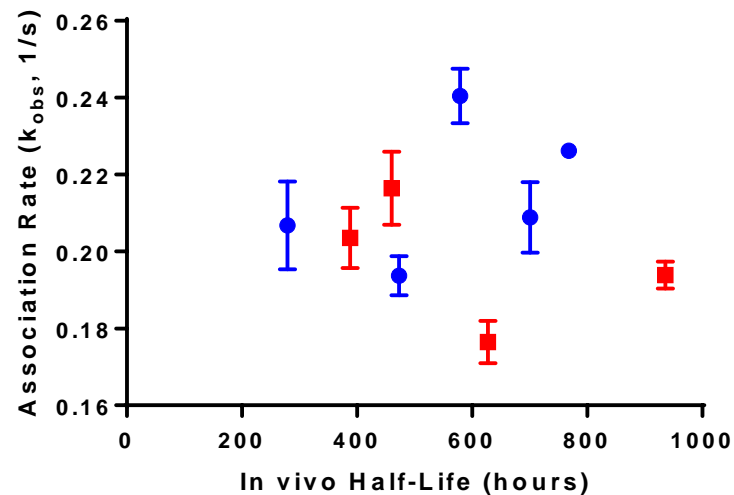
### Dissociation Rate - pH Scouting



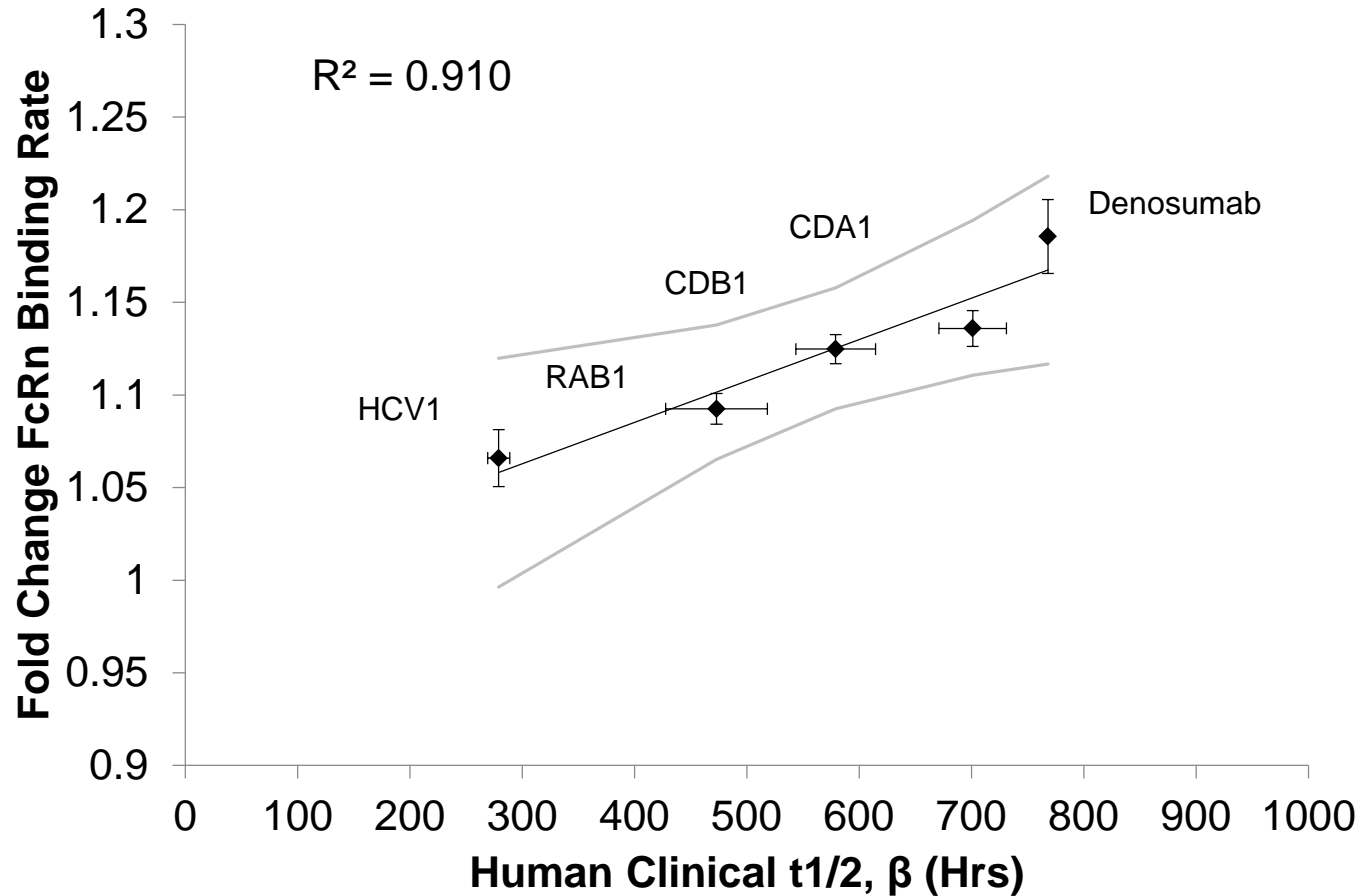
# Predictive Model

Independent Association and Dissociation Rates

mAb	Target	Phase I $T_{1/2\beta}$ (Days)
Denosumab	RANKL	32.0
Actoxumab (CDA1)	C. difficile Toxin A	29.2
Bezlotoxumab (CDB1)	C. difficile Toxin B	24.1
RAB1	Rabies Virus Glycoprotein	19.7
HCV1	Hep C Virus Glycoprotein	11.6



# Predictive Model Combining Association and Dissociation Rates



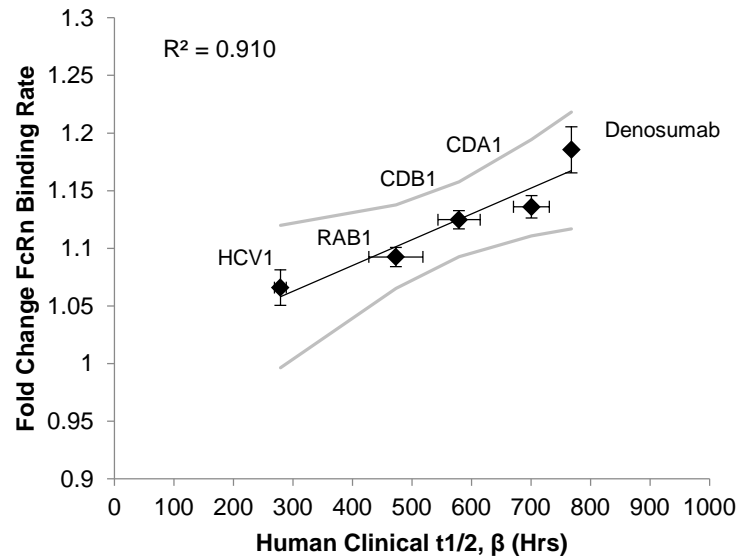
$$\text{Fold Change Association Rate} = \frac{K_{obs}}{K_{obs} \text{ (of slowest on-rate)}}$$

$$\text{Fold Change Dissociation Rate} = \frac{K_{dis}}{K_{dis} \text{ (of slowest off-rate)}}$$

$$\text{FcRn Binding Rate} = \frac{\text{Fold Change Assoc.} + \text{Fold Change Dissoc.}}{2}$$

# Predicting IgG Human Half-Life

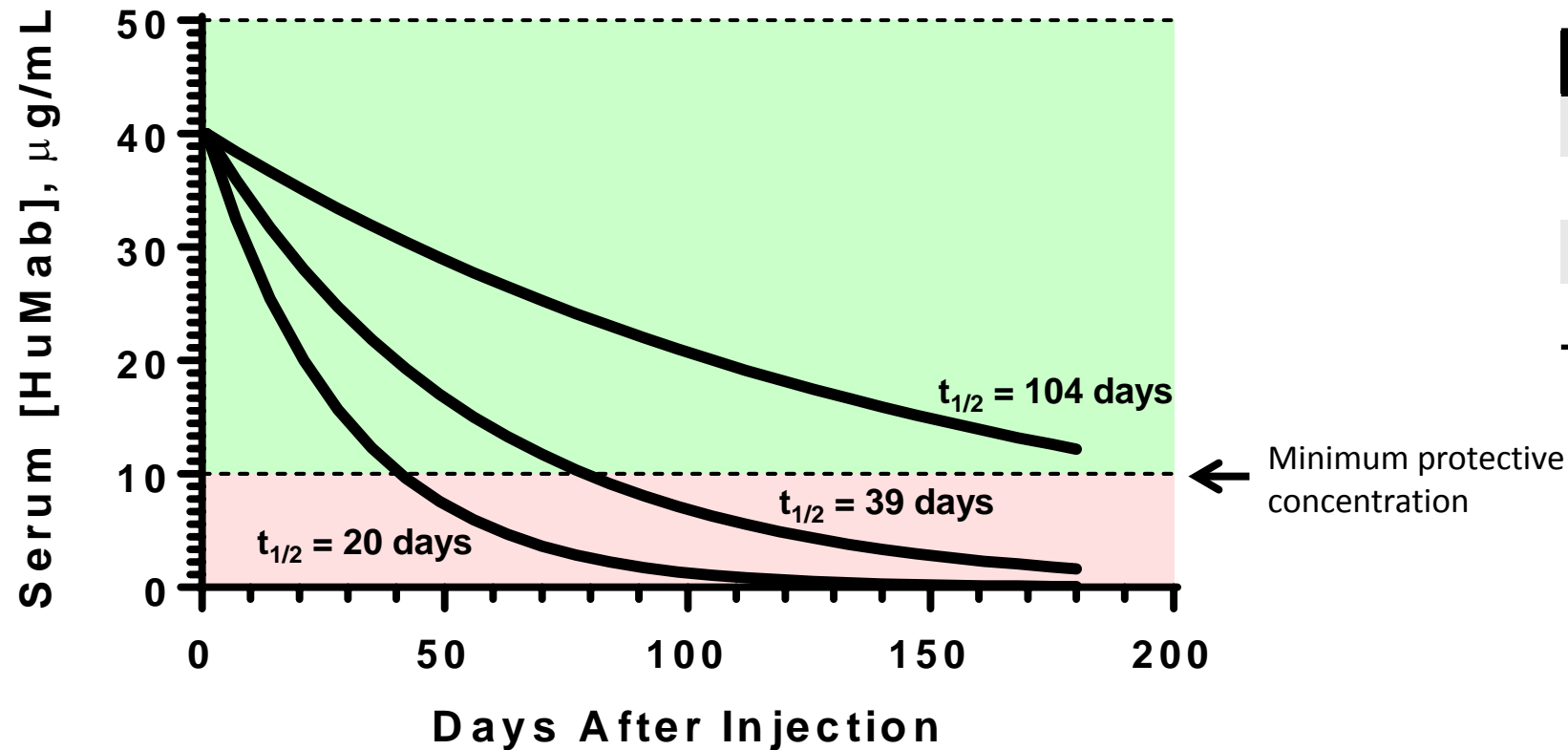
Preclinical Therapeutic mAbs



mAb	T <sub>1/2</sub> (Hours)
<b>CDA1</b>	<b>700.8</b>
mAb1-1	639.4
mAb1-2	629.6
mAb2-1	612.7
<b>CDB1</b>	<b>579.4</b>
mAb1-3	548.0
<b>RAB1</b>	<b>473.0</b>
mAb3-1	451.1
mAb2-2	439.5
mAb2-3	395.6
mAb2-4	378.5
<b>HCV1</b>	<b>279.0</b>
mAb4-1	124.2

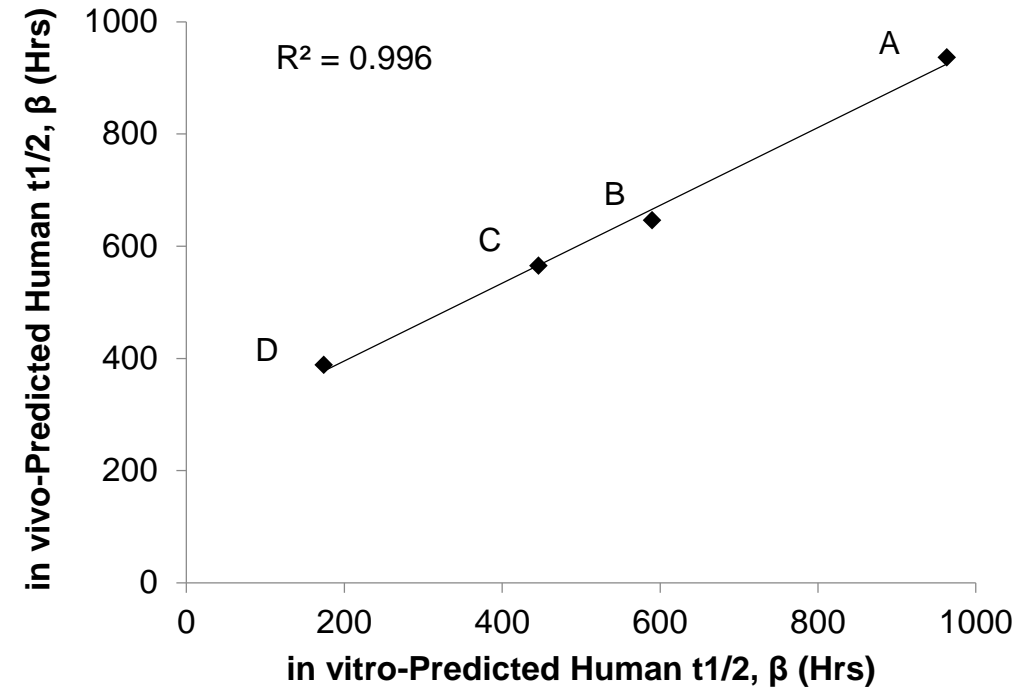
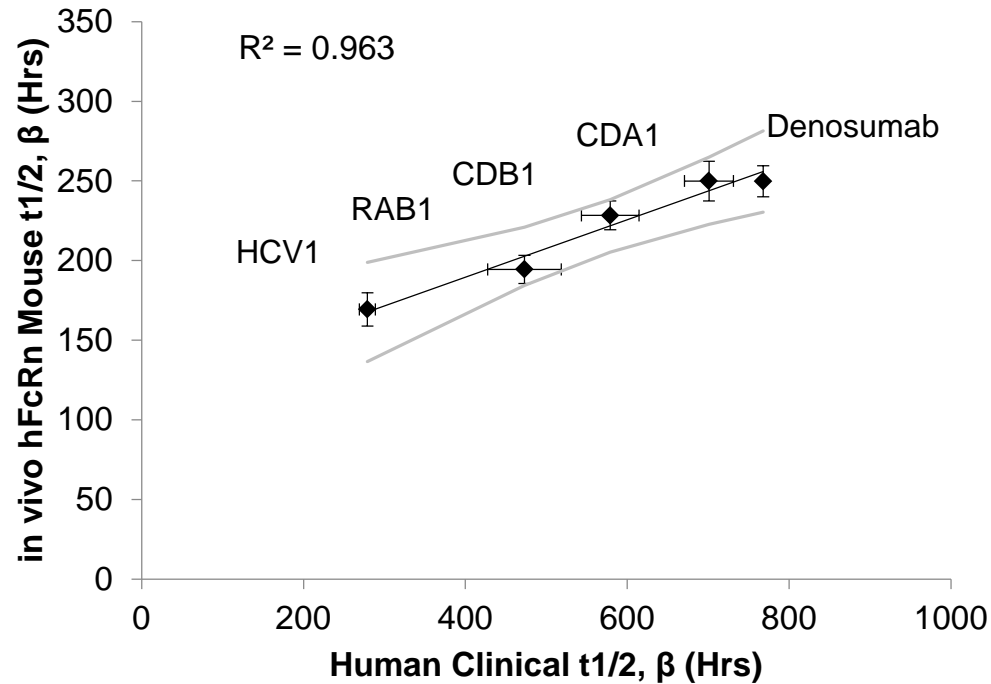
# Predicting IgG Human Half-Life

Therapeutic mAbs for PrEP



mAb	$T_{1/2}$ (Hrs)
A	963
B	590
C	446
D	174

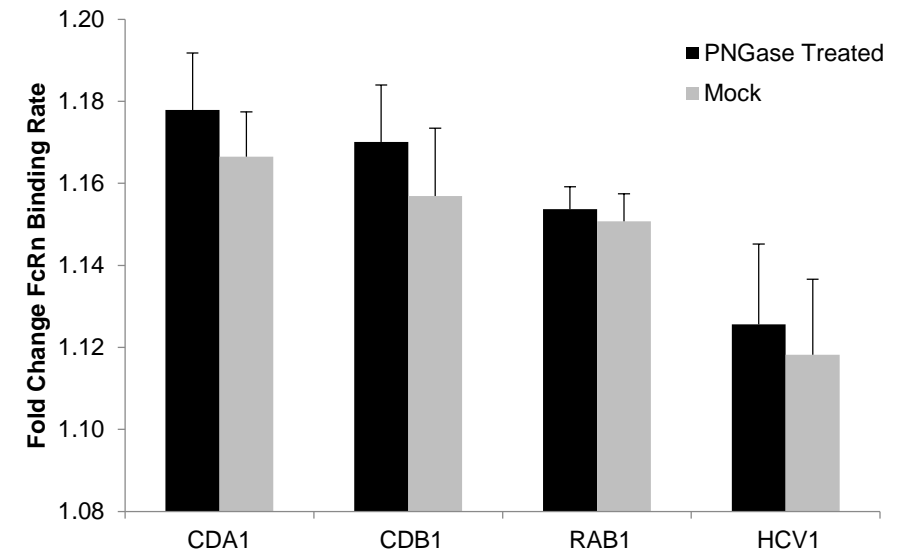
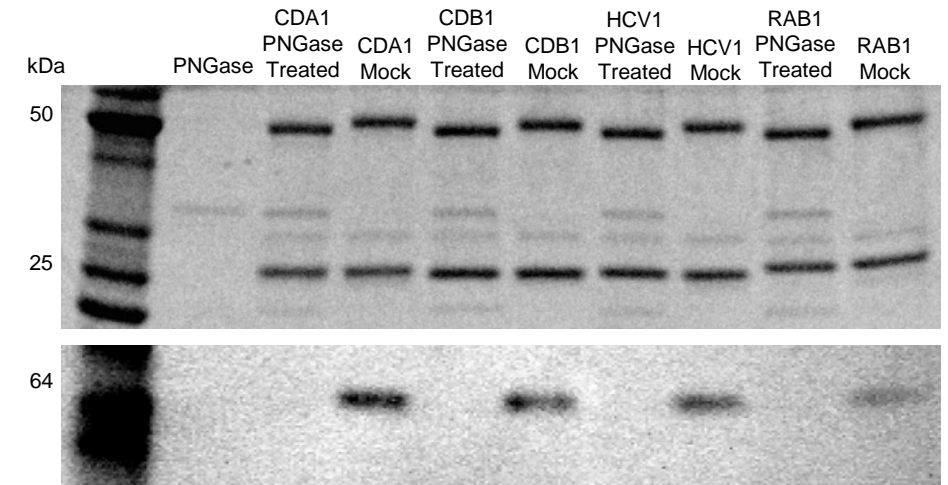
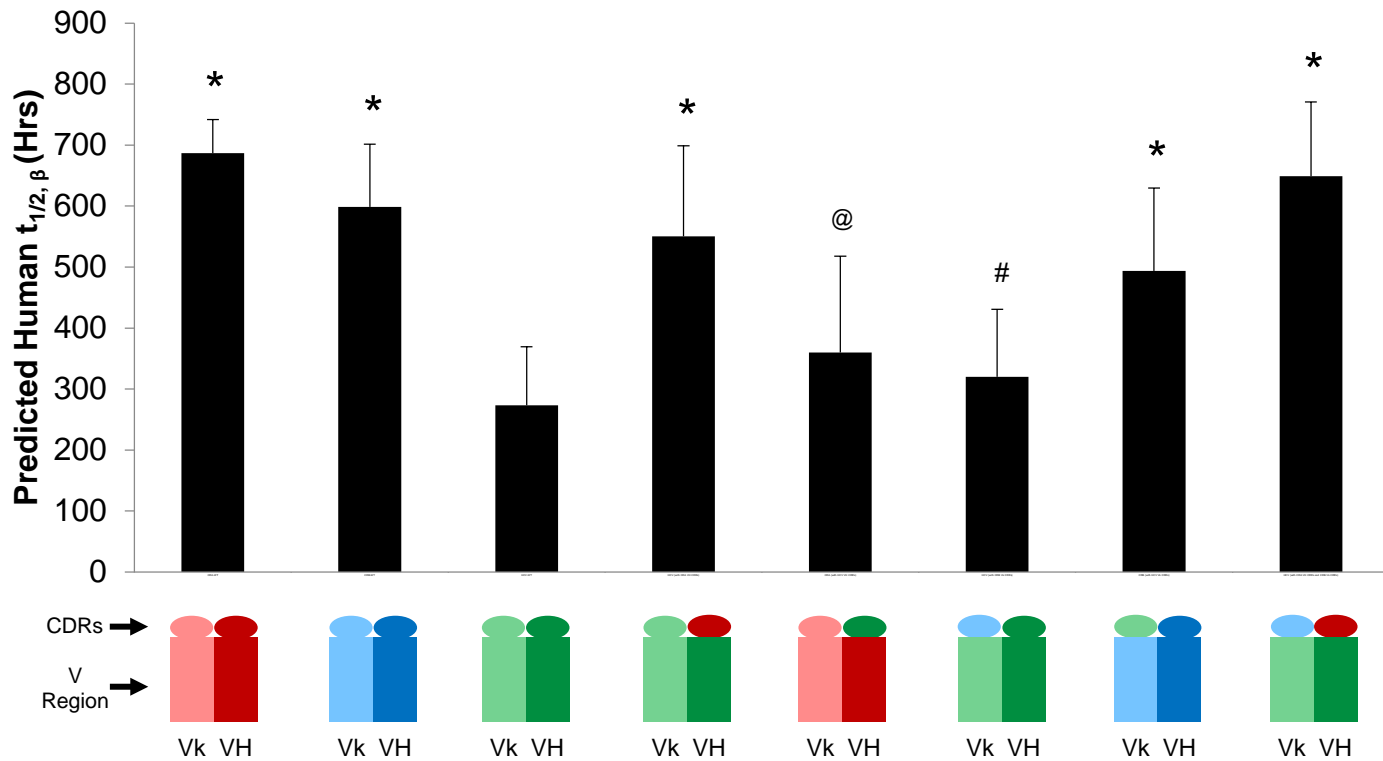
# Predicting IgG Human Half-Life Therapeutic mAbs for PrEP



mAb	in vivo model (Hrs)	in vitro model (Hrs)
A	936	963
B	646	590
C	565	446
D	388	174



# Predicting Half-Life Modifications V Region Sequence & Glycosylation



# Summary

- Optimal half-life is important for clinical success of mAbs
- BLI-based assay to predict human IgG half-life that considers:
  - Both association and dissociation at relevant pH
  - On and off rate
- Confirmed model accuracy with hFcRn transgenic mice
- Useful for screening early stage preclinical candidates and investigating IgG modifications.