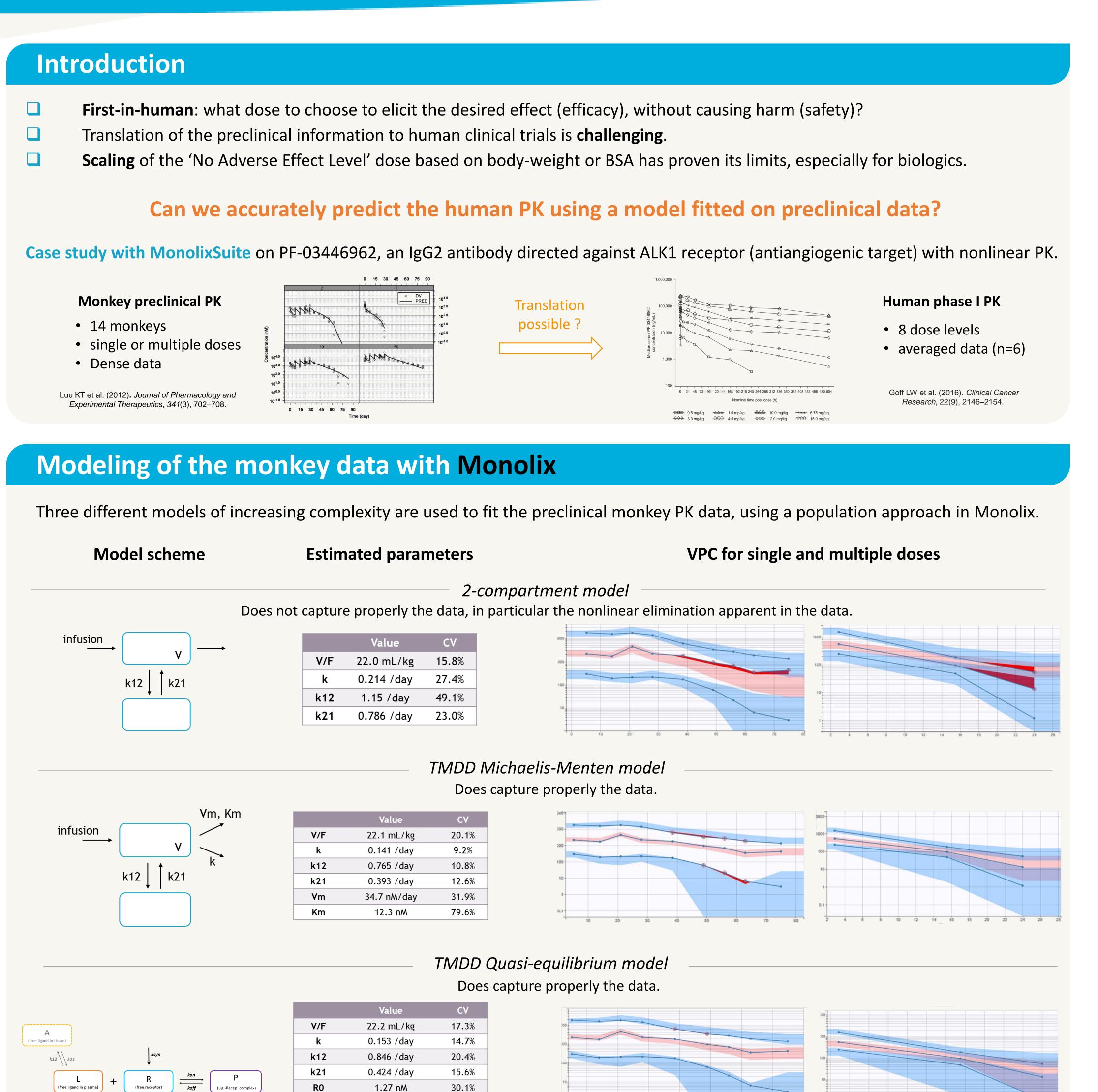
# Simulation of first-in-human using an allometrically scaled population mechanistic TMDD model with preclinical monkey data

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8: V, kel, kint, K<sub>D</sub>, <mark>n, R<sub>0</sub>,</mark> k12, k21

The TMDD QE model has 8 parameters. According to the sensitivity analysis, KD and kint will not be identifiable. Luckily, experimental values are available for these 2 parameters.

RO

kint

kdeg

KD

1.27 nM

14 /day (fixed)

20.1 /day

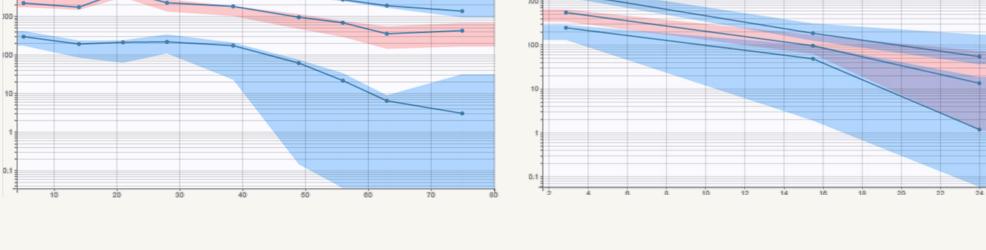
2.4 nM (fixed)

30.1%

-

37.3%

-



#### Sensitivity analysis **Experimental values** QE/QSS model Experiment Value 14 /day internalization via FACS kint KD surface plasmon resonance 2.4 nM 200 400 600 800 1.000 1.2

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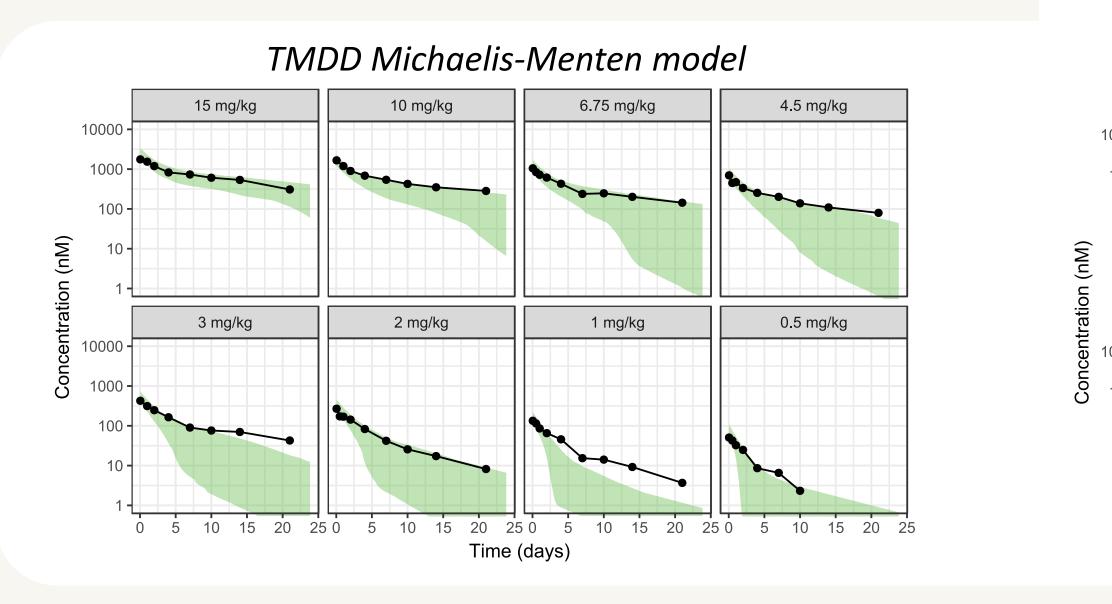


## **Prediction of human PK using Simulx**

The parameters obtained on monkeys are scaled to human using simple allometric scaling for the linear PK parameters, no change for Vm and Km (TMDD-MM model) or using the experimental human values for kint, kdeg and KD (TDMM-QE model). Prediction of human PK for different dose levels are performed in Simulx and the actual phase I PK data is then overlaid.

Parameter scaling								
			2-cpt		TMDD MM		TMDD QE	
		Param	CV	Param	CV	Param	CV	
V/F	Fixed to typical value for IgGs	40 mL/kg	15.2%	40 mL/kg	20.1%	40 mL/kg	17.3%	
k	Allometric scaling $k_h = k_m \left(\frac{70}{4}\right)^{-0.25}$	0.105 /day	27.2%	0.069 /day	9.2%	0.075 /day	14.7%	
k12	Allometric scaling $k_{12h} = k_{12,m} \left(\frac{70}{4}\right)^{-0.25}$	0.560 /day	54.3%	0.374 /day	10.8%	0.413 /day	20.4%	
k21	Allometric scaling $k_{21,h} = k_{21,m} \left(\frac{70}{4}\right)^{-0.25}$	0.384 /day	20.0%	0.192 /day	12.6%	0.207 /day	15.6%	
Vm	Assumed identical	-	-	34.7 nM/day	31.9%	-	-	
Km	Assumed identical	-	-	12.3 nM	79.6%	-	-	
RO	Assumed identical	-	-	-	-	1.27 nM	30.1%	
kint	Fixed to experimental value	-	-	-	-	18 /day	-	
kdeg	Fixed to experimental value	-	-	-	-	5 /day	37.3%	
KD	Fixed to experimental value	-	-	-	-	2.9 nM	-	

#### Darameter scaling



#### Only the TMDD QE model is able to correctly predict the human PK.

## Prediction of human MABEL ('Minimal anticipated biological effect level')

The TMDD-QE model can be used to simulate the free target relative to baseline as a surrogate of the biological effect, in order to determine the MABEL.

This is possible only with the TMDD-QE model, as it is the only one to include the target as model variable.

In the absence of consensus MABEL definition, it is defined in this case study as a 10% decrease of free receptor at peak.

The MABEL is predicted to be around 0.005 mg/kg, well below the lowest dose tested in the first-in-human study.

