

# Building and evaluation of a PBPK model for BAY 79-4620 in mice

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<b>Version</b>	<b>1.0-OSP12.3</b>
based on <i>Model Snapshot and Evaluation Plan</i>	<a href="https://github.com/Open-Systems-Pharmacology/BAY794620-Model/releases/tag/v1.0">https://github.com/Open-Systems-Pharmacology/BAY794620-Model/releases/tag/v1.0</a>
OSP Version	12.3
Qualification Framework Version	3.6

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This evaluation report and the corresponding PK-Sim project file are filed at:

<https://github.com/Open-Systems-Pharmacology/OSP-PBPK-Model-Library/>

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# 1 Introduction

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BAY 79-4620 is an antibody–drug conjugate consisting of a human IgG1 mAb directed against human carbonic anhydrase IX (CA IX) conjugated to the toxophore monomethylauristatin E (MMAE) via a valine-citrulline based linker ([Petrucci 2012](#)).

For BAY 79-4620, tissue concentration-time profiles for a large number of different mice tissues were measured and used together with pharmacokinetic (PK) data from 5 other compounds to identify unknown parameters during the development of the generic large molecule physiologically based pharmacokinetic (PBPK) model in PK-Sim ([Niederalt 2018](#)).

The herein presented evaluation report evaluates the performance of a PBPK model for BAY 79-4620 in xenograft mice for the PK data used for the development of the generic large molecule model in PK-Sim. A standard PK-Sim model was used without an additional tumor organ and without target mediated drug disposition effects from CA IX binding in the tumor - in contrast to the model which has been used in Ref. ([Niederalt 2018](#)).

The presented BAY 79-4620 PBPK model as well as the respective evaluation plan and evaluation report are provided open-source (<https://github.com/Open-Systems-Pharmacology/BAY794620-Model>).

## 2 Methods

### 2.1 Modeling Strategy

The development of the large molecule PBPK model in PK-Sim® has previously been described by Niederalt et al. (Niederalt 2018). In short, the model was built as an extension of the PK-Sim® model for small molecules incorporating (i) the two-pore formalism for drug extravasation from blood plasma to interstitial space, (ii) lymph flow, (iii) endosomal clearance and (iv) protection from endosomal clearance by neonatal Fc receptor (FcRn) mediated recycling.

For model development and evaluation, PK data were used from compounds with a wide range of solute radii and from different species. The PK data used for parameter estimation were from the following compounds: antibody–drug conjugate BAY 79-4620 in mice (Bayer in house data), antibody 7E3 in wild-type and FcRn knockout mice (Garg 2007, Garg2009), domain antibody dAb2 in mice (Sepp 2015), antibodies MEDI-524 and MEDI-524-YTE in monkeys (Dall'Acqua 2006), and antibody CDA1 in humans (Taylor 2008). The PK data used for model evaluation were from inulin in rats (Tsuji1983) and tefibazumab in humans (Reilly 2005).

The PBPK model including the estimated physiological parameters as described by Niederalt et al. (Niederalt 2018) is available in the Open Systems Pharmacology Suite from version 7.1 onwards.

This evaluation report focuses on the PBPK model for the antibody–drug conjugate BAY 79-4620.

Details about input data (physicochemical, *in vitro* and PK) can be found in [Section 2.2](#).

Details about the structural model and its parameters can be found in [Section 2.3](#).

## 2.2 Data

### 2.2.1 In vitro / physico-chemical Data

A literature search was performed to collect available information on physicochemical properties of BAY 79-4620. The obtained information from literature is summarized in the table below.

Parameter	Unit	Value	Source	Description
MW	g/mol	152000	Bayer in-house data	Molecular weight
r	nm	5.34	<a href="#">Taylor 1984</a>	Hydrodynamic solute radius
Kd (FcRn)	μM	0.082	<a href="#">Zhou 2003</a>	Dissociation constant for binding of a humane IgG1 antibody to murine FcRn at pH 6

### 2.2.2 PK Data

The biodistribution data from mice for BAY 79-4620 were Bayer AG in house data taken from two studies:

Data	Description
Whole-body autoradiography	Female nude mice (NMRI nu/nu), bearing HT-29 human colon carcinoma xenografts, were dosed intravenously with 1.25 mg/kg body weight of <sup>125</sup> I-labeled BAY 79-4620. The distribution of total radioactivity in organs and tissues was determined by quantitative whole-body autoradiography after sacrificing the mice (two per time) at various time points after administration.
Wet-tissue dissection study	Female nude mice (NMRI nu/nu), bearing HT-29 human colon carcinoma xenografts, were dosed intravenously with 2 $\mu$ Ci (approx. 500 ng) of <sup>125</sup> I-labeled BAY 79-4620. The distribution of total radioactivity in organs and tissues was determined after sacrificing the mice (three per time) and dissection of the organs at various time points after administration by determination of radioactivity using a gamma-counter. The concentrations were reported as percentage of dose / g tissue. These values were converted to concentrations in ng/ml assuming a density of 1 g/ml for all tissues except for bone for which a density of 1.5 g/ml was assumed (as in Ref. <a href="#">Baxter 1994</a> ).

## 2.3 Model Parameters and Assumptions

### 2.3.1 Absorption

There is no absorption process since BAY 79-4620 was administered intravenously.

### 2.3.2 Distribution

The standard lymph and fluid recirculation flow rates and the standard vascular properties of the different tissues (hydraulic conductivity, pore radii, fraction of flow via large pores) from PK-Sim were used. BAY 79-4620, among other compounds, has been used to identify these lymph and fluid recirculation flow rates used in PK-Sim ([Niederalt 2018](#)).

A standard PK-Sim model was used without an additional tumor organ - in contrast to the model which has been used in Ref. ([Niederalt 2018](#)). It was assumed that BAY 79-4620 is not cross-reactive to murine CA IX, i.e. there is no drug-target binding due to the neglect of tumor tissue in the present PK-Sim standard model (again in contrast to the model used in Ref. ([Niederalt 2018](#))).

### 2.3.3 Metabolism and Elimination

The FcRn mediated clearance present in the standard PK-Sim model was used as only clearance process (in contrast to the model used in Ref. ([Niederalt 2018](#)), where there is an additional target mediated clearance process in tumor tissue). The affinity to FcRn in the endosomal space was fitted to the PK data. The same value as fitted in Ref. ([Niederalt 2018](#)) was used since the contribution from target mediated clearance was small.

### 2.3.4 Tissue Concentrations

For the comparison with experimental data the parameters `Fraction of blood for sampling` used in the Observer for the tissue concentrations were set for all organs to 0.18 for comparison with tissue dissection data and to 0.42 for comparison with autoradiography data according to the fit results

(across compounds) in Ref. (Niederalt 2018). (The parameter `Fraction of blood for sampling` specifies residual blood in tissue as ratio of blood volume contributing to the measured tissue concentration to the total in vivo capillary blood volume.)

In the present evaluation report, the experimental intestine concentrations from the tissue dissection study were compared to simulated organ concentrations for small and large intestine separately in the goodness of fit plots as well as in the concentration-time profile plot.

### 2.3.5 Automated Parameter Identification

The table shows the parameter values that were specified in the model based on the parameter identification reported in Ref. (Niederalt 2018), and which were not included in the PK-Sim database since version 7.1.

Model Parameter	Optimized Value	Unit
<code>Kd(FcRn) in endosomal space</code>	12.7	μmol/L
<code>Fraction of blood for sampling</code> (all organs) - for comparison with tissue dissection data	0.18	
<code>Fraction of blood for sampling</code> (all organs) - for comparison with autoradiography data	0.42	

## 3 Results and Discussion

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The PBPK model for BAY 79-4620 was evaluated with blood and tissue PK data from mice.

These PK data have been used together with PK data from 5 other compounds to simultaneously identify parameters during the development of the generic model for proteins and large molecules in PK-Sim ([Niederalt 2018](#)).

The fitted dissociation constant for binding to FcRn in the endosomal space is rather high compared to usual dissociation constants. This might reflect a lowered affinity to FcRn due to the conjugation of the toxophore or alternatively is a surrogate for a clearance process not represented in the model.

The next sections show:

1. the final model parameters for the building blocks: [Section 3.1](#).
2. the overall goodness of fit: [Section 3.2](#).
3. simulated vs. observed concentration-time profiles for the clinical studies used for model building and for model verification: [Section 3.3](#).

### 3.1 Final input parameters

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The compound parameter values of the final PBPK model are illustrated below.

#### Compound: BAY794620

#### Parameters

Name	Value	Value Origin	Alternative	Default
Solubility at reference pH	99999 mg/l	Other-/Dummy value not used in the simulation	Measurement	True
Reference pH	7	Other-/Dummy value not used in the simulation	Measurement	True
Lipophilicity	-5 Log Units	Other-/Dummy value not used in the simulation	Measurement	True
Fraction unbound (plasma, reference value)	1	Other-Assumption	Measurement	True
Is small molecule	No			
Molecular weight	152000 g/mol			
Plasma protein binding partner	Unknown			
Radius (solute)	0.00534 $\mu\text{m}$	Publication-Taylor1984		
Kd (FcRn) in endosomal space	12.7 $\mu\text{mol/l}$	Parameter Identification		

## Calculation methods

Name	Value
Partition coefficients	PK-Sim Standard
Cellular permeabilities	PK-Sim Standard

## Processes

### 3.2 Diagnostics Plots

Below you find the goodness-of-fit visual diagnostic plots for the PBPK model performance of all data used presented in [Section 2.2.2](#).

The first plot shows observed versus simulated plasma concentration, the second weighted residuals versus time.

**Table 3-1: GMFE for Goodness of fit plot for concentration in blood and tissues**

Group	GMFE
BAY 79-4620 - autoradiography	1.48
BAY 79-4620 - tissue dissection	1.62
All	1.53

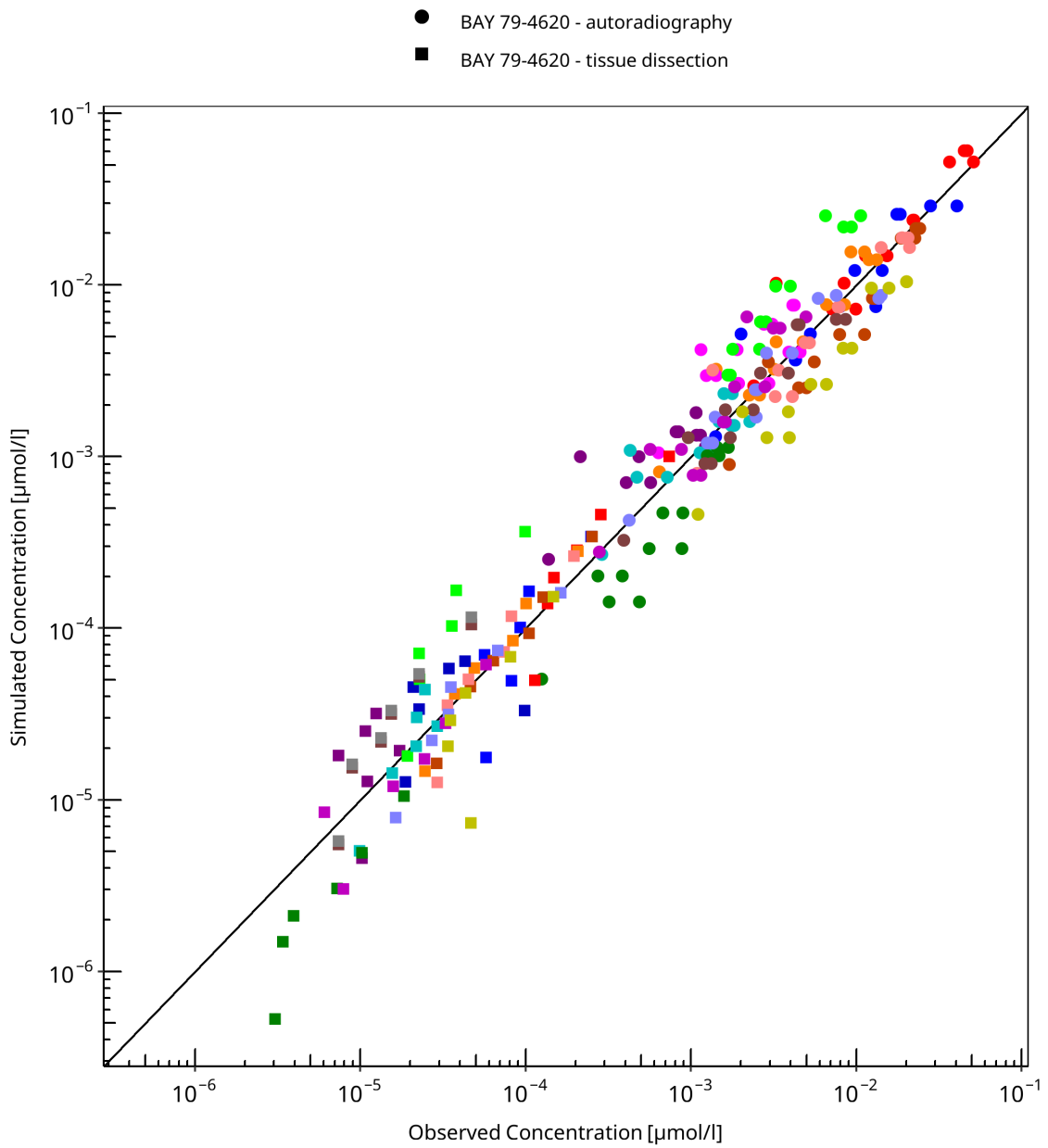


Figure 3-1: Goodness of fit plot for concentration in blood and tissues

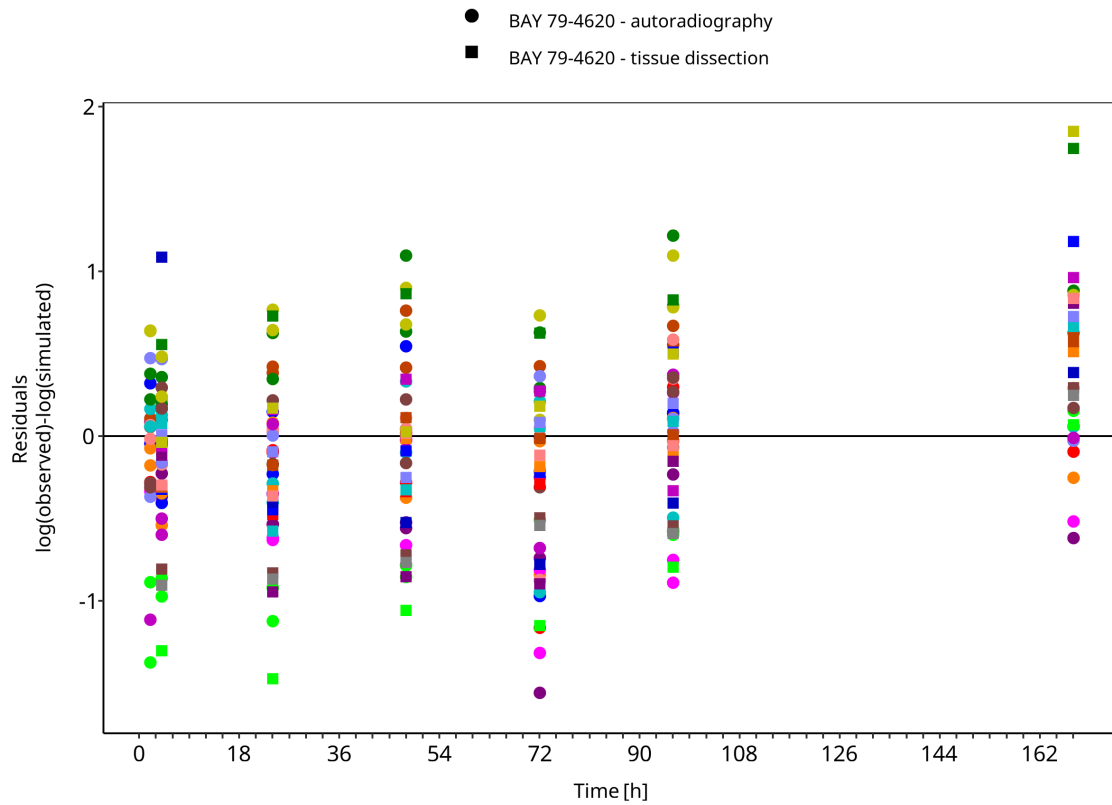


Figure 3-2: Goodness of fit plot for concentration in blood and tissues

### 3.3 Concentration-Time Profiles

Simulated versus observed concentration-time profiles of all data listed in [Section 2.2.2](#) are presented below.

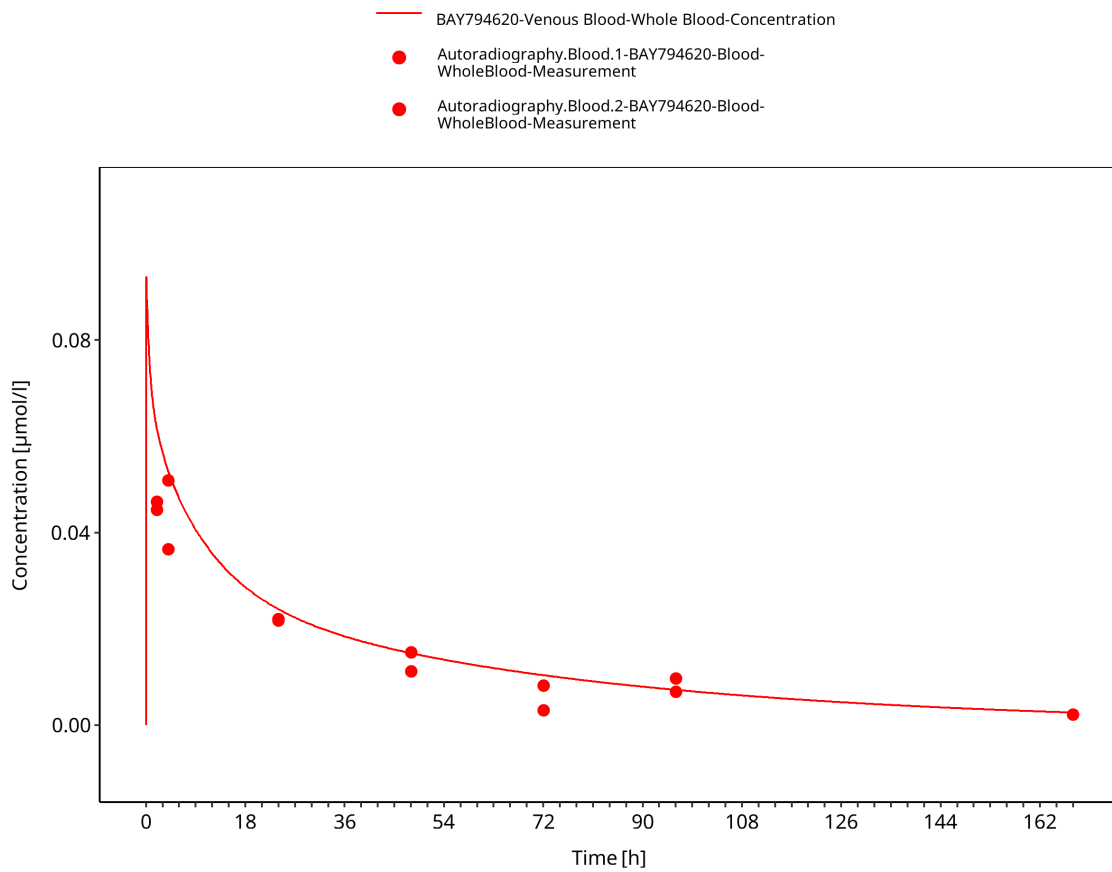


Figure 3-3: Blood - lin scale

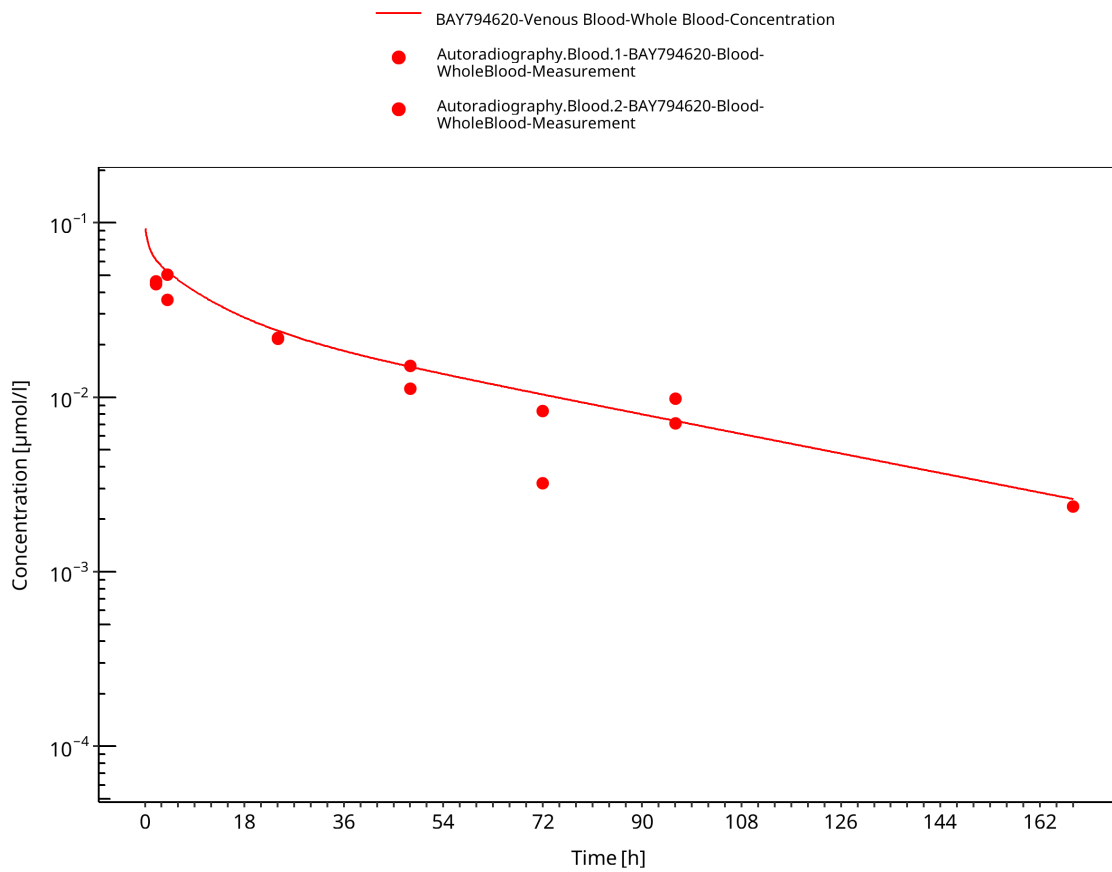


Figure 3-4: Blood - log scale

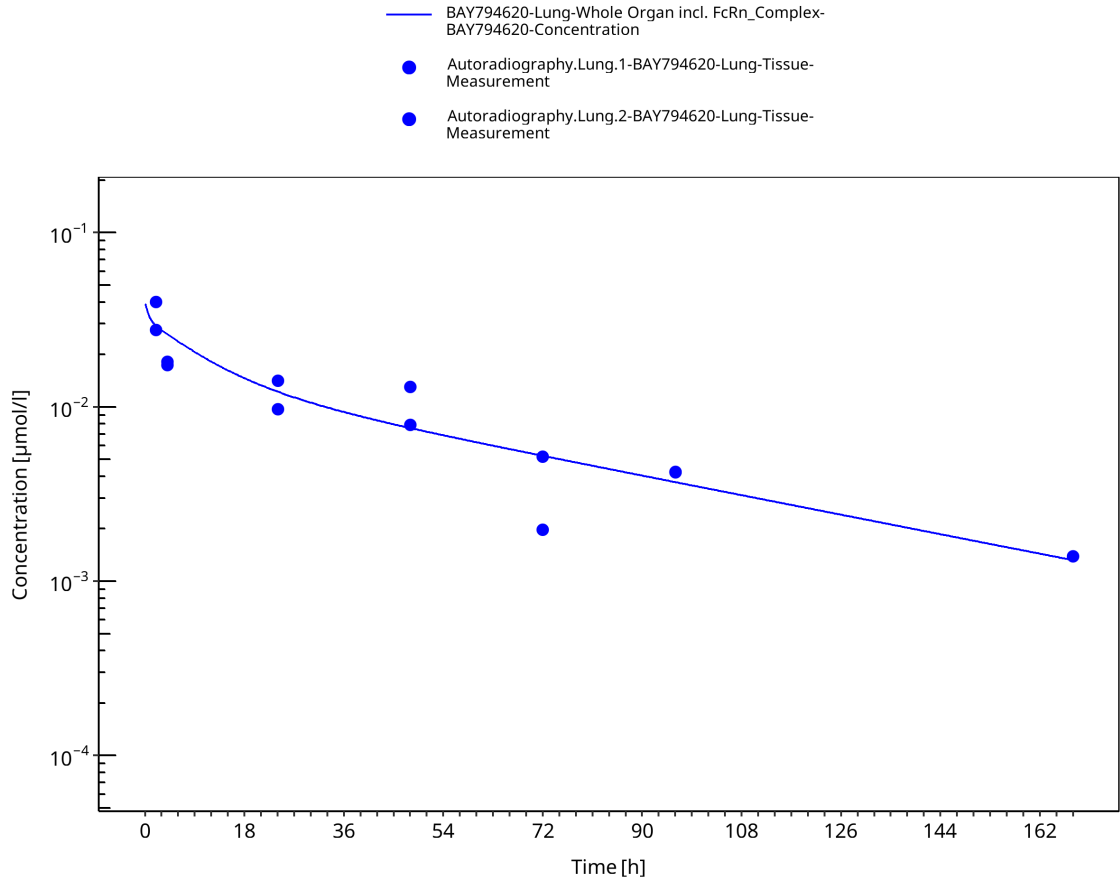


Figure 3-5: Lung

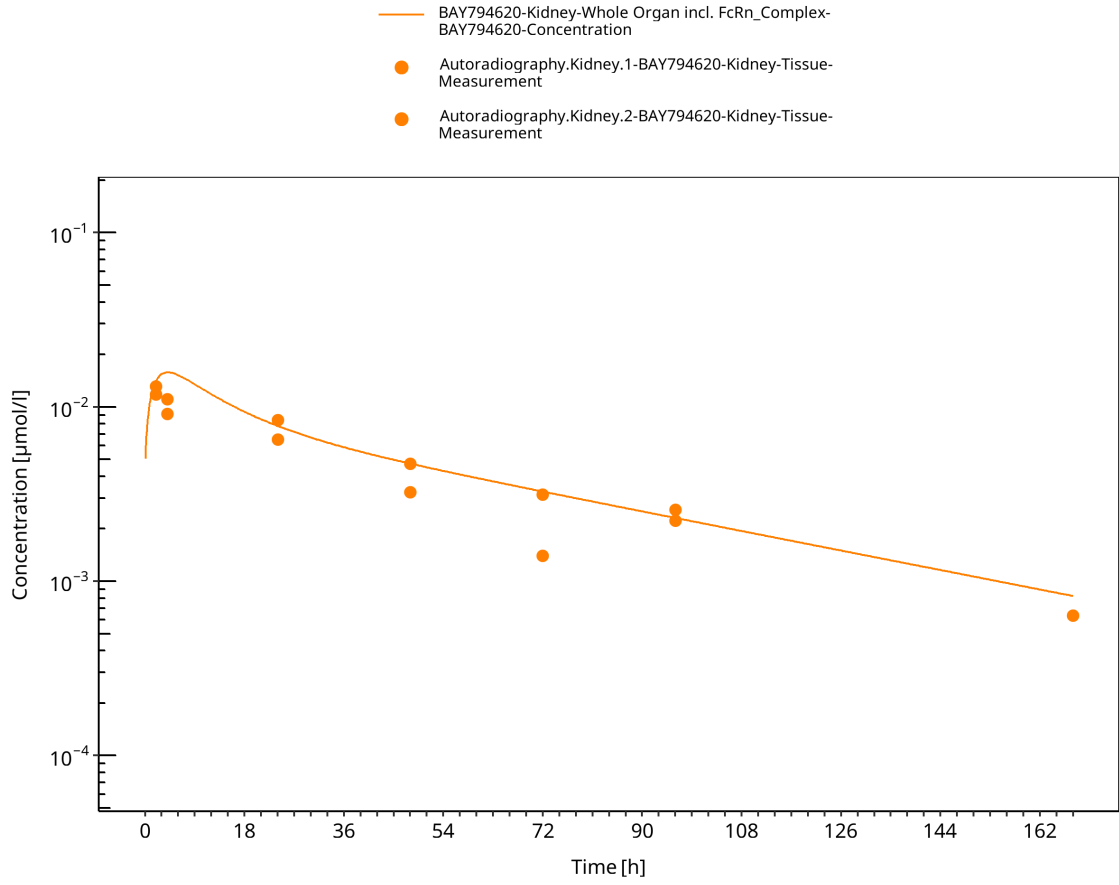


Figure 3-6: Kidney

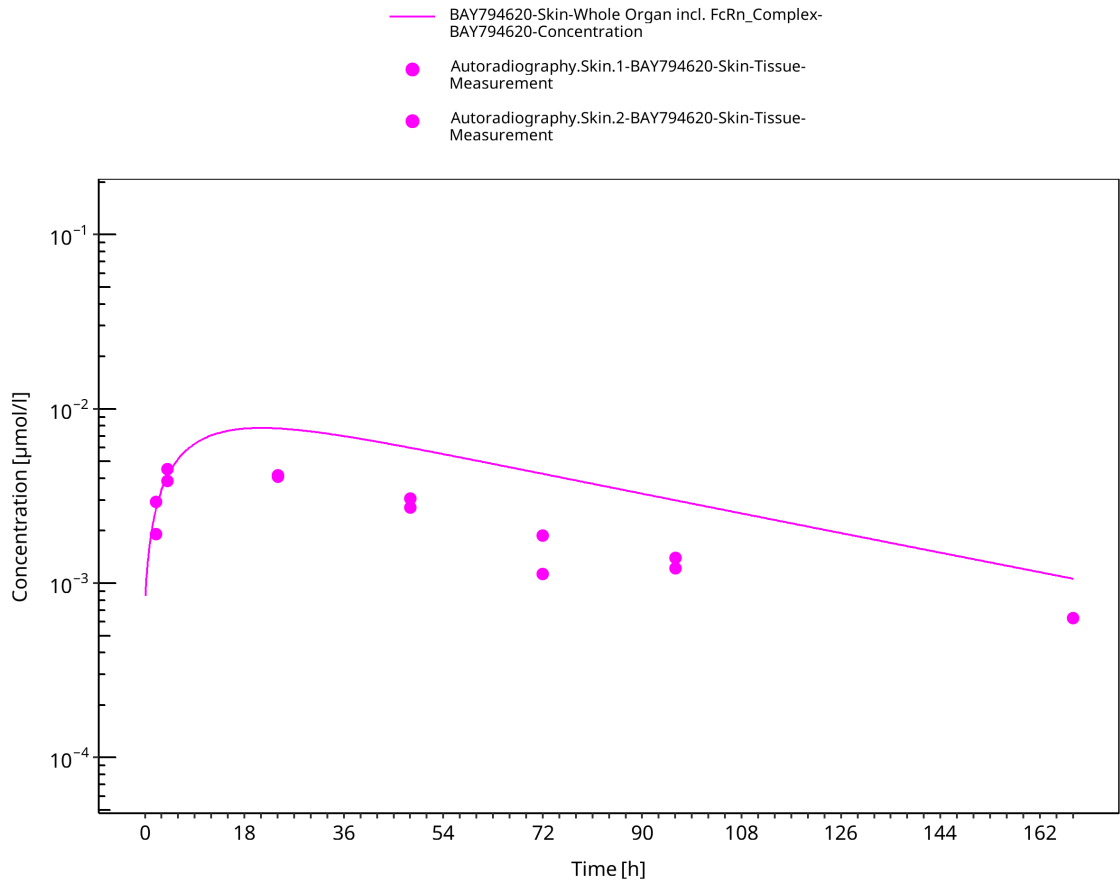


Figure 3-7: Skin

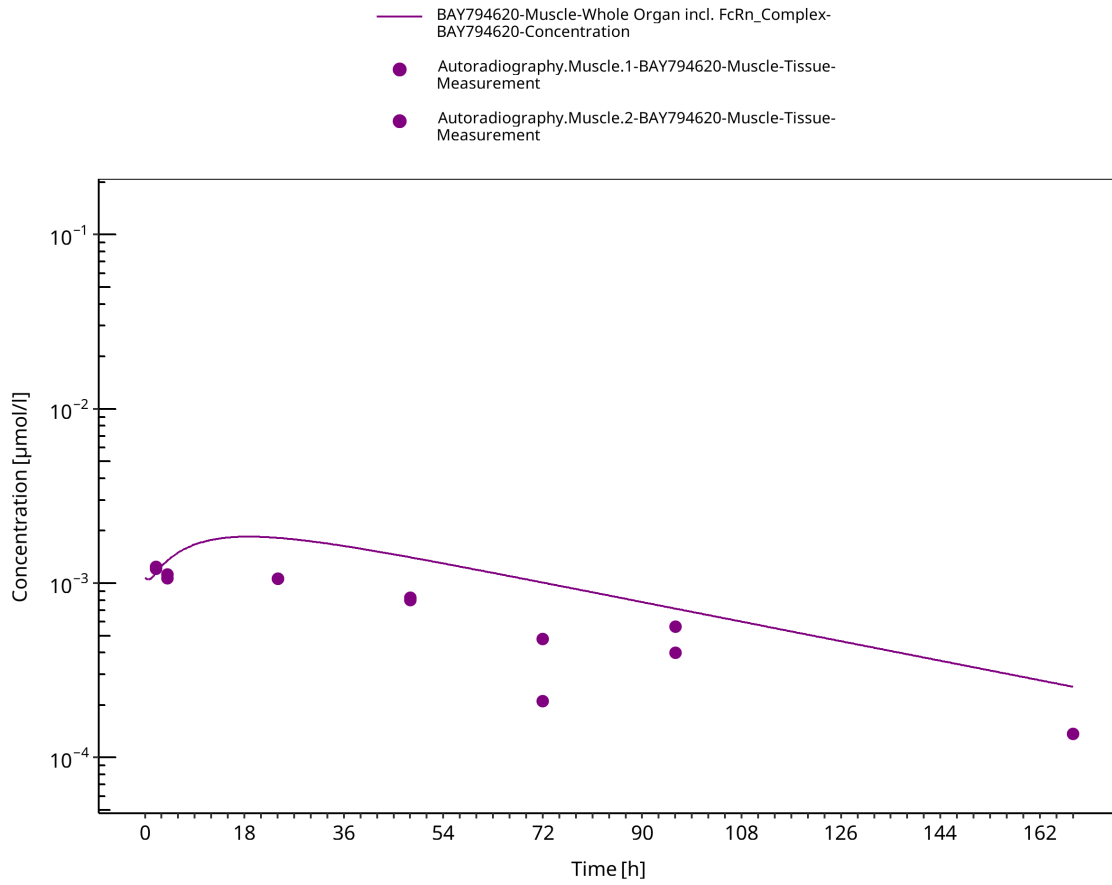
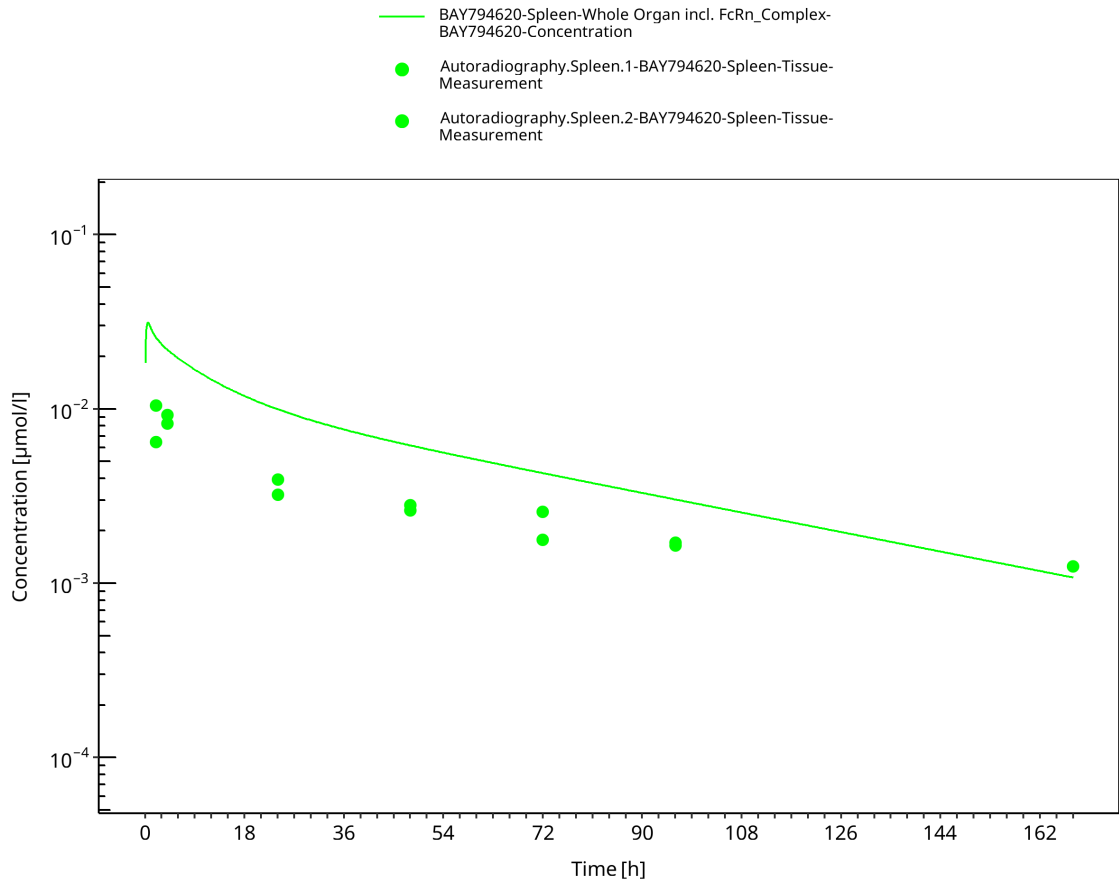


Figure 3-8: Muscle



**Figure 3-9: Spleen**

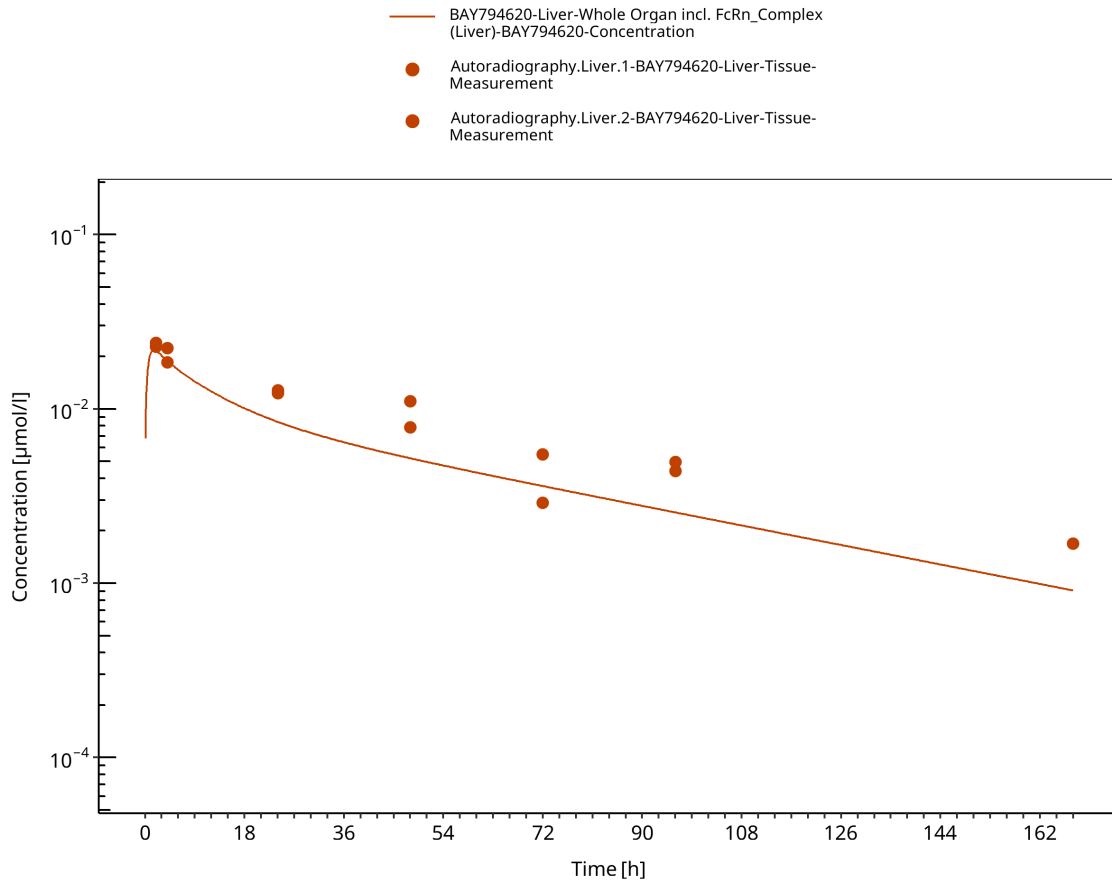


Figure 3-10: Liver

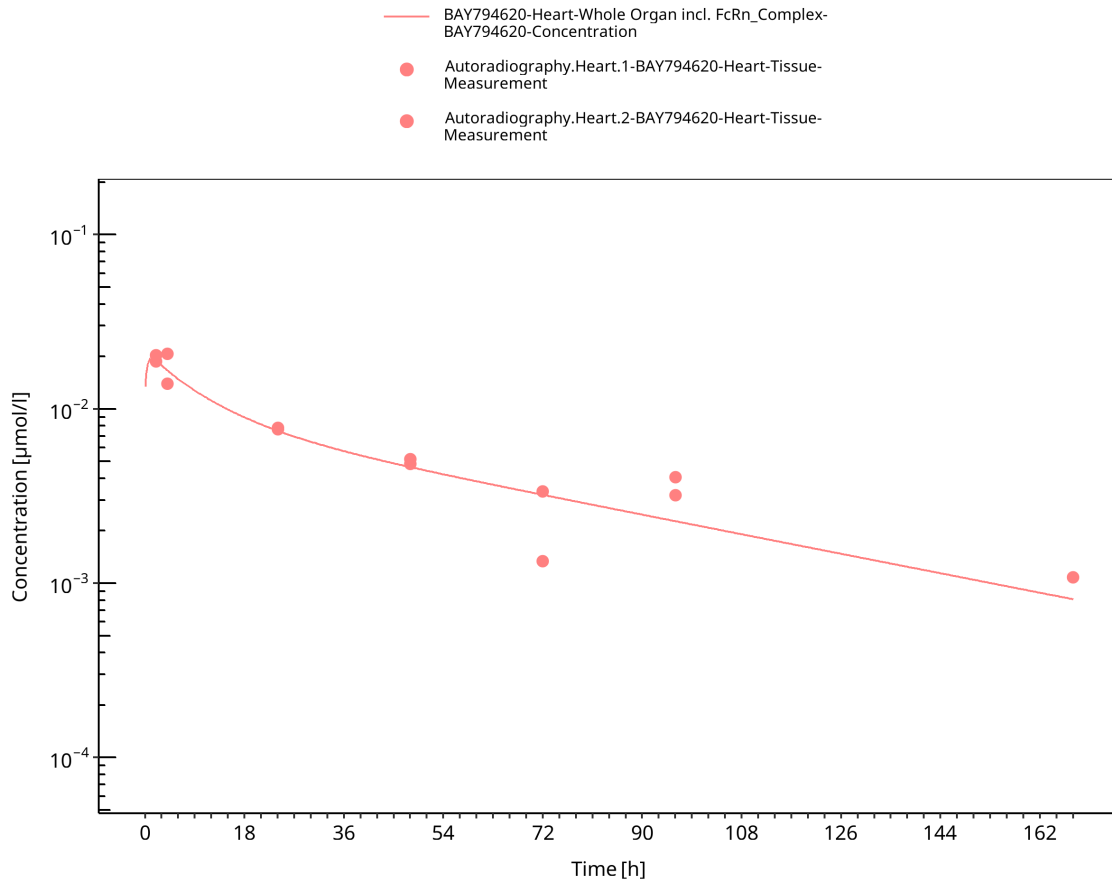


Figure 3-11: Heart

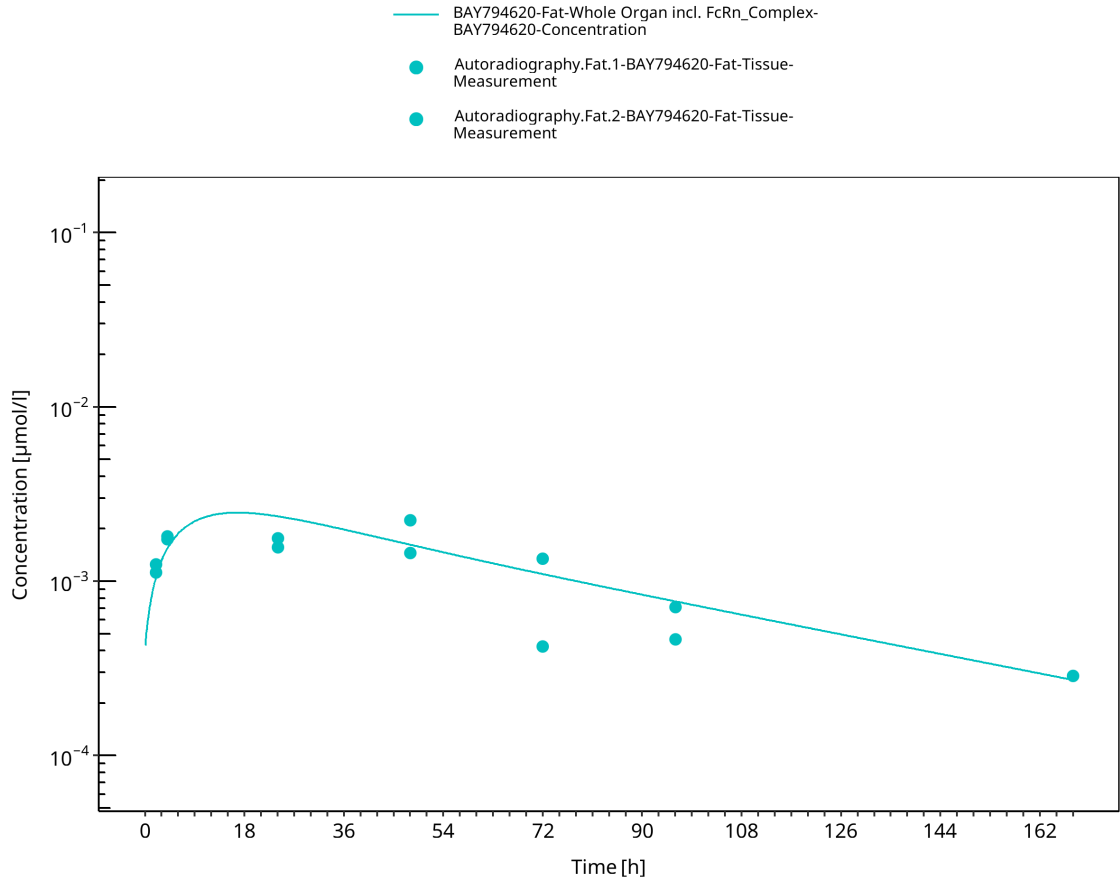
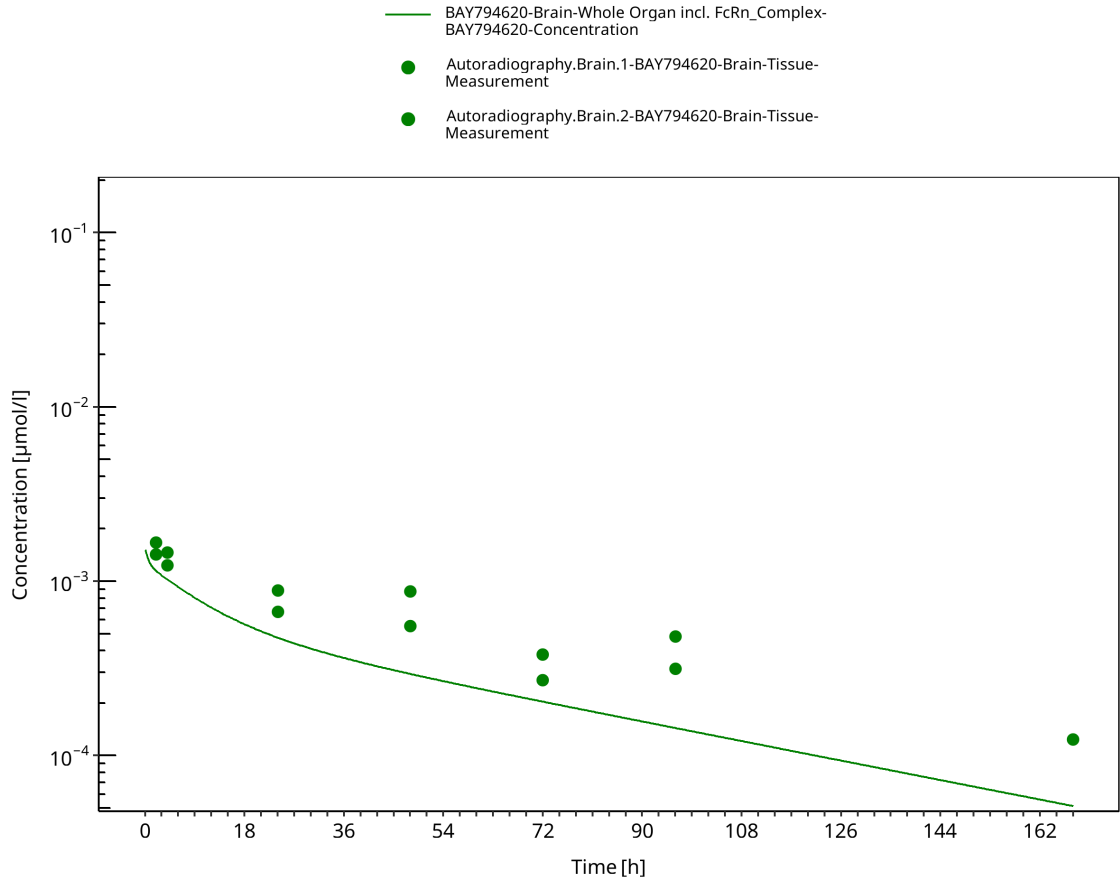


Figure 3-12: Fat



**Figure 3-13: Brain**

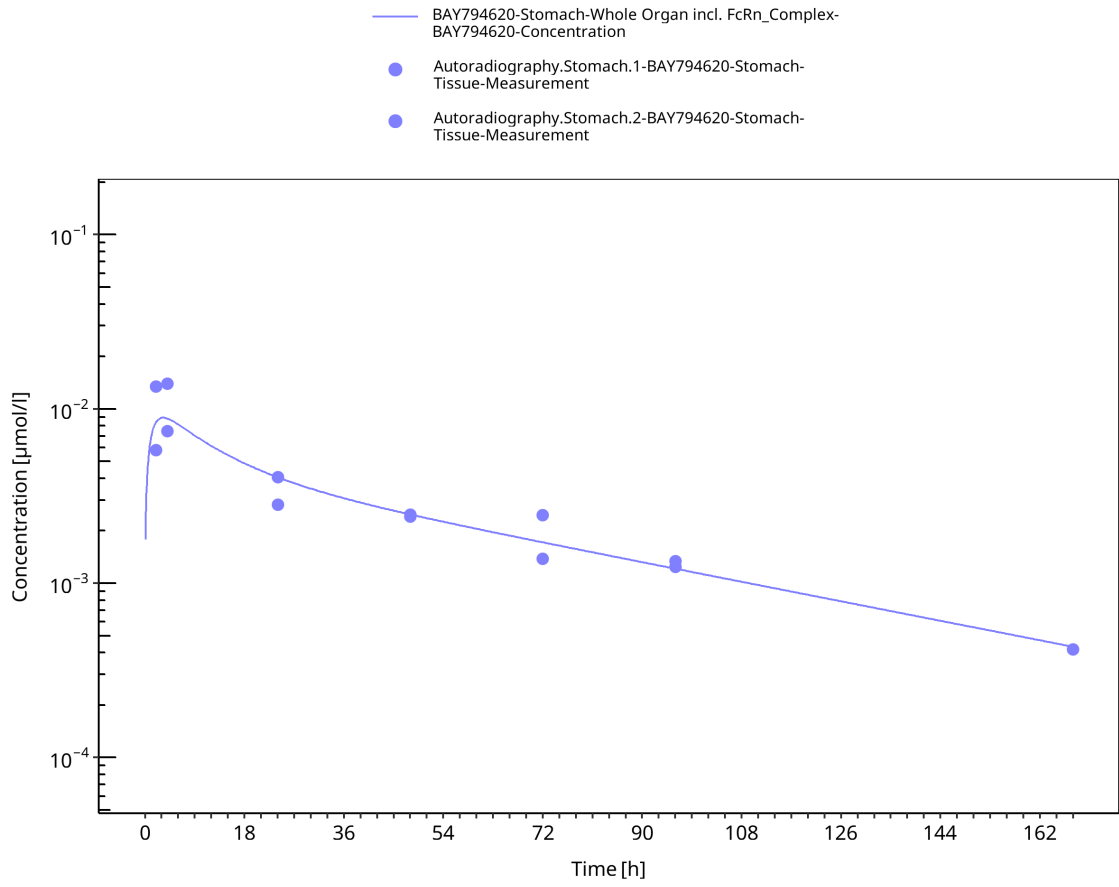


Figure 3-14: Stomach

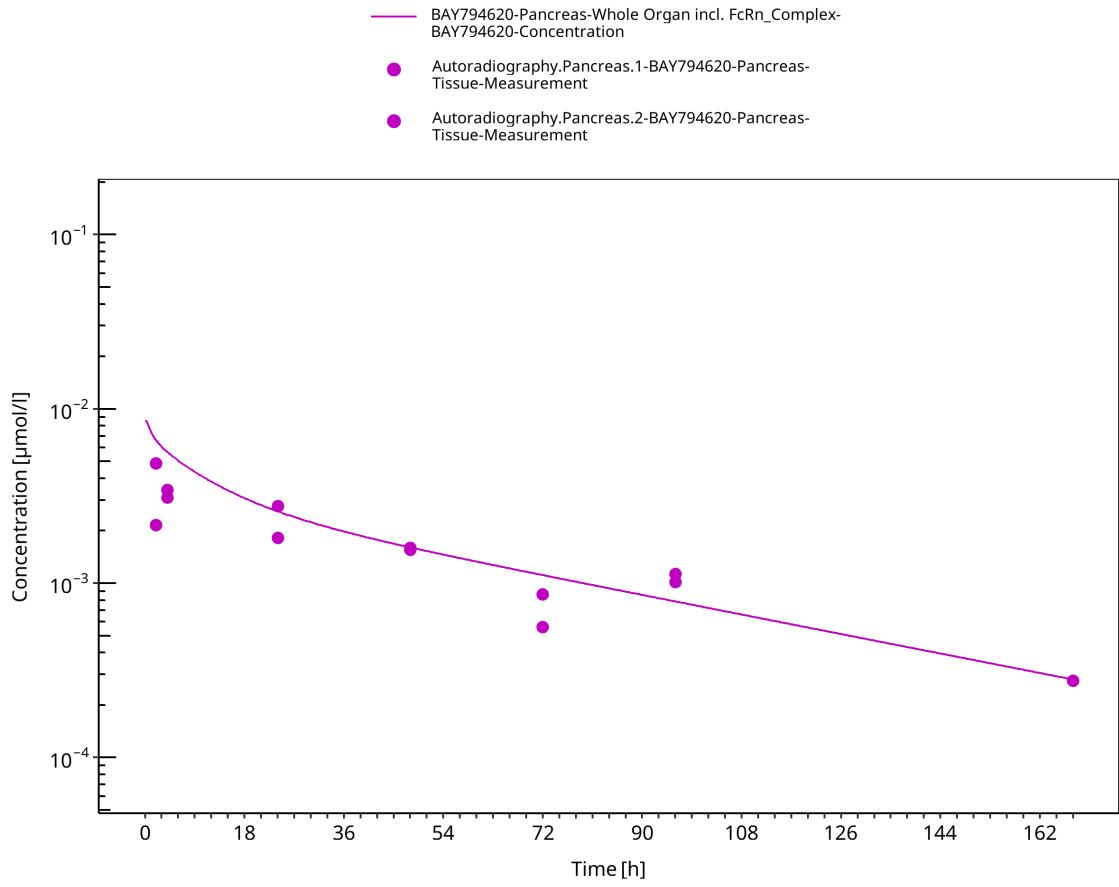
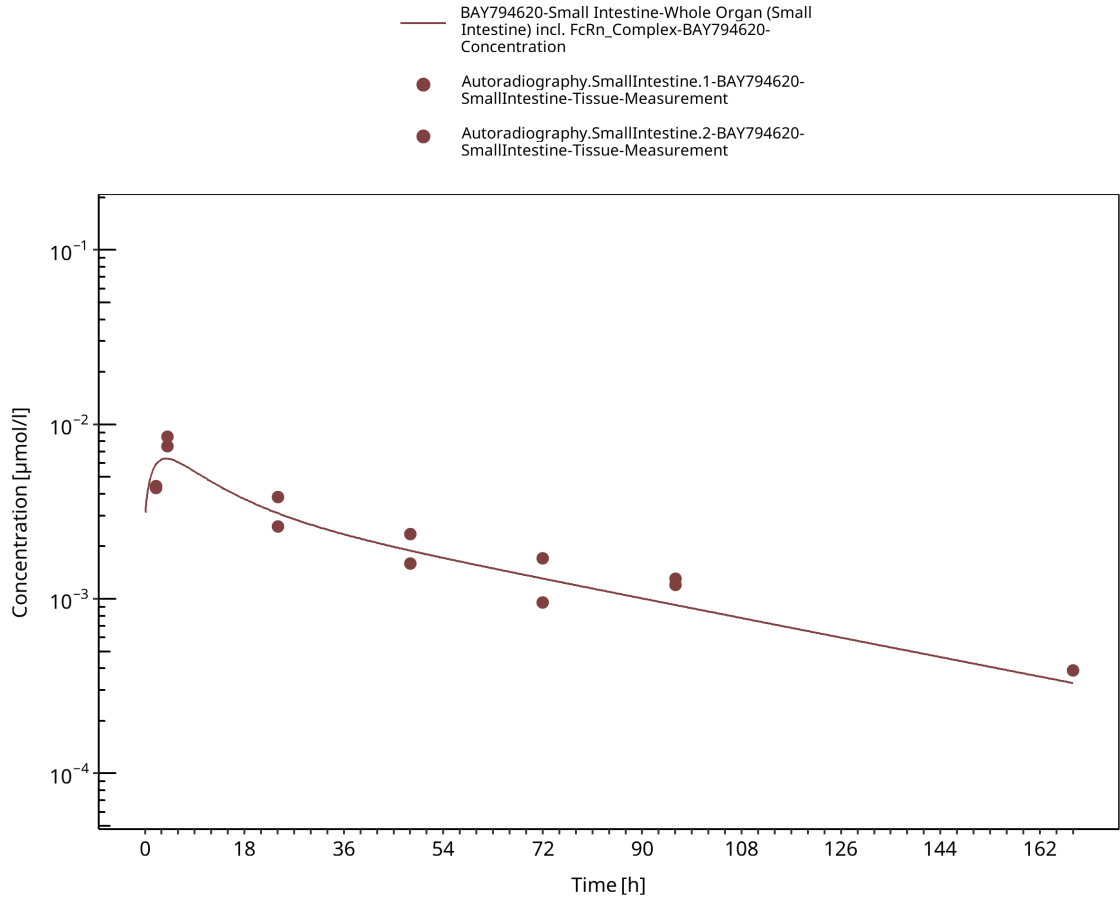


Figure 3-15: Pancreas



**Figure 3-16: Small Intestine**

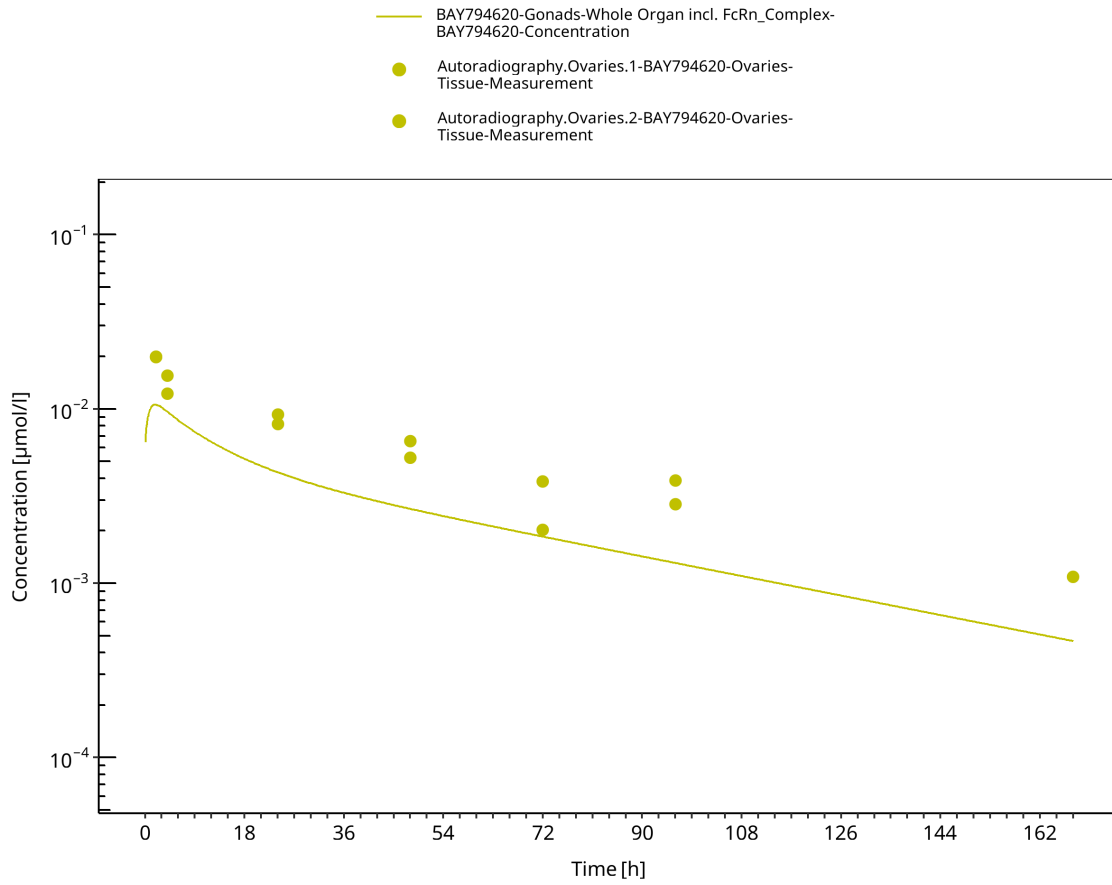


Figure 3-17: Ovaries

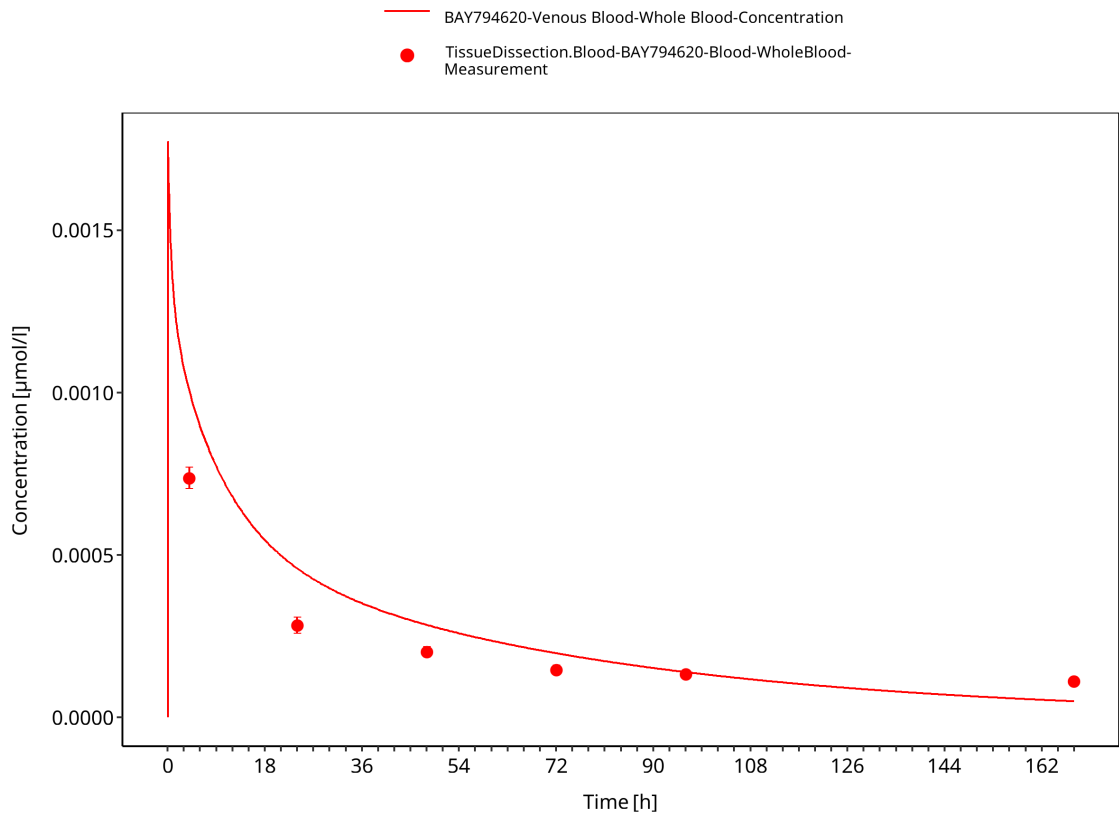


Figure 3-18: Blood - lin scale

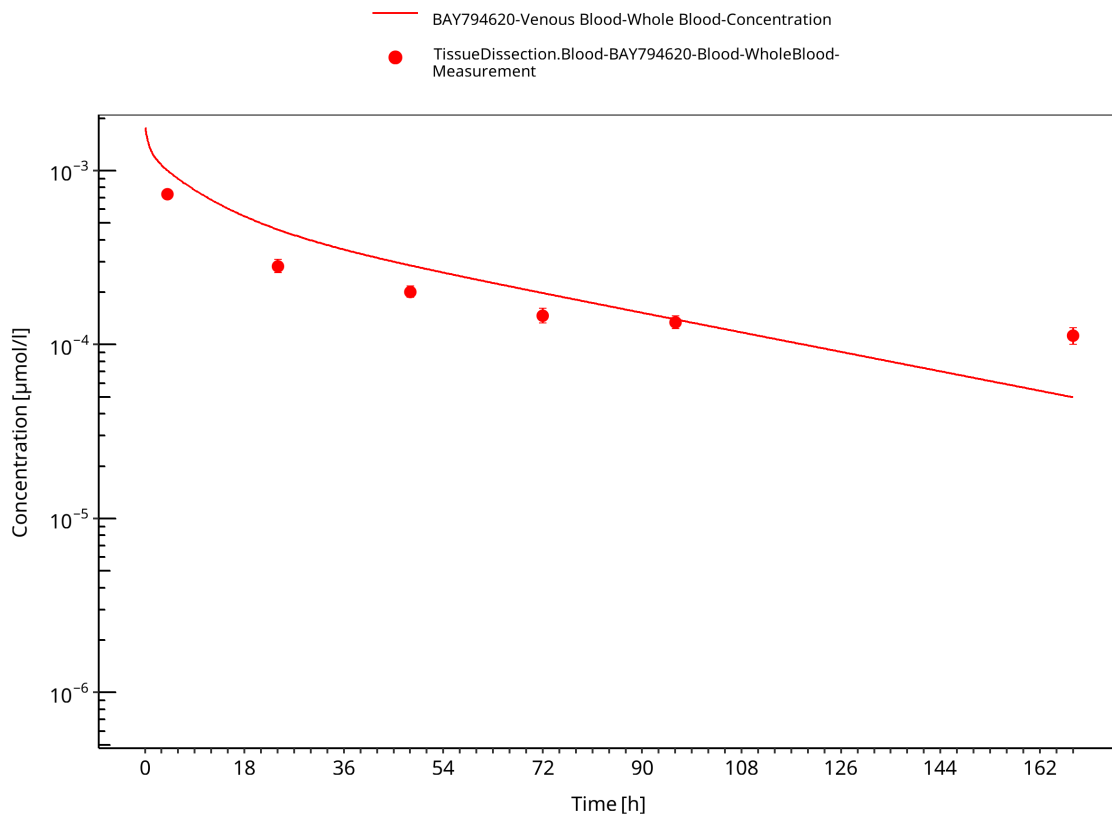


Figure 3-19: Blood - log scale

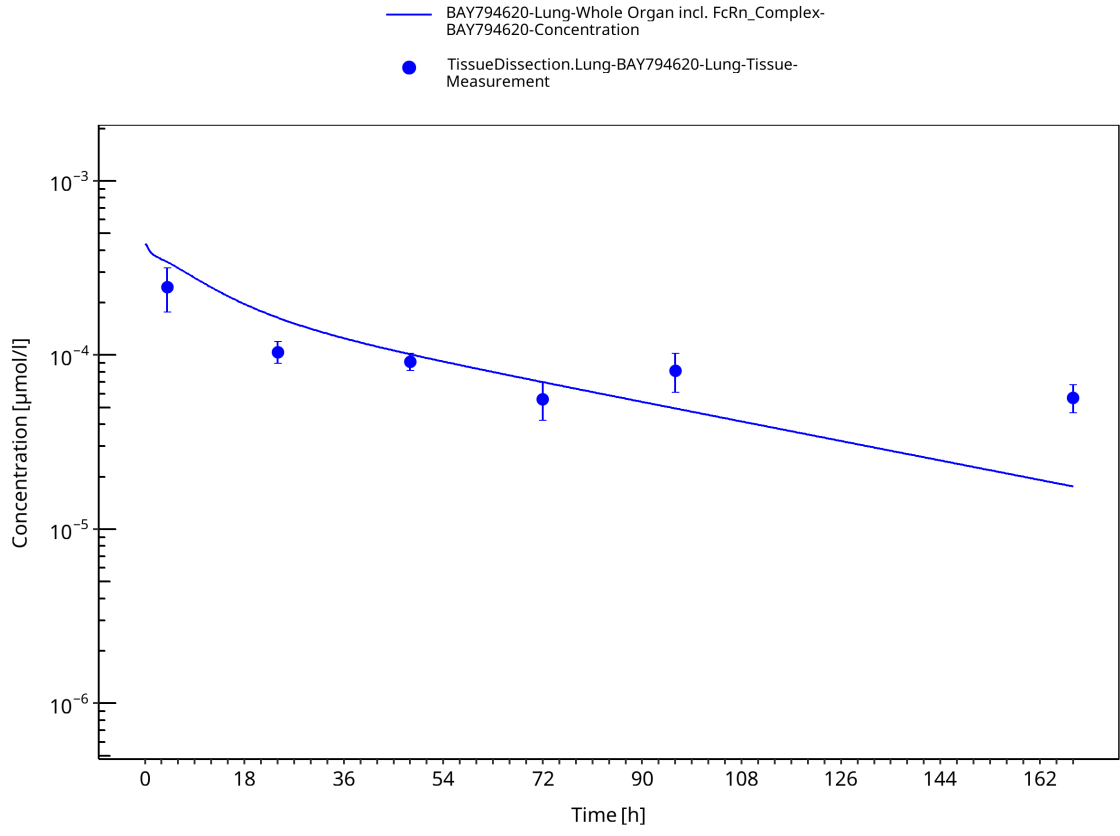


Figure 3-20: Lung

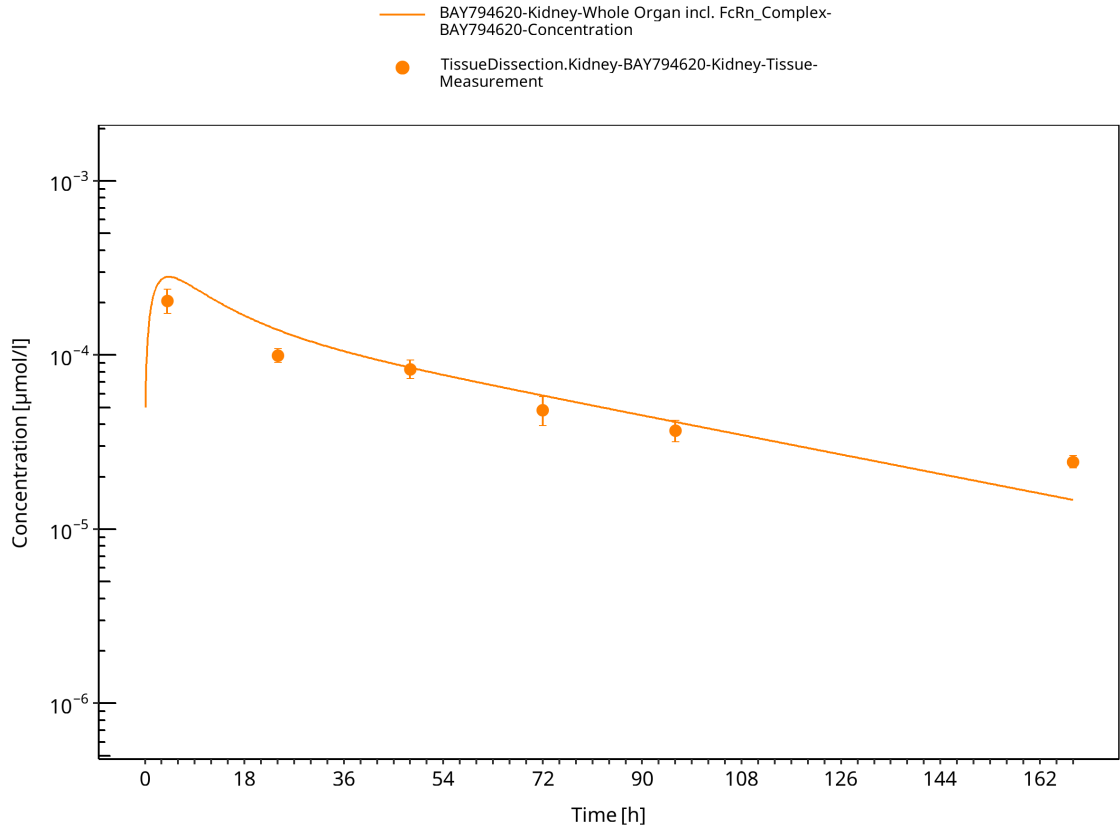


Figure 3-21: Kidney

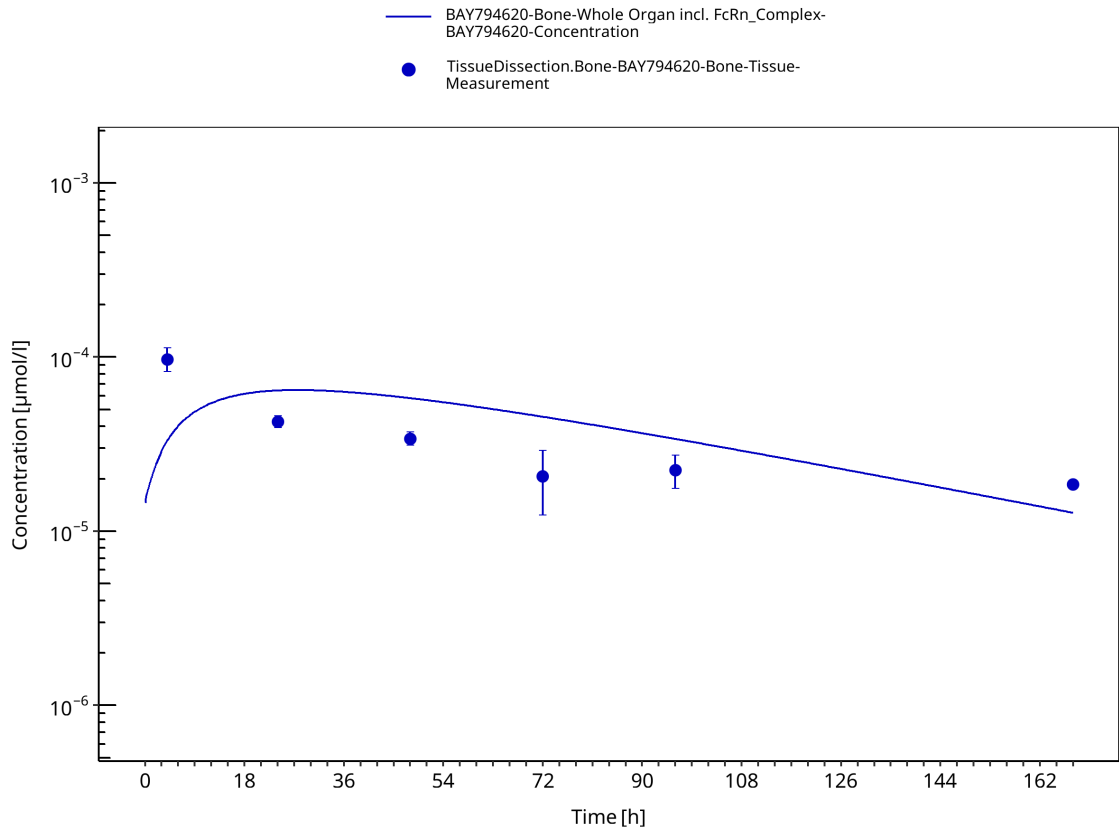


Figure 3-22: Bone

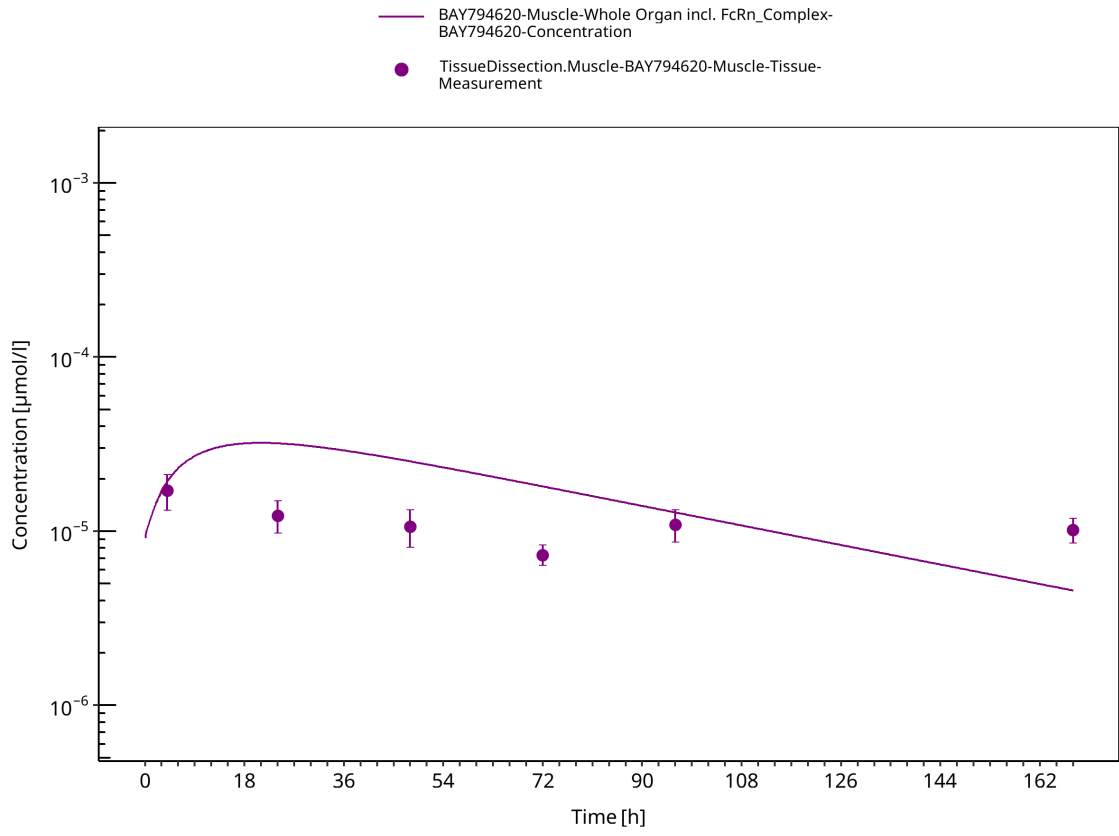


Figure 3-23: Muscle

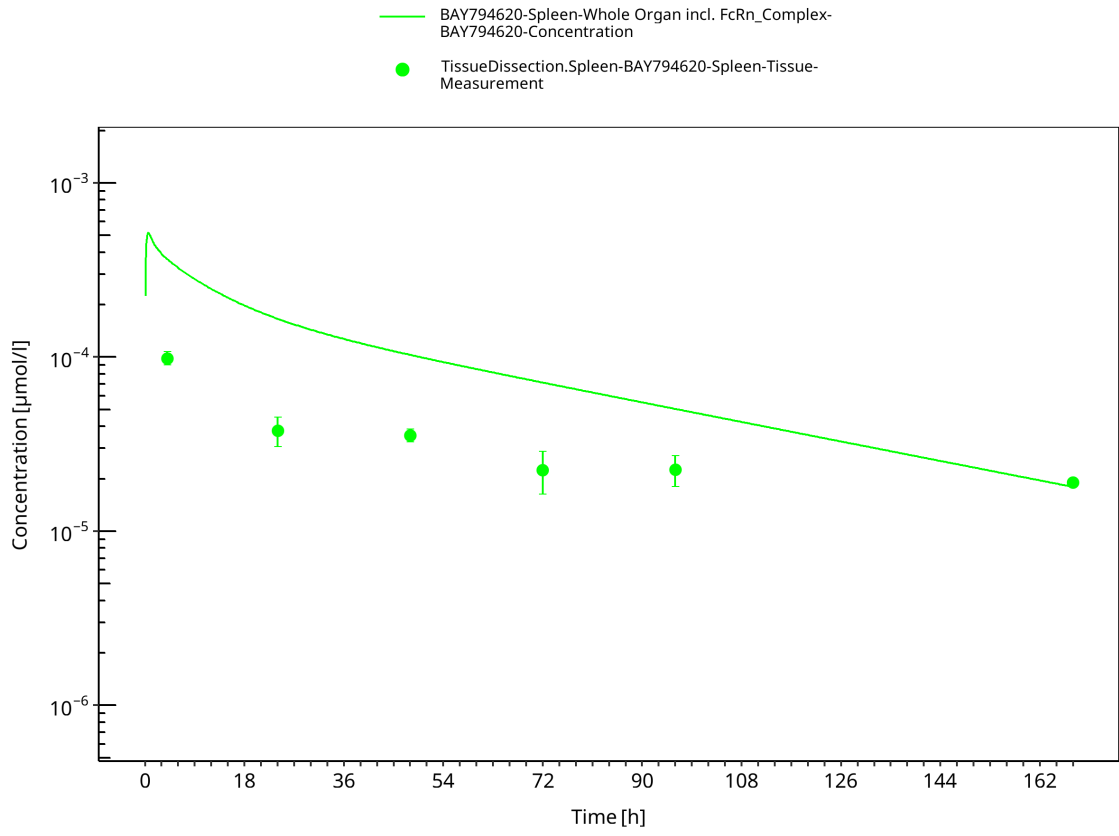


Figure 3-24: Spleen

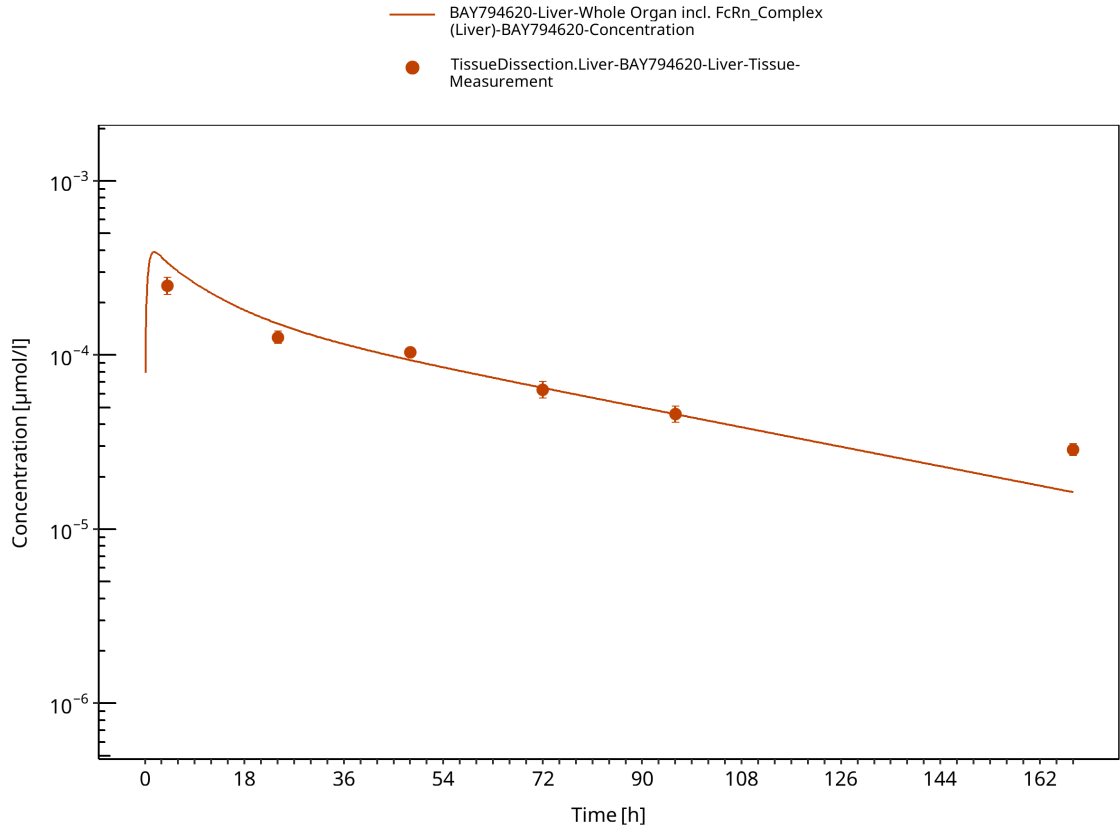


Figure 3-25: Liver

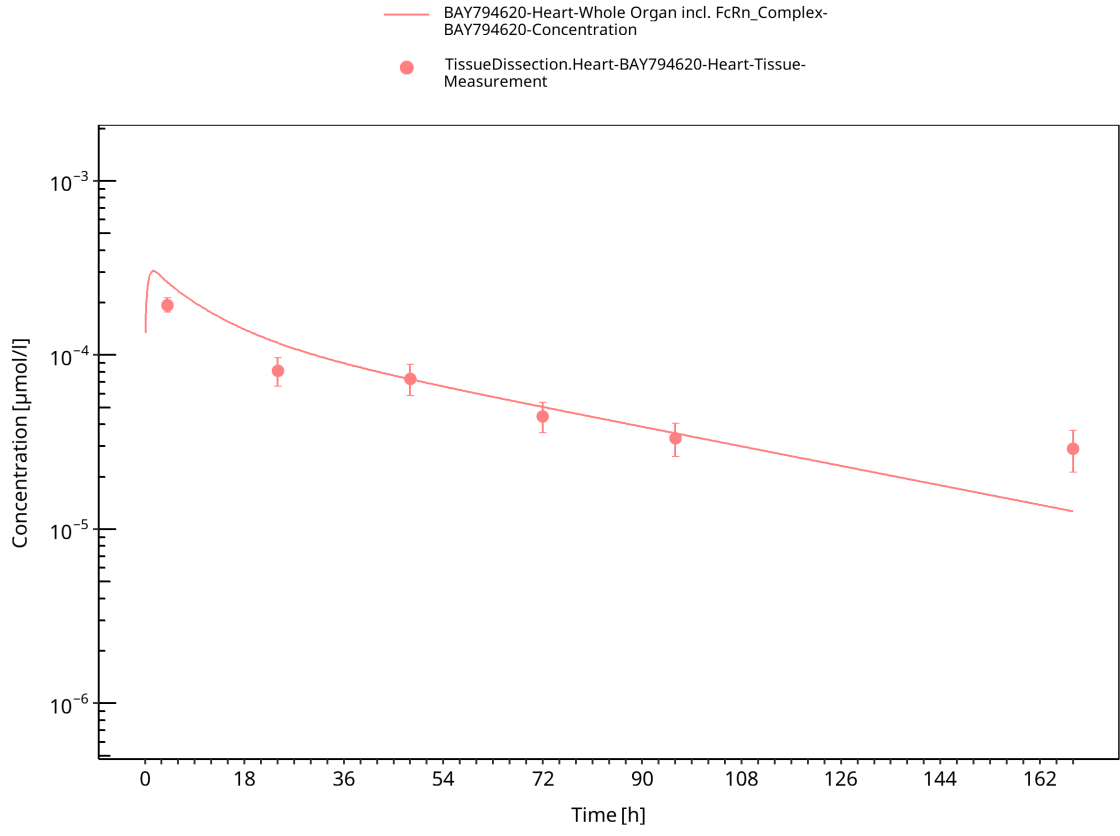


Figure 3-26: Heart

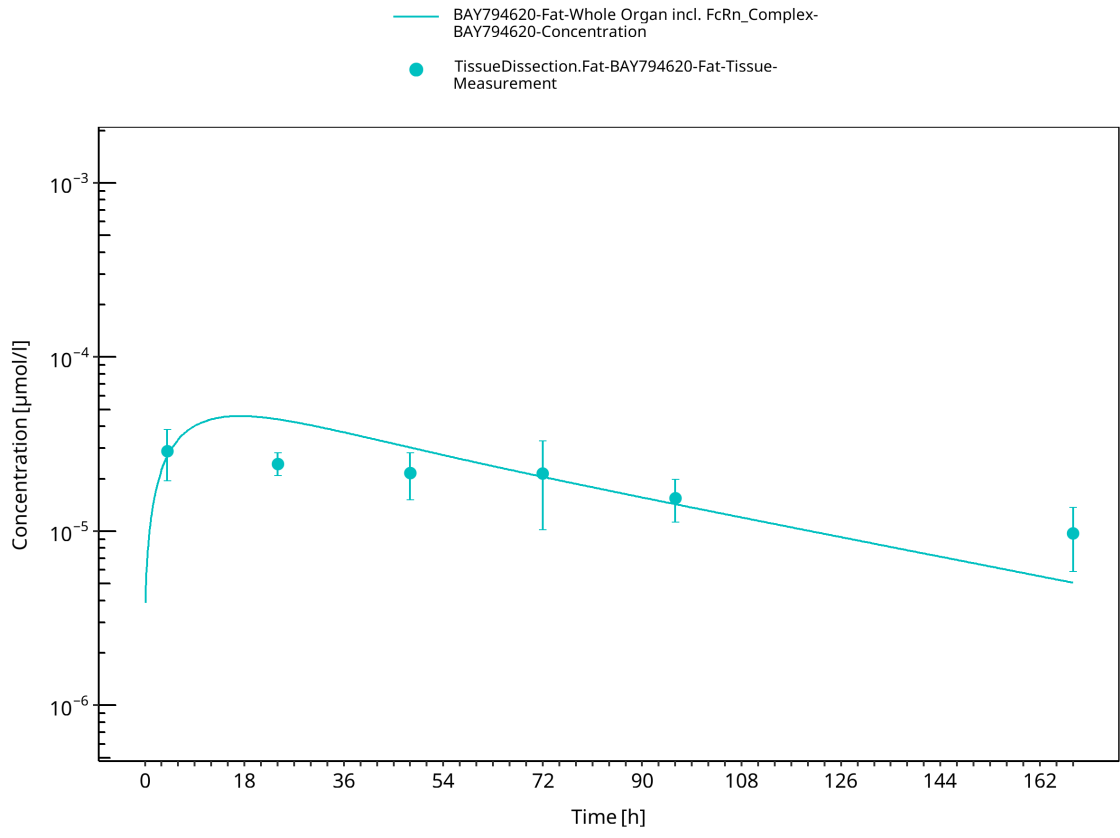


Figure 3-27: Fat

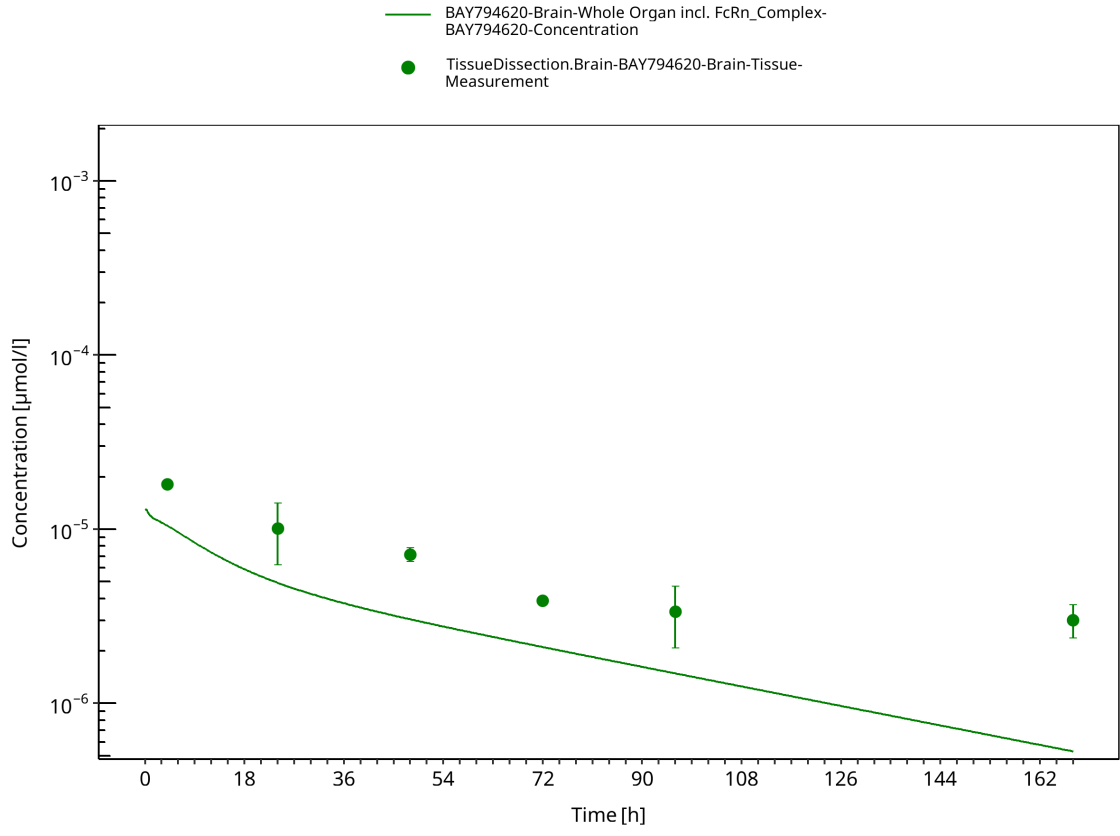


Figure 3-28: Brain

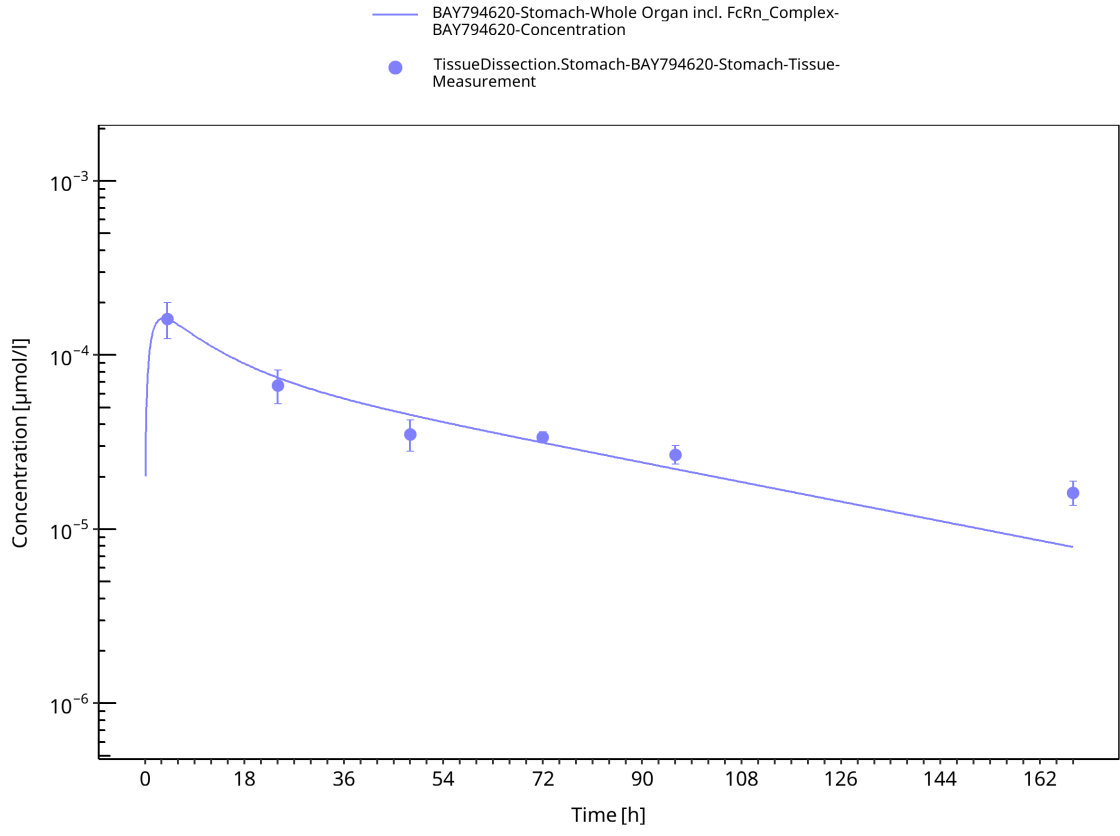


Figure 3-29: Stomach

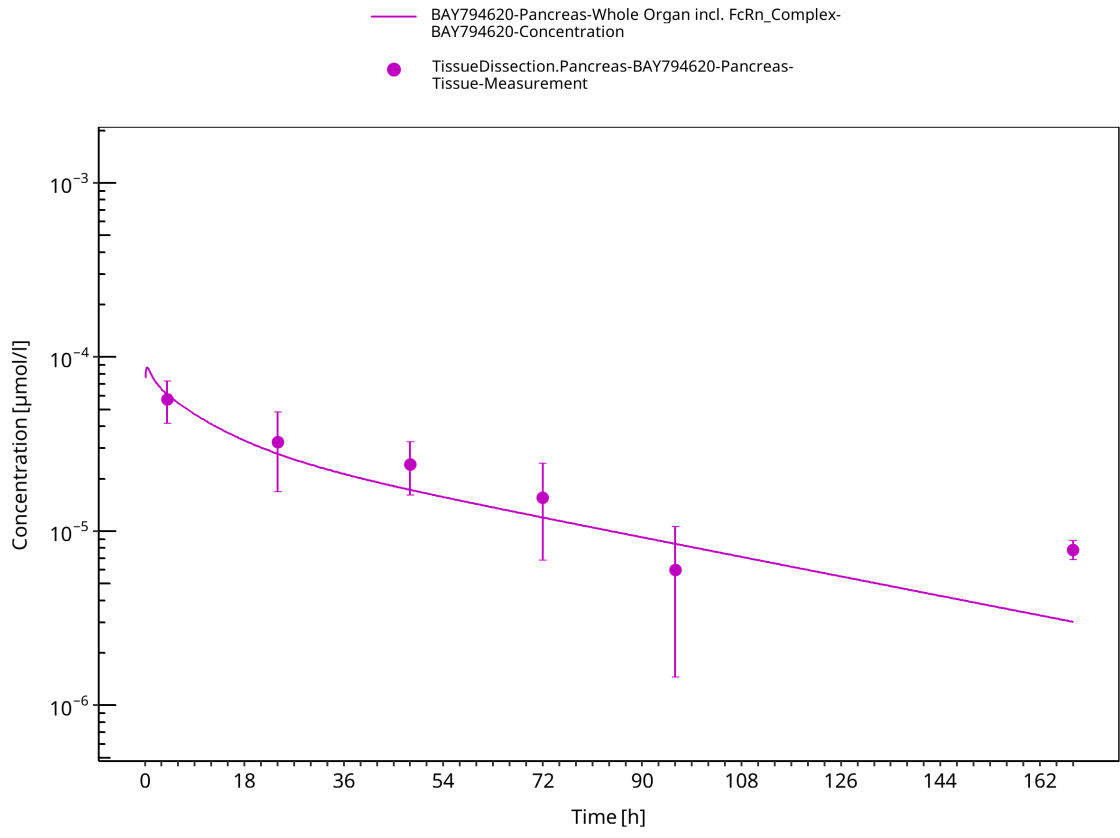


Figure 3-30: Pancreas

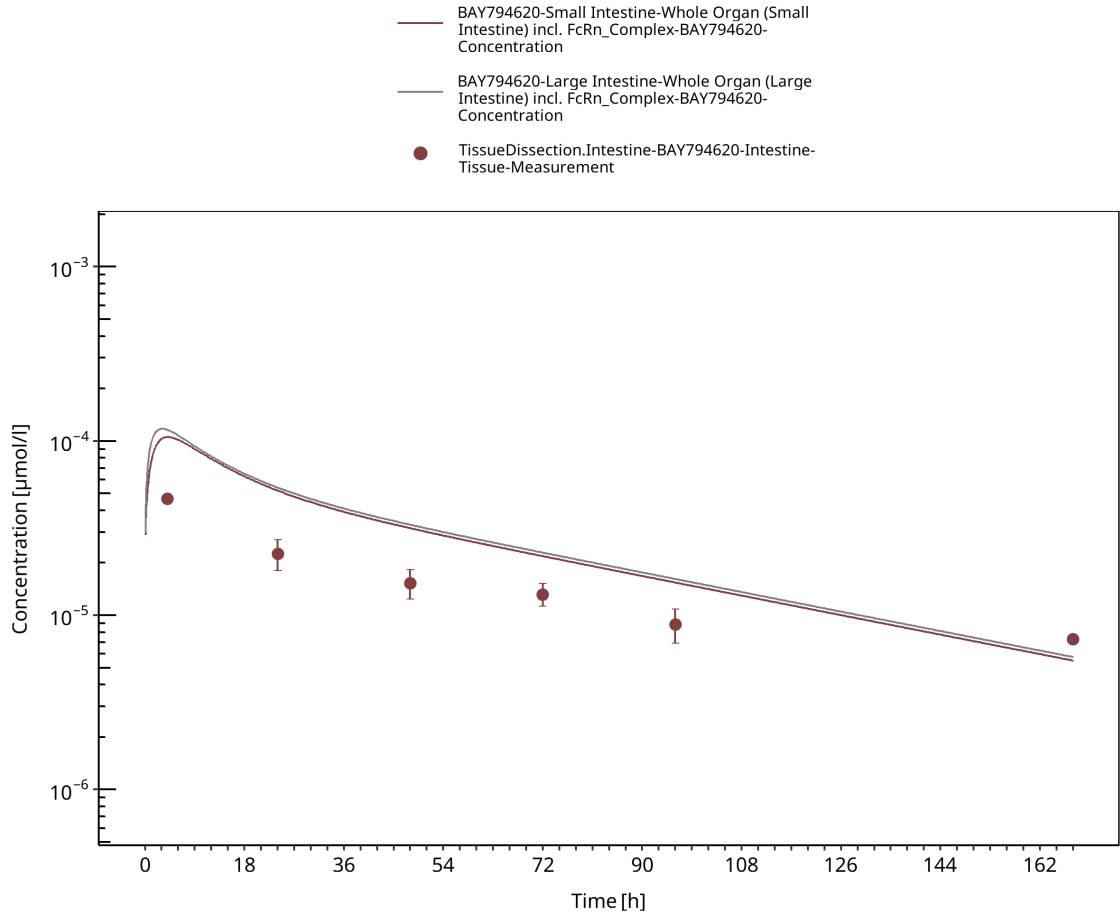


Figure 3-31: Intestine

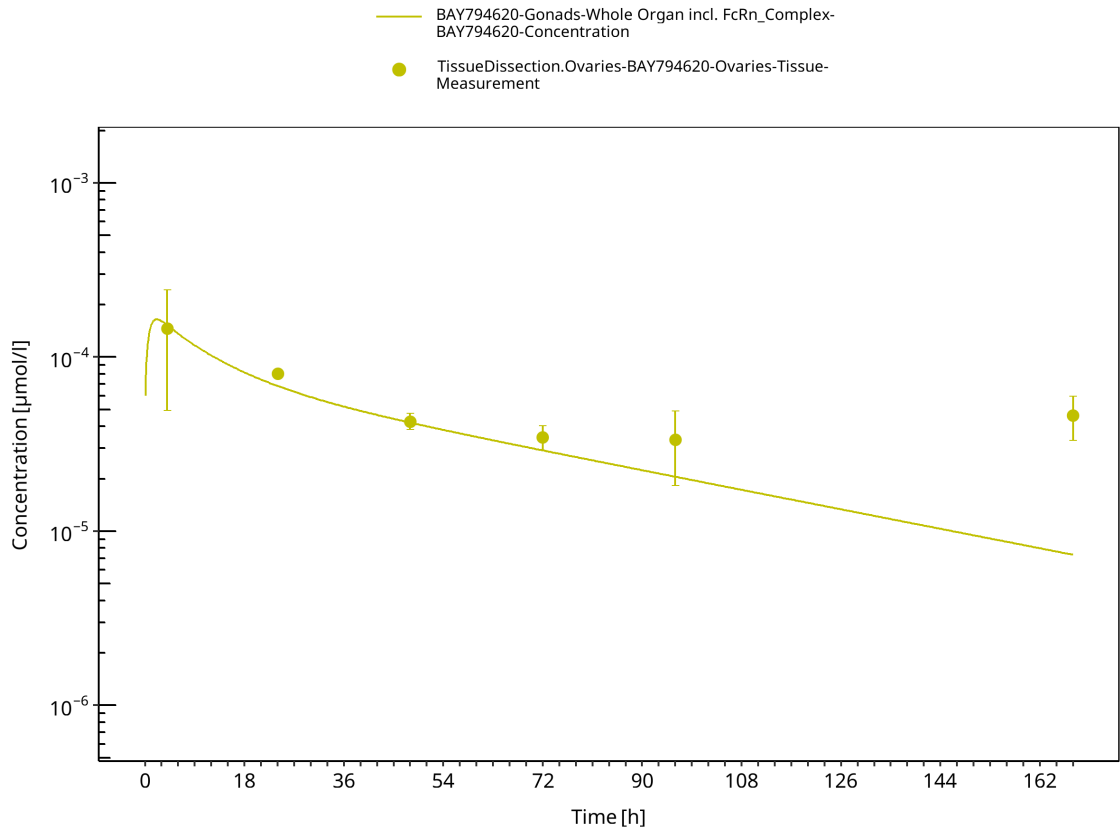


Figure 3-32: Ovaries

## 4 Conclusion

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The herein presented PBPK model overall adequately describes the pharmacokinetics of BAY 79-4620 in mice. The tissue concentrations from the low dose tissue dissection study (dose approximately 0.025 mg/kg) are similarly well described as the tissue concentrations from the autoradiography study (dose 1.25 mg/kg), with the exception of the late concentrations at 168 h after administration from the tissue dissection study which are underestimated by the model. The largest deviations between measured and simulated concentration-time profiles are observed for spleen concentrations which are overestimated by the model and brain concentrations which are underestimated.

The PK data had been used during the development of the generic large molecule PBPK model in PK-Sim ([Niederalt 2018](#)) together with PK data from 5 other compounds (7E3, CDA1, dAb2, MEDI-524 & MEDI-524-YTE).

## 5 References

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