Physiologically Based Predictions of Monoclonal Antibody Pharmacokinetics: Insights from a Large-Scale Data Analysis

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Outline

Physiologically Based Predictions of Monoclonal Antibody Pharmacokinetics: Insights from a Large-Scale Data Analysis



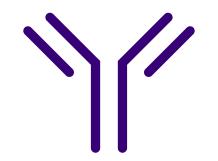
A large database of pharmacokinetic data for mAbs compiled from the literature

Support early-stage pharmacokinetic predictions of mAbs and FIH trials



Monoclonal antibodies and subcutaneous administration

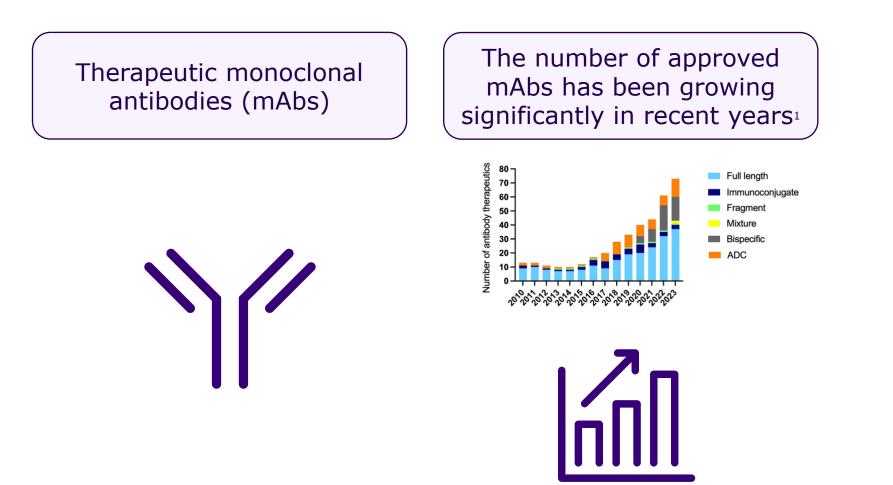
Therapeutic monoclonal antibodies (mAbs)





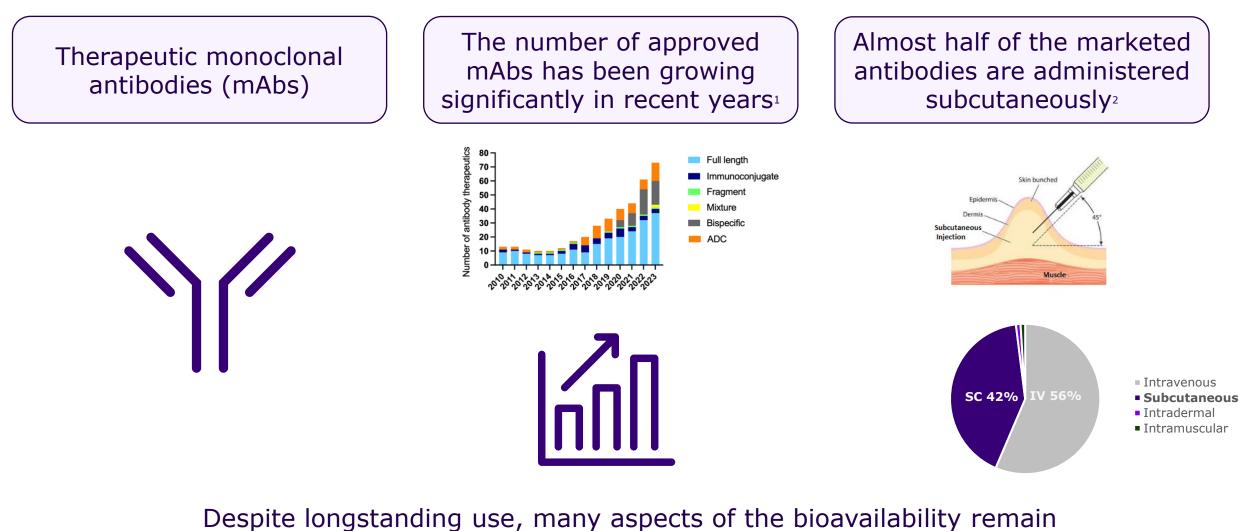
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Monoclonal antibodies and subcutaneous administration





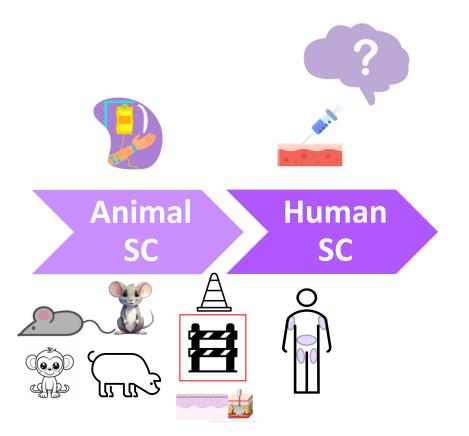
Monoclonal antibodies and subcutaneous administration



poorly understood

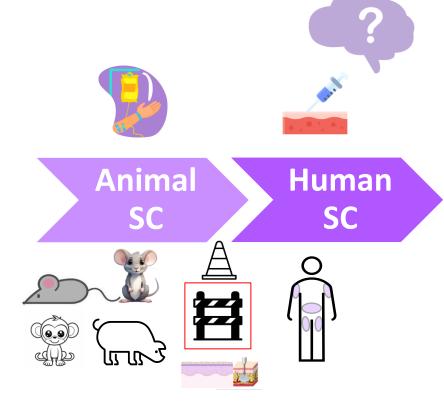


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Why?



FDA U.S. FOOD & DRUG ADMINISTRATION

FDA Announces Plan to Phase Out Animal Testing Requirement for Monoclonal Antibodies and Other Drugs

For Immediate Release: April 10, 2025

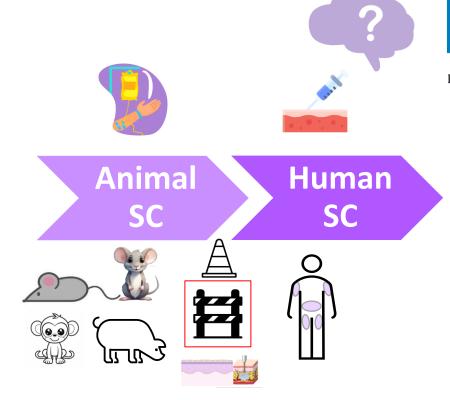
Today, the U.S. Food and Drug Administration is taking a groundbreaking step to advance public health by replacing animal testing in the development of monoclonal antibody therapies and other drugs with more effective, human-relevant methods. The new approach is designed to improve drug safety and accelerate the evaluation process, while reducing animal experimentation, lowering research and development (R&D) costs, and ultimately, drug prices.

The FDA's animal testing requirement will be reduced, refined, or potentially replaced using a range of approaches, including Al-based computational models of toxicity and cell lines and organication toxicity testing in a laboratory setting (so-called New Approach Methodologies or NAMs data). Implementation of the regimen will begin immediately for investigational new drug (ND) applications, where inclusion of NAMs data is encouraged, and is <u>outlined in a roadmap</u> also being released today. To make determinations of efficacy, the agency will also begin use pre-existing, real-world safety data from other countries, with comparable regulatory standards, where the drug has already been studied in humans.

"For too long, drug manufacturers have performed additional animal testing of drugs that have data in broad human use internationally. This initiative marks a paradigm shift in drug evaluation and holds promise to accelerate cures and meaningful treatments for Americans while reducing animal use," said FDA Commissioner Martin A. Makary, M.D., M.P.H. "By leveraging Al-based computational modeling, human organ model-based lab testing, and real-world human data, we can get safer treatments to patients faster and more reliably, while also reducing R&D costs and drug prices. It is a win-win for public health and ethics."



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Why?

FDA U.S. FOOD & DRUG ADMINISTRATION FDA NEWS RELEASE

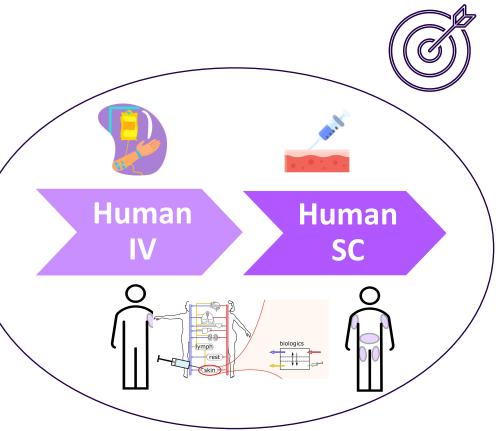
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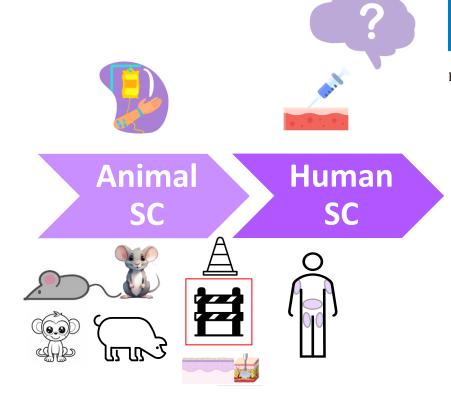
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Establish a model-based strategy for predicting mAbs PK in humans (FIH) following SC administration with and without prior data on IV PK



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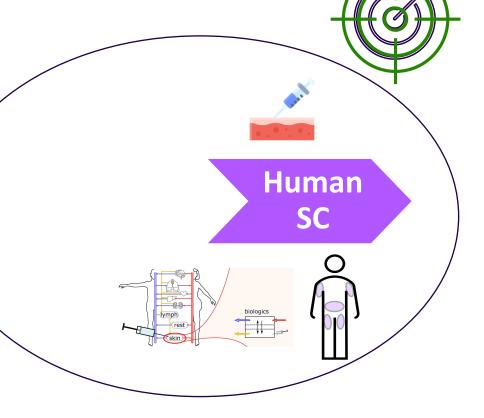
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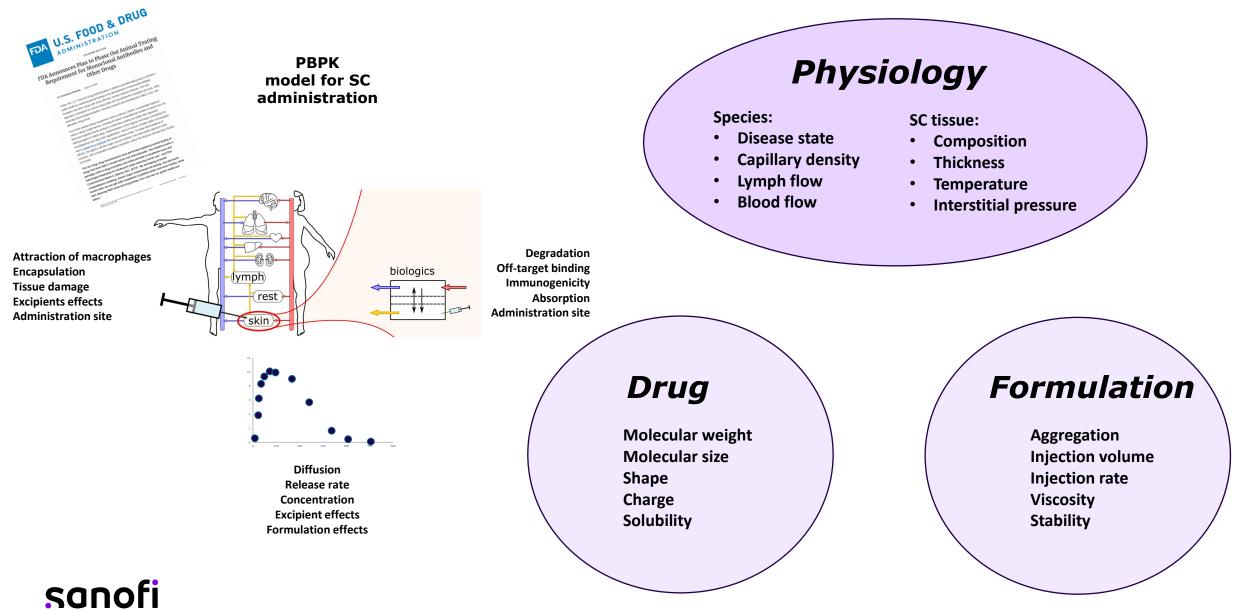
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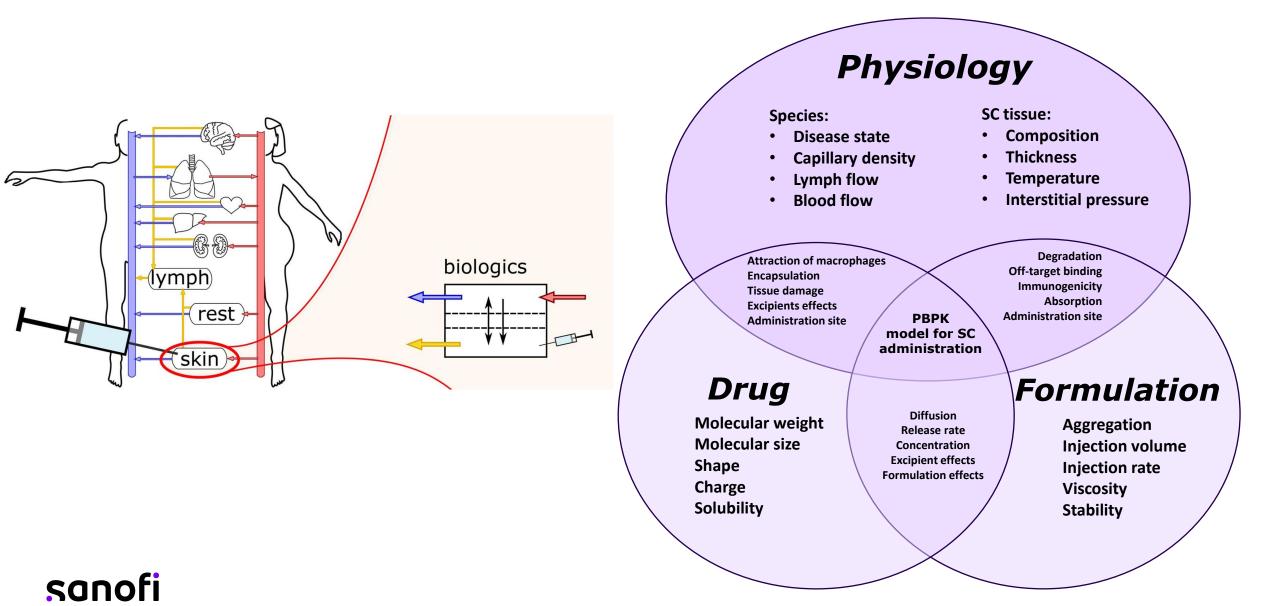
Establish a model-based strategy for predicting mAbs PK in humans (FIH) following SC administration with and without prior data on IV PK

How?

Subcutaneous administration and PBPK modeling



Subcutaneous administration and PBPK modeling



Subcutaneous absorption model

P OPEN SYSTEMS Pharmacology Plasma flow Vascular Space Drug + FcRn Endosomal Space Drug + FcRnInterstitial **Space** Drug + FcRn Lymph flow Organism **Injection site** Depot Stack 1 Stack n° Stack 2 Plasma From Layer 1 Lymph Stack 3 Layer 2 Stack 4 Layer 3 Stack 5 Layer 4 Stack 6 Central Lymph Layer 5 Node Stack 7 Layer 6 Stack 8 Layer 7 Stack 9 Layer 8 Stack 10 Local Lymph Layer 9 Stack 11 Node

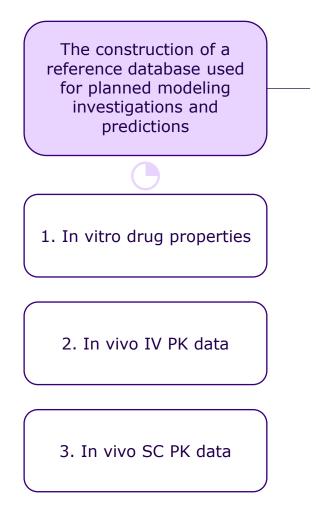
Physiologically based model structure

Describe the spatial-temporal drug disposition in the SC tissue (3D)

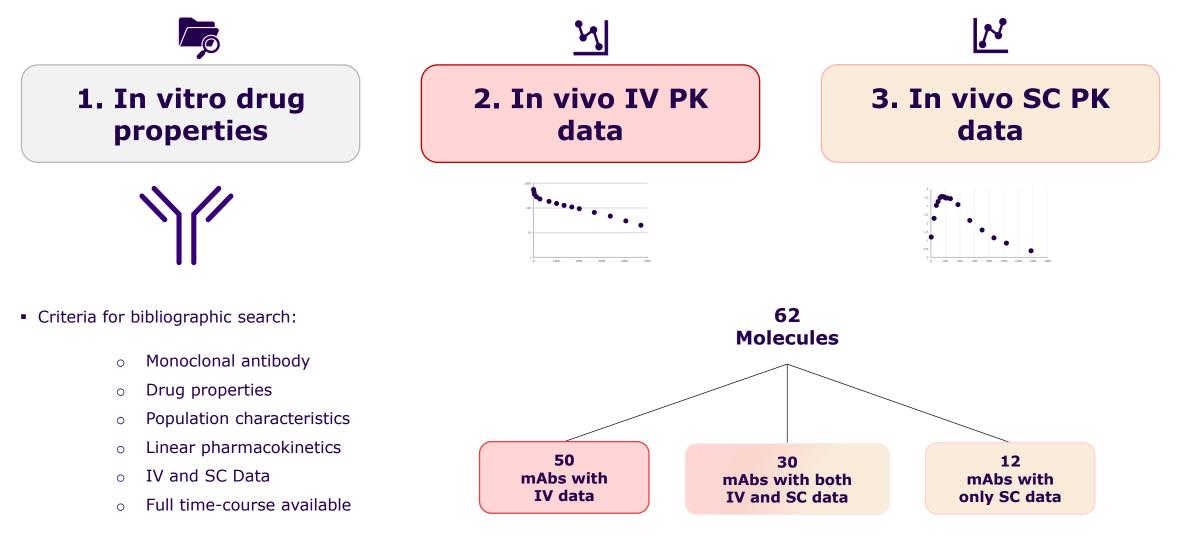
Model elements

- <u>Depot = Injection</u>
 - Injection volume
 - Injection rate
 - Undissolved drug particles
- Layers = representing the tissue surrounding the depot
 - Dynamic layer sizing to allow for sufficient space
 - Geometry: sphere or cylinder
- <u>Dispersion in tissue</u>
 - Defined by user
 - 1/3 shells may be filled at administration
- Alignment to OSP PBPK structure
 - Parameterization and structure
 - 2-pore theory for extravasation
 - Endosomal clearance/FcRn-binding

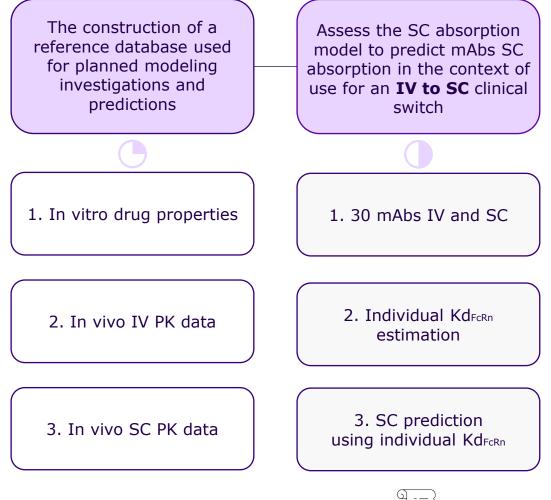
Establish a model-based strategy for predicting mAbs PK in humans following SC administration with and without prior data on IV PK



The construction of a reference database used for planned modeling investigations and predictions



Establish a model-based strategy for predicting mAbs PK in humans following SC administration with and without prior data on IV PK



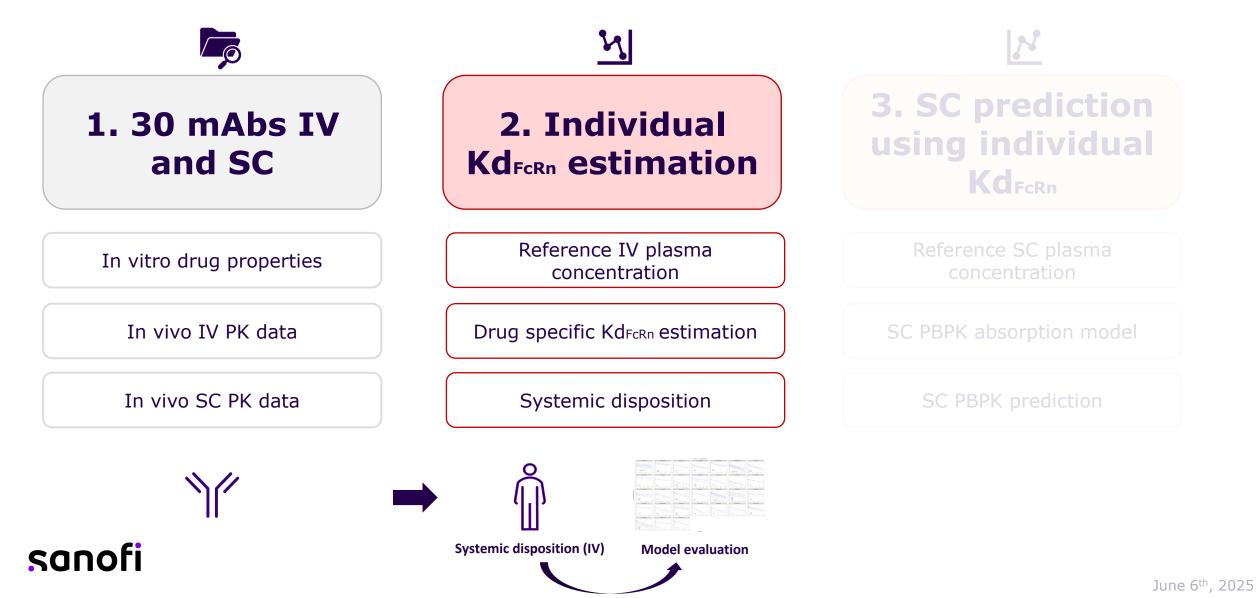


Assess the SC absorption model to predict mAbs SC absorption in the context of use for an IV to SC clinical switch

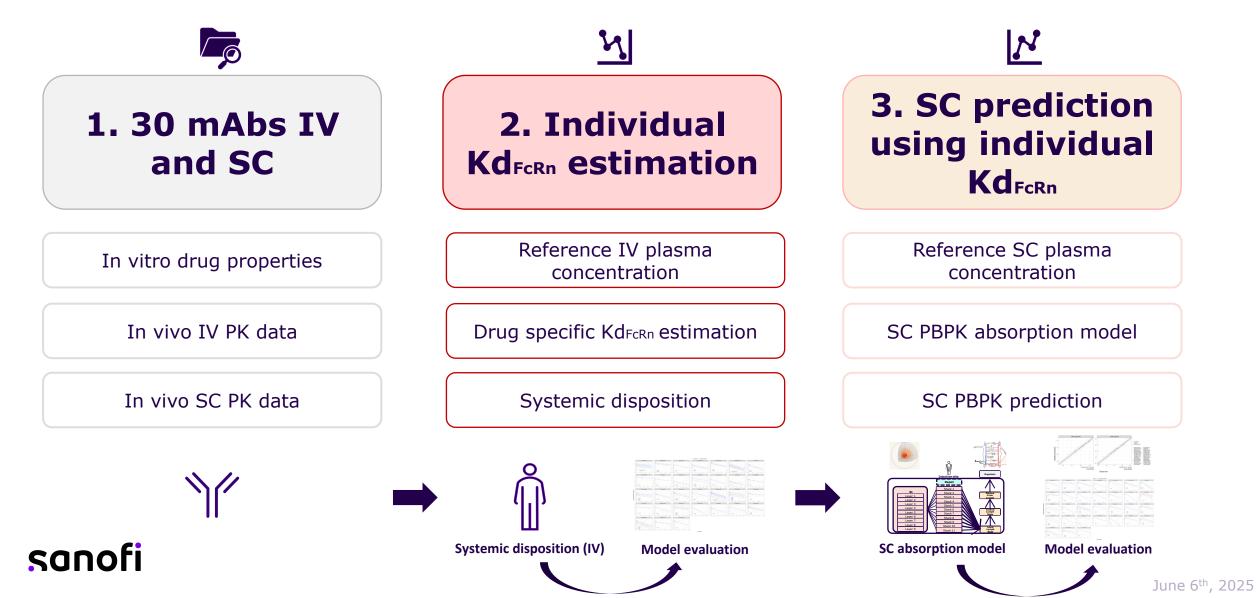




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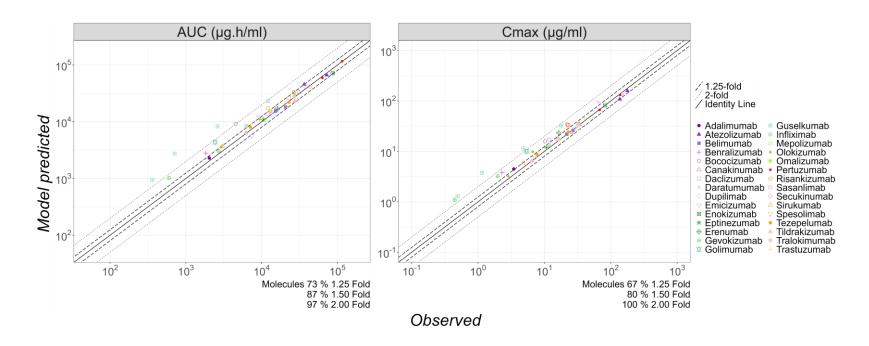


IV to SC

3. SC prediction using individual Kd_{FcRn}

SC PBPK prediction

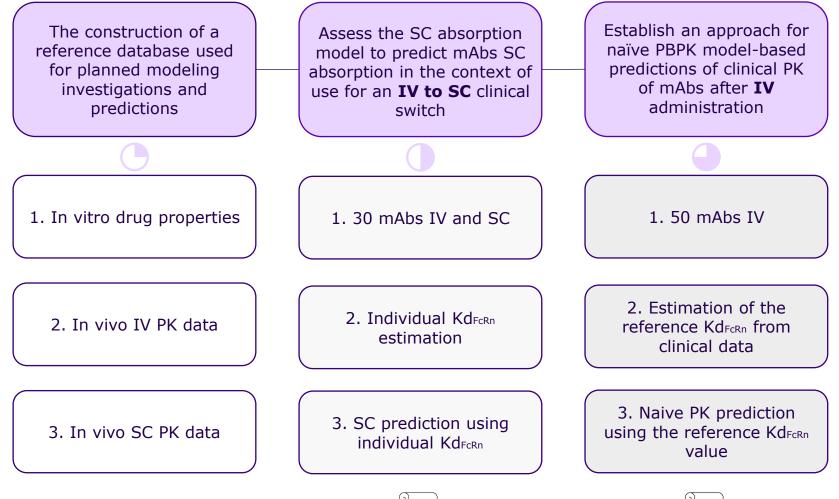
Good predictive performance of the SC absorption model in the context of a clinical switch from IV to SC



29 of 30 mAbs with model predicted AUC and Cmax values within the two-fold (0.50-2.00) range compared to the observed data

✓ The predictive performance of the SC absorption model for switching from IV to SC administration of mAbs was successfully evaluated

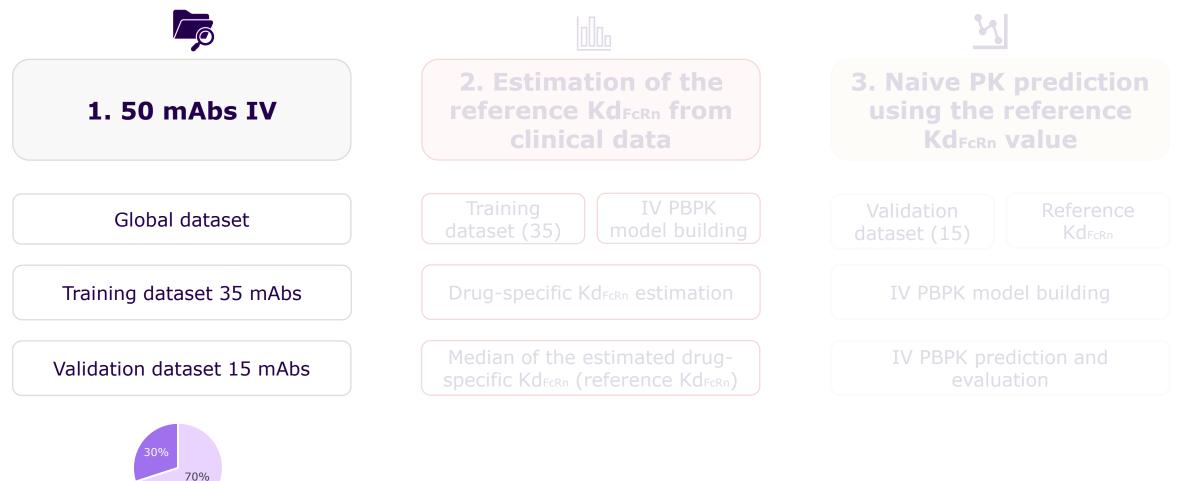
Establish a model-based strategy for predicting mAbs PK in humans following SC administration with and without prior data on IV PK





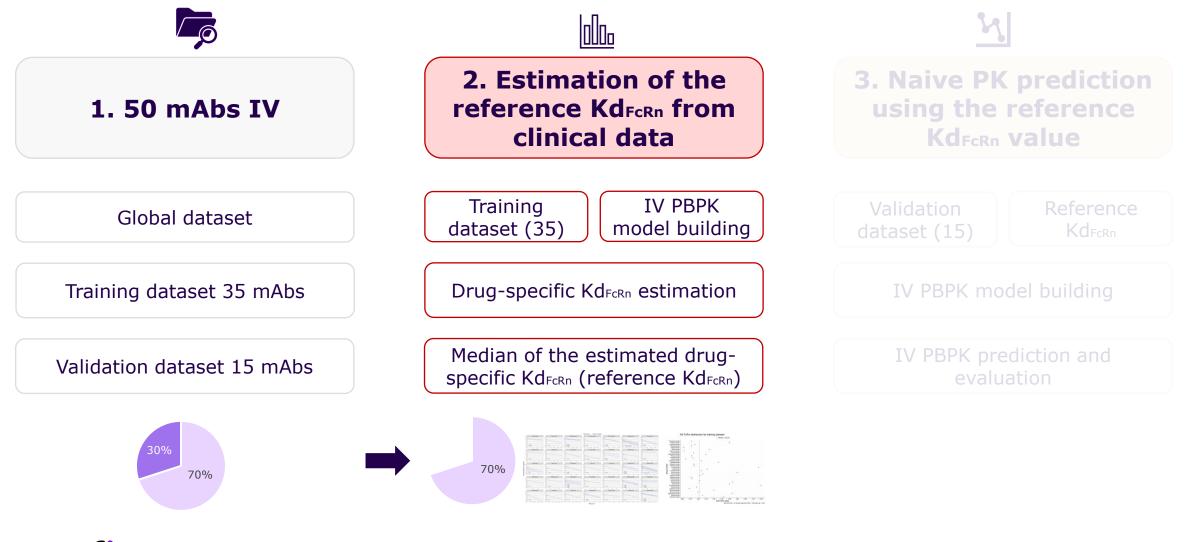


Establish an approach for naïve PBPK model-based predictions of clinical PK of mAbs after IV administration



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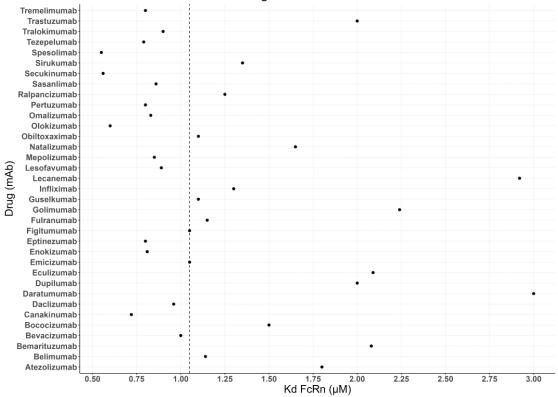


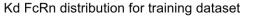
June 6th, 2025

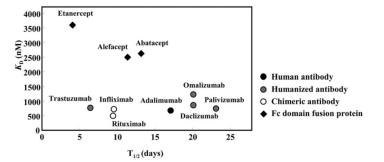
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2. Estimation of the reference Kd_{FcRn} from clinical data

Median of the estimated drug-specific Kd_{FcRn} (reference Kd_{FcRn})





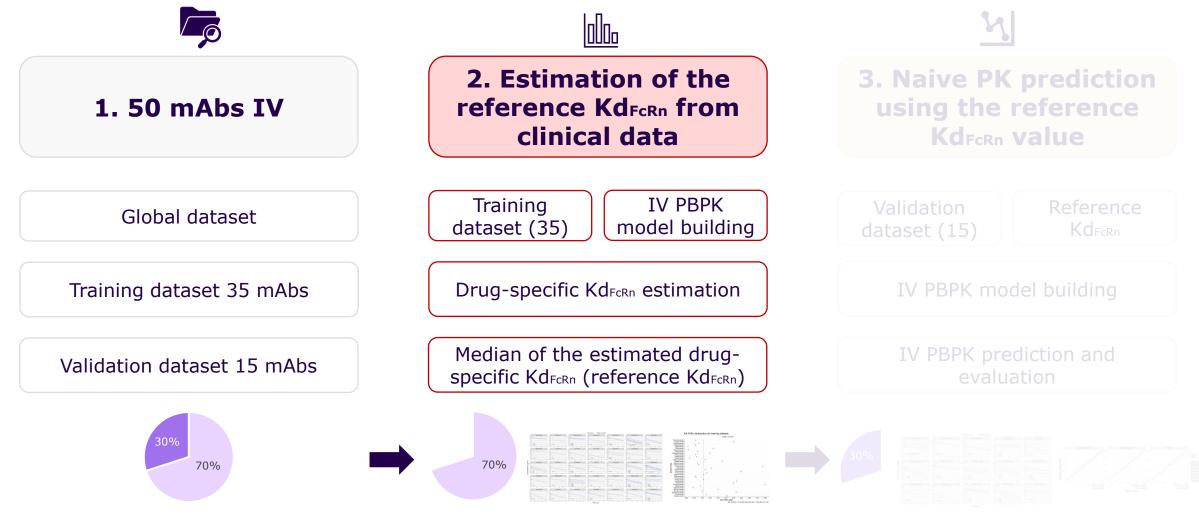


Structure	Nonproprietary name	Binding target	Affinity to FcRn $K_{\rm D}$ (nM)	Half-life (days) cited from the literature	
Human antibody	Adalimumab	TNFα	672	14.7-19.3	Weisman et al., 2003
Humanized antibody	Daclizumab	CD25	846	20	Vincenti et al., 1998
	Omalizumab	IgE	1237	20	Casale et al., 1997
	Palivizumab	RSV F protein	750	19-27	Subramanian et al., 199
	Trastuzumab	HER2	773	2.7-10	Tokuda et al., 1999
Chimeric antibody	Infliximab	TNFα	727	9.5	Comillie et al., 2001
	Rituximab	CD20	508	9.4	Maloney et al., 1997
Mouse antibody	Muromonab-CD3	CD3	ND	0.75	Hooks et al., 1991
Fc-fusion protein	Abatacept	CD80/CD86	2633	13.1	prescribing information
	Alefacept	CD2	2506	11.3	prescribing information
	Etanercept	TNFα	3612	4	Lee et al., 2003

- ✓ Kd values of binding between Fc domain-containing therapeutic proteins and human FcRn⁷
- ✓ Distribution of estimated Kd_{FcRn} values for the mAbs included in the training dataset (median represented as dashed line)

6. Suzuki T, al (2010) Importance of Neonatal FcR in Regulating the Serum Half-Life of Therapeutic Proteins Containing the Fc Domain of Human IgG1: A Comparative Study of the Affinity of Monoclonal Antibodies and Fc-Fusion Proteins to Human Neonatal FcR

Establish an approach for naïve PBPK model-based predictions of clinical PK of mAbs after IV administration



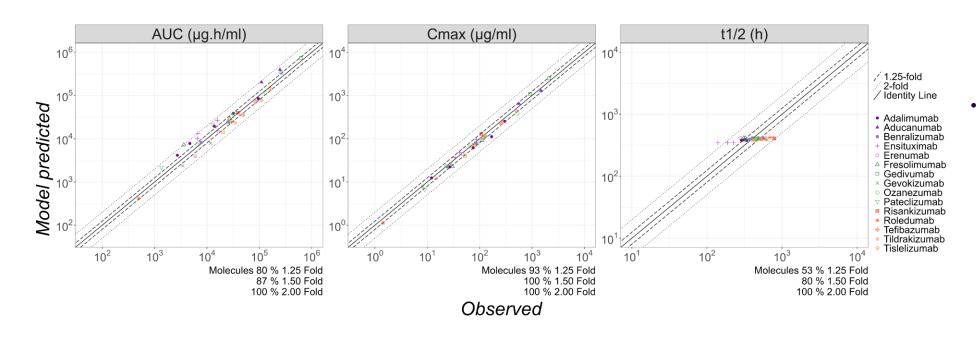
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3. Naive PK prediction using the reference Kd_{FcRn} value

IV PBPK prediction and evaluation

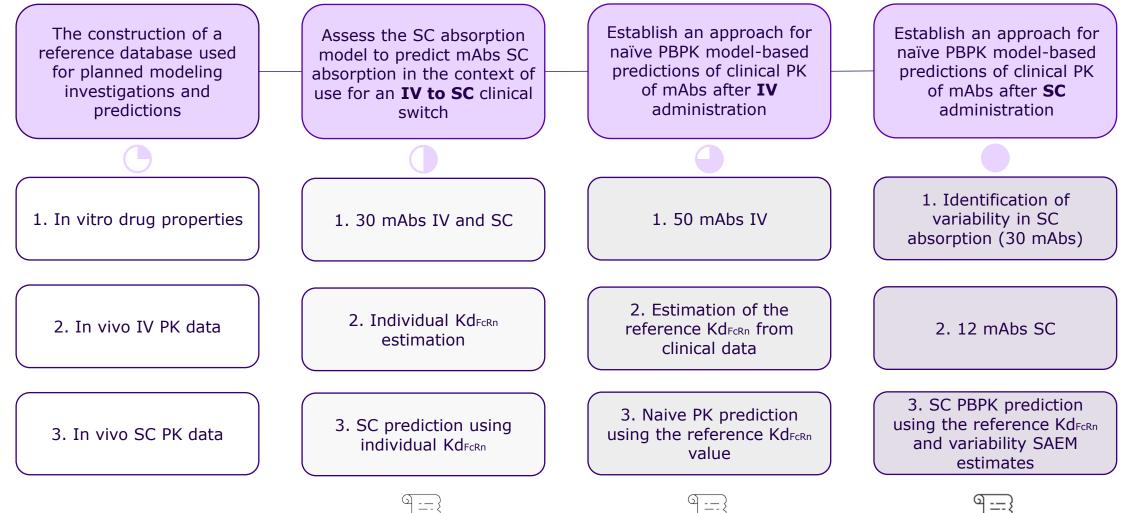
Good predictive performance of the reference Kd_{FCRn} value is observed when used to predict mAbs PK



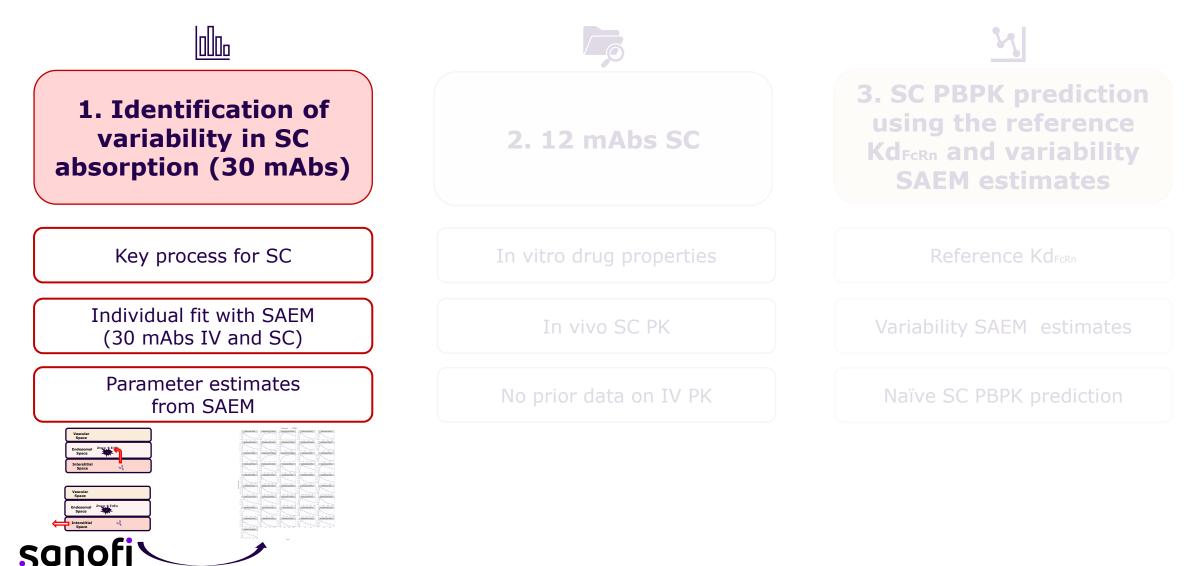
All 15 mAbs with model predicted AUC, Cmax, and $t_{1/2}$ values within the two-fold (0.50-2.00) range compared to the observed data

 \checkmark This median value was considered as a reference value for $Kd_{\mbox{\tiny FcRn}}$

Establish a model-based strategy for predicting mAbs PK in humans following SC administration with and without prior data on IV PK



Establish an approach for naïve PBPK model-based predictions of clinical PK of mAbs after SC administration



1. Identification of variability in SC absorption (30 mAbs)

Key process for SC

Injection site endosomal clearance



Vascular Space	
Endosomal ¹ Space	Drug + FcRn
Interstitial Space	-

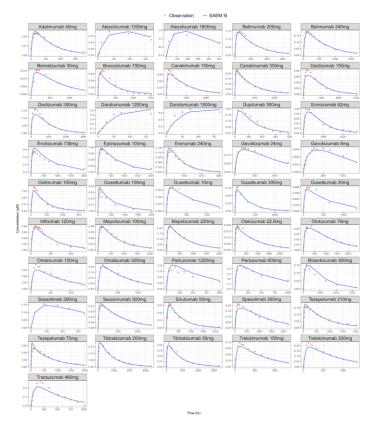
Injection site lymph flow transport



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	Vascular Space	
	Endosomal ^{Drug +} Space	FcRn
_	Interstitial Space	=l

Individual fit with SAEM (30 mAbs IV and SC)

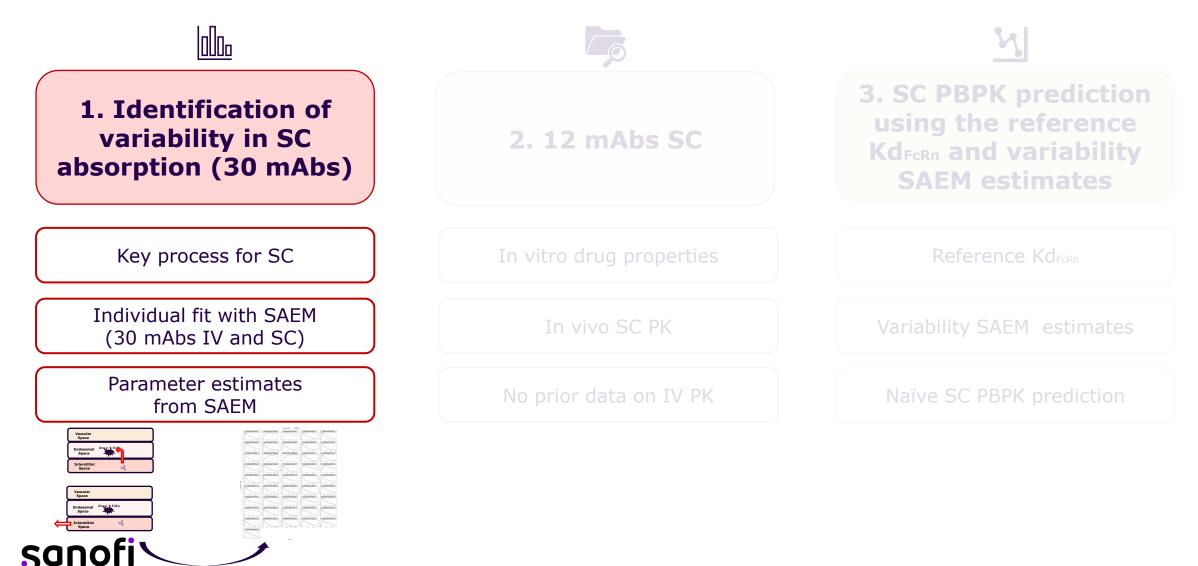


Parameter estimates from SAEM

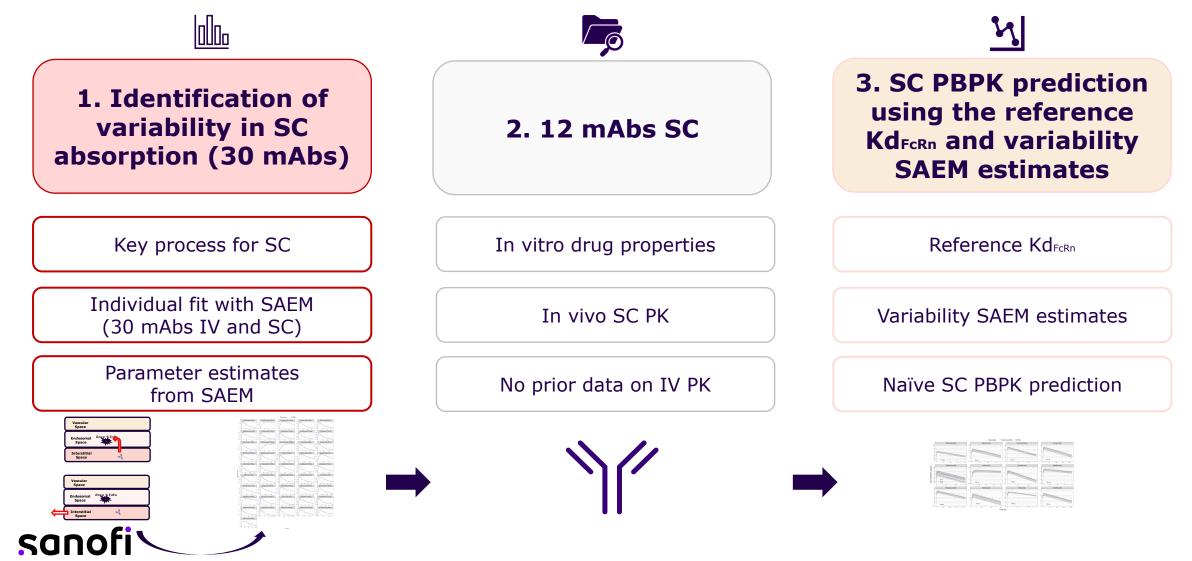
Parameter	Estimate	RSE (%)	p-value
Lymph flow proportionality factor	0.0075	Fixed	-
Rate constant for endosomal uptake (1/min)	0.7409	18	-
beta_DOSE (Rate constant for endosomal uptake)	-0.0016	35	0.002
IIV Lymph flow proportionality factor (%)	69	23	-
IIV Rate constant for endosomal uptake (%)	75	26	-
Proportional residual error	0.1420	5	-
Additive residual error (µM)	0.0029	6	-

✓ In order to integrate variability in the absorption phase, these parameters with their intermAbs variability were estimated using SAEM algorithm coupled with the WB-PBPK model 28

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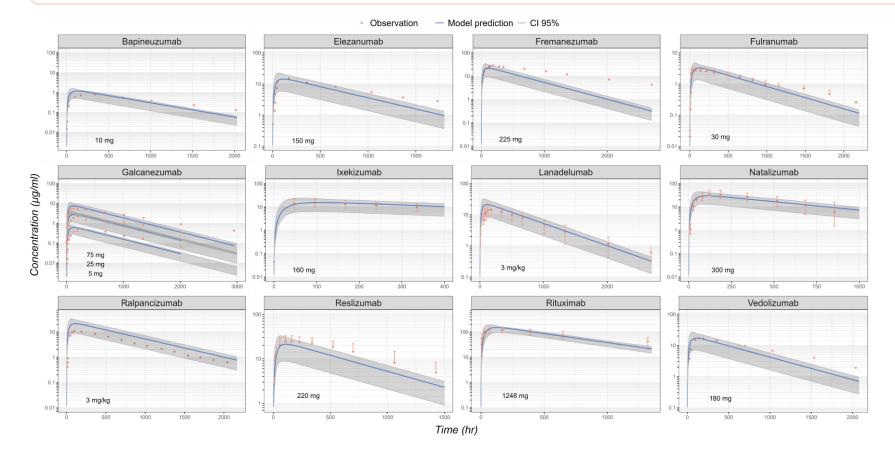


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3. SC PBPK prediction using the reference Kd_{FcRn} and variability SAEM estimates

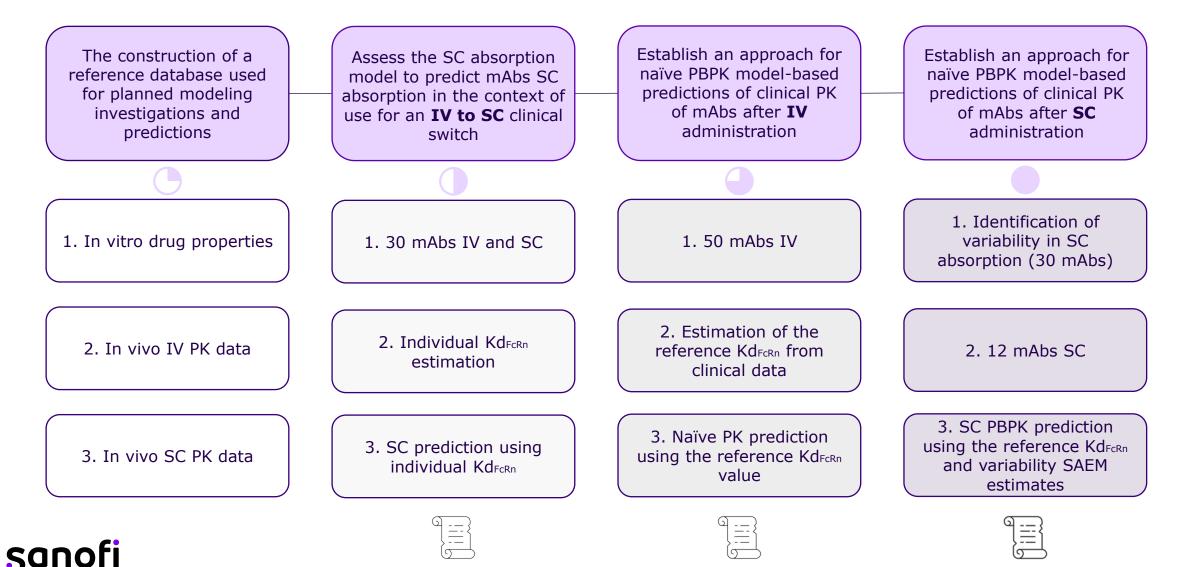
Naïve SC PBPK prediction



- The WB-PBPK model
- The SC absorption module
- Pop WB-PBPK approach for parameter estimates and inter-mAbs variability
- Reference value for human Kd_{FcRn}

 \checkmark The absorption falls within the prediction interval for most of the mAbs included in the database

Establish a model-based strategy for predicting mAbs PK in humans following SC administration with and without prior data on IV PK



Conclusion

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This approach provides a PBPK framework for predicting human PK of mAbs based on FcRn affinity, in order to support drug development and FIH trials.



The results align well with FDA's plan to phase out animal testing for mAbs, where it is possible to achieve reliable results using modeling and simulations.



Local SC processes, including interstitial retention and endosomal uptake, were identified as key areas for further investigation in relation to mAbs properties (formulation, physicochemical parameters).



Further perspectives include the validation with mAbs incorporating specific mechanisms such as target-mediated drug disposition (TMDD) and anti-drug antibodies (ADA).

Acknowledgements

- Sanofi, Translational Medicine Unit (TMU), Quantitative Pharmacology, Vitry-Sur-Seine, France: Donato Teutonico, Antoine Deslandes, Laurent Nguyen.
- Pharmetheus, Uppsala, Sweden: Erik Sjögren, Moriah Pellowe, Gianluca Selvaggio, Johanna Eriksson, Marylore Chenel.
- Uppsala University, Uppsala, Sweden: Ilse Dubbelboer.
- Computational Pharmacology and Clinical Oncology (COMPO), Aix-Marseille University, Marseille, France: Florence Gattacceca.

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Thank you for your attention



